(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

| | GCTGACATAA | TTGCATCAAA | TTTCACATCC | CCATAAAAAT | CGCTACCĂCA | TAACCTACGA | 60 |
|------------|------------|------------|------------|------------|------------|------------|-------|
| 5 . | TAATACCTAC | AAGAACTGGA | ATTAAAGATA | GGAATCCTTT | AAAAAATCCT | TGAACGACTA | 120 |
| | TTGTTACAAG | CAAGGTTATC | ATTGCAACAA | TTAAGAAACT | GATATTGTAA | CCTTTCATAT | 180 |
| | CTCCAGGATT | TTCATACATT | GCCATATTGA | CTGCAGTAGG | CGCTAAGCTT | AAACCAATTA | 240 |
| 10 | CCATGATGAC | TGGTCCAACA | ACAACTGGTG | GTAATAATTT | CATTAACCAT | GCTGTCCCAC | 300 |
| | TTAATTTGAT | TAGAATCCCG | ATGATGACGT | ACATAACACC | ACTCATGAAT | AATGCTACAA | 360 |
| 15 | GCATGTCTCC | TAAGCTATGC | GTACTTAATC | CCGTGATAAT | TGGCGTGATA | AATGCAAAGC | 420 |
| | TAGATCCCAA | GTATGCTGGT | ATTTGCGCCT | TCGTTATTAA | GATATAAAGT | AATGTACCGA | 480 |
| | TTCCCGAAGC | TAGTAACGCT | GCTGATATTG | GTAGTCCTGT | TAAGAATGGT | ACTAGTACTG | 540 |
| 20 | TTGCGCCAAA | CATCGCAAAT | AAATGTTGTA | AGCTTAAAAÄ | TGCCCATTGC | GCTGGTTGTG | 600 |
| | GTTTTTCATT | TACATCTAGT | ACGGGTTTTA | CTGTTCGTTC | AAACATTTCA | TCATTTTGCA | 660 |
| | TAATATTCAT | TTCCTCCGAT | AAAAAAAA | TCTCTTTACA | TCAGTATATG | TAAAGAGACA | 720 |
| 25 | AAAAGTGTGA | CAAGTTGCTA | CAAGTCATTT | TCGTCCATAG | AAATTGACTT | ATAGTTGTCG | 780 |
| | AACATGAGGG | TATTATTAGA | TAAACAAGCA | TATGAAAACT | TATTTATCAT | TCAACTCCCC | 840 |
| | CACCTTTTTC | AGTCTCTCGT | ACTGAATTAA | AAGGGGLATT | ATTTAATTAT | AACTGCATTT | 900 |
| 30 | CTTTGATCcA | TTECTTCYAA | ATAGACACTT | ACCGTTTCCT | CTTTAGAAGT | AGGTAWATTT | . 960 |
| | TTACCAACAA | AATCTGCTCG | AATTGGTAAC | TCACGATGTC | CTCGATCAAC | CAAAGCAGCT | 1020 |
| 35 | AAACCAATTT | TAATAGGTCT | AGCATTTAGC | AAAATAGCAT | CAAGTGAAGC | ACGAACCGTT | 1080 |
| | CGACCAGTAT | ACAGCACATC | GTCAATAATG | ATGACTACTT | TATCTGTAAT | ATCTGTGTCG | 1140 |
| | ATGTCTATTG | CGTCTTTTGT | CGTAAGTGAT | GACATGTGCT | CTATATCATC | TCTAAAGTAT | 1200 |
| 40 | GTAATATCAA | TTGTTCCAGT | AGGTATACGT | TGTTGCTCAA | TTTGATGAAT | TTEATCTTGT | 1260 |
| | ATACGATTCG | CTAAATATTC | ACCTCTTGTn | TTGATACCTA | AAAGATTAAA | TTATCAGTAC | 1320 |
| | CTT | | | | | | 1323 |

(2) INFORMATION FOR SEQ ID NO: 634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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| | ACCCATCTCA TCGTATTTTG AATTTAATAG ACGAGATCGA TGTATATCTG AATTCATCCC | 60 |
|------------|---|-----|
| | AACTATGGAT TAATGTTGGT ACATCATLAA CGCATAACCA ACATTTTGAG CAGTTGTTTT | 120 |
| 5 | ATAAGTAACG TGATTTTAT CTAATTGCCC TCTTAATGCG TCCTCTGTAA ATTCAACACT | 180 |
| | ATCAGAACCA TTAGAGGTCG CTTCATATAA GTTATTAGAT GCAATATGTG CTAAATCGCT | 240 |
| | ATTGATTTTC AATGGTTTTA ATCCTTTTAA TTTTCTCATT TCATTCGTTA CTTCATAAAG | 300 |
| 10 | AGAAATTAAT TGATTTGGAT TTTGCTCAAC TGGACGCTTA TTATGCTCTT CTGACGTAGA | 360 |
| | ATTAGAATTT AATTGATAAG GTTCAATATC TGCTAACATT TCTTTTGTTA AAAATCGTAC | 420 |
| 15 | ACTTAGCACC TITTTCGATT GTTGATCAGA ATACACTTGT GCATATATGT CGCCATATTT | 480 |
| | AATCAGTGTT TGTGTTTTTA AATCTTCATC TGAAAGTTCA AATTCATATT TTTTACCATC | 540 |
| | AACTTTAAAG GACGGTTCTG GATTAATACT TGTATGATTA AAAATTTCTG CAGAATGTTG | 600 |
| 20 | TCCTATTTT AACGGACTAA CATTGACTTT CTCACCTGTA GCATACACTG AAACGATTTC | 660 |
| | TTCACGTTTA-GTTGAAACAA_TGTAATAACT_GTTTTTGTCT_TTAAACACAT_AATTTTTGTA | 720 |
| | rCCATCTCTA AAAGGGTAGA CrCGATCTGC TTGTCCAAAT T | 761 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 635: | |
| 3 0 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 827 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

TTAAATATAT TTATATATTA TAGAATAGAA AGACCTGAAG ATTGAATATC TTTCGCAAAG 60. CCTTTAACTG TATCTACTGA TAATTCGTTA ATATCGCGAC CTAAGTTTGT ATTCACTTTT 120 TTCACAACAT CTGCTGGGCA TGTAATAATA TCTGCACCAA TTTCATCAGC TTGAATCACA 180 TTGAATAATT CGCGGCAACT TGCCCATAAT AATTTAACGC CGTCTTTACT ATGCGTAACT 240 TTNACAGCCT CTKTCATTAA TGGTAATGGA TCTACGCCTG TALCTGCAAT ACGTCCTGCA 300 AATACTGAAA CATATGTTGG CACACCTTCA GTTACTGCTT CAGTTATTTC TTTAACTTGT 360 TCAATTGTGT AAACAGCCGT AACGTTTAAT CTCACATTGT CAGCTGAAAG TTTTTTAATT 420 AAAGGAATCG TTGATTCACC TTTTGTATTT ACAATAGGAA TTTTAACAAA TACATTTTCG 480 CCATATTGTT TTAAAATTGC TGCTTCTTTK TCCATAGTTT CTAAATCGTC TGCAAATACT 540 TCAAATGARA TTGAAGCATC TGGAATTTCT TTCACAGCTT CTTCAGCAAA AGCTTTGTAA 600

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| TITTTATAAG CTGCTTTCAT TnCTTCAATA TCTGCACCGk CCGCAAATAC | TTCTACATTT | 720 |
|--|------------|-----|
| AGTTTAGCCA TATAAYATAG CCTCCTTGAT TCTTATTAAA ATTTTAACAA | CATCTGCATG | 780 |
| KCTTTTTCTT ACAACCATTT GTAAAAAATG ATTTTTATTT CTTLGTT | • | 827 |
| (2) INFORMATION FOR SEQ ID NO: 636: | | |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1478 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

TTAGTCGGTA TAACCATCGG CTAGGTGGTT TTTGTATTAA AAAAGTGGAT aCCAAAATTT 60 ATTAATAATT ATTTTAATGT TAGAAAAAAA CTAAATAAAA ACTCGCTAAT GATATCCAAT 120 AATATGTATA CAAAACGAGA CATATATTGC ATATGATTAA CGAGATACTG AAAATATTTT 180 ATCACCCCTA AAATGATTAT TCATTTTCAG CGGTAATTCG ACCTAAAGTC AAACTTACAA 240 TAAAACCGAT GATAAATACT ACTAATGAAA CGAACCACAT CACGATATTA GTTGGTAAAC 300 CTGGAAATAC TGCAAAGAGG GAGCCAACAA CAAAACCAAT GATTAATGCA AAAGTCATTA 360 GTTTATGATG TGTTAGGAAA TACTGGATAA TTTTGCTTGA AATAATGAAT CCAGCAAGCA 420 CGCCAAATCC GACTGCAAGT AATATAGGAA GACCTGCAAA GTTAAGTTTA ACAACTTCAG 480 ATATTGCTAG CATGACCGTA CCATAGACGC CAAATACTAA TAACATAAAT GACCCTGAAA 540 TACCTGGGAG TAACATAGCA CTAGATGCAC ACATACCTGC AATAAAATAT TTAATAATAA 600 GACTAGTTGA TAGAGTAAGT GTTTCTCCAG CATGTTTATC ACCATTATTC ATTAATGTAA 660 TAACAATTAA GATAGCGATA CCAGCTATAA CCATCATGTA ATGTYTAGTT GTAAATGACG 720 TTTTATAGTT AGAAATTTTC AATAAATATG GAACGATACC AATGATTAAT CCACCAAAGA 780 AAAACATAGT TGGAATATGG TGTTGGCTTA ATAAATAATT AAAAAGATTA CTTAGTGATC 840 CCATTGCCAG TAACATTCCA ATTATAATGG GGATTAAAAA TGTAAAACTT GGCCAAAAAC 900 GTCGTGAGAA TATGCCGCTA ATTGAAGCGA TAAATTGATT GTAAATACCT AACAATAATG 960 CGATAGTCCC ACCGCTAACA CCAGGTACCA AGTCACTCGT TCCCATAGCA AAACCTTTTA 1020 GAATATTAAT CCATTTAAAT TGTTGCATGA ATAACTCCTT TCAAACGATT GGAATAAAAT 1080 CATAAATAGC ATCATACCAT ATTACAAATG TCCTAGTGAA ATGATAACAT ATTTTAAATT 1140 CATAAAATCC ATTGAGAAAT TATGTGCACT TATTATCATT TATATTTTTA AAGAGAGCGG 1200

| (2) INFORM | ATION FOR SI | EQ ID NO: 63 | 37: | | | |
|------------|--------------|--------------|------------|------------|------------|------|
| TGTTAACTTG | ACAATTAACA | CTGATGAAAT | ACATGCGA | , | _ | 1478 |
| ATCAACATTA | GAAATYAAAG | ACCTACATGT | GTCTATTGAG | GATAAAGAAA | TCTTAAAAGG | 1440 |
| TAAAATTATT | ATAAACTAGT | TAAGAAAACT | TTATATTTTA | CGGAGGGAAT | ATAAAATGGC | 1380 |
| AGGTATAAGT | AAGTTATAAT | TAACTGAACG | CATTATTACA | AAGTCTTTTT | GACTACAAAT | 1320 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1995 base pairs (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

| 20 | ATTACAGCAT | CITCTCTAGG | TAGATTATTA | AAAGATAGAG | GTCTAAATGT | AACAATTCAA | . 60 |
|----|------------|------------|------------|------------|------------|------------|-------|
| | | | | | | | |
| | AAATTCGATC | CATACTTAAA | TGTTGACCCA | GGTACAATGA | GTCCTTATCA | ACATGGTGAA | 120 |
| | GTATTCGTAA | nGGATGATGG | TGCAGAAACT | GACCTAGACT | TAGGACATTA | CGAAAGATTT | 180 |
| 25 | ATTGATATTA | ATTTAAACAA | GTTTTCAAAT | GTGACAGCCG | GTAAAGTGTA | TTCACACGTA | . 240 |
| | TTGAAAAAAG | AACGTCGTGG | TGATTACTTA | GGCGGAACAG | TTCAAGTTAT | TCCGCATATT | 300 |
| | ACAAATGAAA | TTAAAGAACG | TTTATTACTT | GCAGGGGAAA | GTACGAATGC | AGACGTTGTT | 360 |
| 30 | ATCACTGAAA | TTGGCGGTAC | AACAGGTGAT | ATTGAGTCAT | TACCGTTTAT | TGAAGCGATT | 420 |
| , | CGTCAAATTC | GTAGCGATTT | AGGTAGAGAA | AATGTTATGT | ATGTTCACTG | TACATTACTG | 480 |
| 35 | CCTTATATTA | AAGCTGCTGG | AGAAATGAAA | ACGAAGCCAA | CACAACATAG | TGTTAAAGAA | 540 |
| | TTACGAGGCT | TAGGTATTCA | ACCAGACTTA | ATCGTTGTAA | GAACTGAATA | TGAAATGACA | 600 |
| | CAAGATTTAA | AAGATAAAAT | TGCATTATTC | TGTGACATTA | ATAAAGAAAG | TGTTATTGAA | 660 |
| 40 | TGTCGTGATG | CAGACTCTTT | ATACGAAATT | CCATTACAAT | TAAGCCAACA | AAATATGGAT | 720 |
| | GATATCGTTA | TTAAACGTTT | ACAATTAAAC | GCGAAATATG | AAACACAGCT | TGATGAATGG | 780 |
| | AAACAGTTGT | TAGATATCGT | TAATAATTTA | GATGGTAAAA | TTACAATTGG | TTTAGTAGGT | 840 |
| 45 | AAATÄTGTTA | GCTTACAAGA | TGCATATTTA | TCAGTTGTTG | AATCATTGAA | ACATGCTGGA | 900 |
| | TATCCTTTTG | CCAAAGATAT | TGACATTAGA | TGGATTGATT | CAAGTGAAGT | AACAGATGAA | 960 |
| | AATGCAGCCG | AATACCTTGC | AGATGTCGAC | GGTATTTTAG | TACCAGGTGG | ATTTGGTTTC | 1020 |
| 50 | CGTGCAAGTG | AAGGTAAAAT | TAGTGCAATT | AAGTATGCTA | GAGAAAACAA | TGTACCATTC | 1080 |
| | TTTGGTATTT | GTTTAGGAAT | GCAACTTGCA | ACAGTTGAAT | TTTCAAGAAA | CGTATTAGGC | 1140 |

| | TTACCAGAAC | AAAAAGATAT | CGAAGATTTA | GGTGGTACAT | TACGCTTAGG | CTTATATTCA | 1260 |
|------------|------------|------------|-------------------|------------|------------|------------|------|
| | TGTTCAATTA | AAGAAGGCAC | ATTGGCACAA | GATGTTTATG | GTAAAGCGGA | AATTGAAGAA | 1320 |
| 5 | AGACATCGTC | ATCGTTATGA | ATTTAATAAT | GACTATAGAG | AACAATTAGA | AGCAAATGGT | 1380 |
| | ATGGTGATTT | CTGGTACAAG | LCCAGATGGA | CGTTTAGTAG | AAATGGTAGA | GATTCCGACA | 1440 |
| n | AATGETTCTT | TATTGCTTGT | CAATTCCACC | CAGAATTCTT | ATCTAGACCA | AATCGTCCGC | 1500 |
| | ACCCGATTTT | TAAATCATTT | ATTGAAGCTT | CATTÀAAATA | TCAACAAAAT | TTTAAATAAA | 1560 |
| | GCTAATAAAA | CCGGTACTTT | CATTGTTAAA | CATTGAAAGT | ACCGGTTTnT | CGTATAATTT | 1620 |
| 5 . | TAATATTATG | TTAGTGACAA | ggtatgaaat | AACAATAGTG | ACTTTTATAA | TTCTAAGTCT | 1680 |
| | CTTGTCATTT | CAATCATTTG | TGTATAAATG | TCATAGTATA | CATAATTCAA | TGCCATCGCA | 1740 |
| | TGTGGTyGGA | CAATCTTATC | GTAATCTTCA | GTGTAGACTA | TAGGTCTTGG | TGTAGATAAA | 1800 |
| 0 | TCGATAAAAT | GTACGAGATG | ATCAGGGAAA | TCATCTGTTT | TAGGTTTGTT | GCTTATTAAG | 1860 |
| | ACCACATCGA | TATCTAAGTC | GATAAGTTTT | TGAATATCTA | ATGCAACTTG | АТУАТТАТАА | 1920 |
| 5 | AATGGTGCGA | ATAATAATAC | ACGATCAGTT | GAGTCAATTT | CTTTAAwkTC | TTTAATAGCG | 1980 |
| | TaAGTTTnCG | GCTAG | | | 1. | | 1999 |

(2) INFORMATION FOR SEQ ID NO: 638:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1107 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

60 ATTAGTGATG AAAGTCAGAT TGAAGCTTTA TTAACAGCTG AAAAATATTC AGAAATGATT GGTGAATAAT CACCGTGTAA CTCCTTAATC TAAGATTGAG GAGTTTATTT TTAGTCTGAG 120 AAAATAAATG ATATGAAAGA AAAATTATTA GGTACTATTA TTTGGAGTAT TGCTACATTT 180 TATTATTCAA GAATGATGGA AATAATGAAT TTAGCTATTT TAAAAATAAA AATTGGGGGA 240 AGTTAATATG CTAAACATTC AAGACGTTAN CATNCTTTCT AAAAAGGAGC AAAAAGCATA 300 TAACCGTTTC GTAGAATCTG TAGAAAACGG TAATTTACCA GTACTACCAT GTATTGAAAT 360 GGATCTAAAA GAGATGCAAG AAGAAACATT AAACCAGAGT AAGATTGGTG GAATGCCATT 420 TTTAAAATCT TTTAAAGATA TACCATTAGA TGAAAATAAT GTACCAATGG TATTGCTAGC 480 ACAGATTAAT TTGGATGATC TTCCAGAACA ACAAGAATTA TTTCCTGTAA AAGAAGGGAT 540

| AAACAATATA | AACTCAAGGC | TTGTTTATAT | AAAAGAGCCA | ATTACAGATT | TATCACTCGA | . 660 |
|------------|------------|------------|------------|------------|------------|-------|
| AAATATTCAA | GCGCATTTGA | AGTCATTAGA | TGCTGATAAT | GAGGATATCC | CGTTCAGTGG | 720 |
| AGCATTTTCT | ATAGAATTTA | GATTGTCGAA | ACAAACTATT | ACATGTACTG | ATTATAAGTA | 780 |
| CGATGAGGAC | GTGCTTGCAT | TGTGGAATAA | AGTCAATCCA | TCCTTCGCGC | TAAAATCAAT | 840 |
| GTTTGGTGGT | TATGATGAAT | TGATGGAACC | TGTGTGTAmC | AywTTTACTG | CTAAGGAACC | 900 |
| ATTTAATCAA | CTTGGTGGTT | ATCCATATTT | TGACCAAATA | GATCCAAGAA | CGAACGATCA | 960 |
| AGAACTGAAA | ATGTATGATA | GAGTCTTACT | GCAAATTGaT | TCTACAAGAG | ATGGTAATTC | 1020 |
| TTCGATTATa | TGGGGTGaTT | TAGGTATTGC | CAATATCETA | GTGaAATCTA | CTGrACCTTG | 1080 |
| aGGcTAtGaa | GTTTTGAATG | ATTACCT | | | | 1107 |
| | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

| | ATTCATATTA | TTATAAATTA | TTTCTACACC | ATCCCAATTG | AGTTGTTTTT | CATAATTTAA | | 60 |
|---|--------------------|------------|------------|------------|------------|------------|-----|-----|
| | ATGTAATTCC | ACTAACTCCC | TACCAATTTC | AACAAATCCA | TATACATCCT | TTAATATCGG | | 120 |
| | TATTCGCGGA | AAACCTTTAC | TCAAATCACT | TGAATATTTG | TTCACATAAT | ATTTATGATG | | 180 |
| | CAAAATTGCA | TATATATAAT | ATACTATCTC | TTCTGAATTA | AGATTTATTT | TCTTTTTAAA | | 240 |
| | AGAATTAGgA | AATATTATCT | ACATGCCTCA | AACTATCTTT | ACCTTTGtAT | GTAGCAAAGC | • | 300 |
| | CTTkGCCATT | ACCAATAAAt | TGGAAATTAG | GTAATATGTC | CGTGATCATA | GCCGAGAATT | | 360 |
| | CTTTATTCAT | TCCCTGTCCT | TGTATATAAA | TCACCTGTCC | AGTATTCTCC | ATTATATTAT | | 420 |
| | AATATCTACT | TGGCATTTCC | TTTTATATTA | TGTCGTACAC | TATCCATTTT | TTTGTAAATG | | 480 |
| • | GTCTATGCAT | AAATTTAACA | ATTCTCTCTG | GATTAATTGA | TTTTTTATAA | CCTTTAGAAA | | 540 |
| • | ATTTTTGGGT | AAGTCCTCGT | GTCCAACTAA | Taaatgtttc | ATCTTTGTTC | ACTAAATTTA | . 0 | 600 |
| • | TACGTTCTCT | TGAATCTAAG | ATATCAATTA | ATCTATCTAT | TTCAGAATTA | TAGTTATCTA | | 660 |
| (| CAAGTAATTT | TGCATTTACT | AATGCTTTTT | CATTCGAAAA | ATTTGTTACC | CAATTATCTC | | 720 |
| • | ITGCTG aATT | TACTCCATTA | AATKGAKCTA | AATATATAGA | ATTTTCAATA | TCCTTGGAAT | | 780 |
| • | CATACATTGG | TAAATAATTC | CCCATAGTTT | ATGTCTCGGT | GATTAATCCA | ATCATTGGGG | | 840 |

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| | AAAG | * *** | 904 |
|-----------|---|------------|-----|
| | (2) INFORMATION FOR SEQ ID NO: 640: | | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 436 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | |
| 10 | (D) TOPOLOGY: linear | 1 | |
| | | - | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640: | | ٠. |
| 15 | CGATGTCTTT ACTATTAGAC TTAGCCATTG GTTTCACCTC TCCAAAAATT | GTAAATGTGT | 60 |
| | ATCATCAATA TGAAAGTTAC ATAAAACTGA CATATTTCTT TAAAATATCA | ACGCCATTGA | 120 |
| | TAACTTCCTG TTTTAATTGA TACGCTGTAA CAAAATACTA TAGTTAGTGC | TTACATGTAT | 180 |
| 20 | ATGTTAAAGC AAGCAGTGGT AAATGTAAAT TATAATTATT CATTAACTTT | GCAATATATT | 240 |
| | AAATCTTTTA TTCATAGAAG ATAAATATCA AATCAATCAT AATTATTTGA | CAACAAATAG | 300 |
| | CTAACGATTG TTTTAATCTA CATTTGGCTT ATAGCATTTT AAACCTATAC | TCTATTTTGA | 360 |
| 25 | TACAATATAA GTGTAAAATC AATCATAAAA AGGATATTCA ATATCTGCAT | CCAAGAAAA | 420 |
| | CATTACAATT ACCTTT | | 436 |
| - · 30 | (2) INFORMATION FOR SEQ ID NO: 641: | | • 3 |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 442 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641: | | ٠. |
| 40 | GTTATTAAAT TCAGAGTGGT AGCAAATTAA AGTTAnTCAA GAGTTAAGAT | GAATTTAATT | 60 |
| | CATGAACACG TCTATTATTT TTATAATTGT AGCAAATAAA GCTTTACATC | | 120 |
| | TTAAATATGT TCAAAAAATA TGACTCAAAA AATTCAATCG TATTAAAATC | | 180 |
| 45 | CTAGGTATCA TCTATGGGGG AACATTTGGA ATATATCCAA AAGCAGACGC | | 240 |
| * | AATTCCTCAA GTGTACAAGA TAAACAATTA CAAAAAGTTG AAGAAGTACC | | 300 |
| | | | |
| 50 | GAAAAAGCTT TGGTTAAAAA ACTTTACGAT AGATACAGCA AGGATACAAT | | 360 |
| | TCTAATAAAT CTAGGAATTG GGTTTATTCA GAGAGACCTT TAAATGAAAA | CCAAGTTCGT | 420 |
| | ATACATTTAG AAGGAACATA CA | | 442 |
| 55 | | | |

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

| . 10 | | | | | | | |
|------|------------|------------|------------|------------|------------|------------|------|
| | CCAATTTTGG | TATGAATTAT | ACAGATAATT | Cuccecce | AGGATCATTT | GCTTATTTAA | 60 |
| | ATCAATTCGG | TGTGGATAAA | TGGATGAATG | AAGGGTATAT | GGCATAAGGA | GAACATTTTA | 120 |
| 15 | ACTACTGCCA | ATAACGGAAG | ATATATTTAT | CAAGCTGGAA | CTTCATTAGC | CACACCTAAA | 180 |
| | GTTTCGGGAG | CACTAGCTTT | AATCATTGAT | AAATATCATC | TTGAAAAACA | TCCAGATAAA | 240 |
| | | | | • • | ATAAACCATT | | 300 |
| 20 | | | | | | AGCAAGTTAA | 360 |
| | • | * . | | | GAAAACATTT | | |
| - | | | | | GAAAATAACG | | 420 |
| 25 | | | | | | GTGGCATACT | 480 |
| | | | | | | • | 540 |
| | | | | | ATGACACGAA | T. | 600 |
| 30 | | | | | CATTTAAGTG | | 660 |
| | | | • | | GAAATTAATA | | 720 |
| | | | | | GACTTTTCTT | | 780 |
| 35 | ACAAAGACTT | GGAATTGCAA | TGGCaTTAAT | TAAAAaGCCA | GAAATTTTAG | TATTAGACGA | 840 |
| | ACCATCTAAT | GGTTTAGACC | CATATGGAAT | CCAAGAACTT | AGAGAACTTC | TAAAATTATT | 900. |
| | AACAGAACAA | GGTACTAGTA | TTATTATTTC | AAGTCACATT | TTATCTGAAA | TCCAAGTTTT | 960 |
| 40 | AGCAGATCAT | ATCGGTATTA | TTCATGAGGG | TGAGCTAAAA | TATCAGCAAA | GAAATAACAA | 1020 |
| | AGATGAAAAC | TTAGAAGAGA | TATTCTTCAA | AATAACGAAA | GGTGATTACA | AATGATACAT | 1080 |
| | TTAAAGATaG | AAGGTATCAA | ATTTAAAAAt | TCTTTCAGTA | TGTATGTTTT | ATTAATAAGT | 1140 |
| 45 | | | | | TCGCCAAAAG | | 1200 |
| | | • | • | • | ATATTTGGCC | | 1260 |
| | | | | | AAATTGAAAT | | |
| 50 | | | - | | AAGAAATAAG | | 1320 |
| | | • | , | | | | 1380 |
| | TTONITIMI | CAMINGCATT | TTTGGTACAT | TGCTTTTTAG | TATTTATTAT | TGCTTATATA | 1440 |

| | TTGATGTATG | TAGTATCTCT | ACCATTGATA | CCGCTCAACT | TTTTATTAAC | TCGATACTTT | 1560 |
|----------|------------|------------|------------|------------|------------|------------|------|
| | GGTGTGTTCG | TATCAATATT | AATAAACTTA | GTATTATCAG | TCATTTGTGT | CTTGTTTTTA | 1620 |
| <i>5</i> | ACATTGAAGA | GTTTATTTTG | GGTGTTGCCG | TGGGGGATAA | TGCAGAGAAT | CCCGCTTATT | 1680 |
| | ACGCTTGGTA | TACTACCTAA | TGGtTTAGTT | GTAAACCATA | ATTCAAAATA | CTTTAATGAT | 1740 |
| 10 | CTCAATGCCT | TATATATTTC | GATTATTGTT | AGCATCATTA | TTTTCGCGAT | AGTAACATTT | 1800 |
| | TTAAATAATA | AGAAAAGTTG | GCGATTAAAA | TGATAATTAA | CGAATTAAAG | TCATGTAAGT | 1860 |
| | TGAAATTTTC | TAAGCAAGCG | CTCACATTTG | TACCCATTAT | TGTAACCATA | TTGTTTATAT | 1920 |
| 15 | TATTTATAAA | TTGGTATTTA | AACGTAAATT | TATGGAATGG | TCGACAAATm | AGTTTGTTTA | 1980 |
| | CAGCGAGTTT | TAATGCAATT | ACATCGCTAT | TAATTTCTAT | AAACGTCTAT | CAAGTTATCA | 2040 |
| | ATTTTGAAGA | AAATATTGGT | CACTTTAATC | ATATTTTAGG | AAAAGCTAAT | AGGCTAAATT | 2100 |
| 20 | GGTTAAATGC | ATCAATGATT | TTTACTTATA | CTATTACAGC | CATATGTATT | CTATTAGCAT | 2160 |
| | CAATTAATTT | ATTGTGGCAT | TCACATGATA | TGAAAATAAC | ACTTATGTTT | ATAGGCGTaT | 2220 |
| 25 | CATTGTTTTT | CAATGTAATT | ATATTACTGC | TACTTTTTAT | TTTTAGTATT | TTCATTAAAG | 2280 |
| | ATGTAATGGC | TATTGTTGTC | GGAGTTTTAA | TGTTTATTTT | TAACGTTTAT | TTTGGATTAG | 2340 |
| | AAGTGCTTGG | AGATCATTCG | TGGTTCTATT | TACCAATCAC | ATATGCTACA | CGTTACGTTT | 2400 |
| 30 | ATATGTTTAn | CGAAGGGGAG | TATACCAGTT | ACATTAACAT | TGGGCAATCT | ATATNATTAT | 2460 |
| | CACGNTGCCG | AT | | | | | 2472 |

(2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 646 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

| MINIMINGO | AATTATTICG | ATIMCAGATT | IIACGAAICG | IGCIACGAIG | CAMANIGAMII | 01 |
|------------|------------|-------------------|------------|------------|-------------|-------|
| ATAAAGATCC | ATATGGCGAA | AAGTTAGCTT | ATGGAATTGC | TTTTAATGGC | AGTGTGGATA | 120 |
| TGCAAGGGGA | TAAACAAGTC | ACAATTCCAA | AATATAGTGT | AGTTACAATT | ACTGGCGAAA | 180 |
| ATAGTAAAAA | TTATCGTGTT | ACCGCCGATA | ATAAGACTTA | CTATGTTAGT | AAAGATAAAT | 240 |
| TAGAATATTT | TAACCCGGCA | GGTTTATATC | AAACGCATAG | TTTTAAAAAA | TTAGCACCAT | 300 |
| שמבמשמשת | AAATTĀTACT | באת מידים מידים מ | СУБУСТАТОВ | TACTOAATTA | CATABABACC | . 26/ |

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| | CACAACAACC GATACAATTA CTTTTCAATG ATAATAATCA GTTATACGGT TTTGTTTATC | 480 |
|----|---|------------|
| _ | CAATTGTAGA TAAAAAAGAA TTAAAAGATA AGTTTAATAT TAACAATAAC ATTTGGATTA | 540 |
| 5 | CTAAAGTTGG GAATGGATAT TGTATTGCCA ATTTGAAAGA AGACAAATGG ATTTATATTG | 600 |
| | AATTGTAGGT GTAAAGATGC TAGATAATAT TATTTTATAT TTTAAA | 646 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 644: | |
| | (i) SEQUENCE CHARACTERISTICS: | • |
| | (A) LENGTH: 426 base pairs (B) TYPE: nucleic acid | n 200 3 5 |
| | (C) STRANDEDNESS: double | |
| 15 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644: | |
| 20 | TAATATCGGA ATTTGATAAT GAAGATATCT AATTTTTTAA TATTCGTAGC TTTTATTTTT | - · · · 60 |
| | CTACTTATTT TATGTTTATT TTTAATCTTA CAAATGACAA ACCATTAAAA GTAGCATCCC | |
| | · | 120 |
| 25 | AACATCAAAC AAAAAACAA TTCATCAAAT AAAAATCGCT ACAAAACCAA GTCATTAAAC | 180 |
| | ACGCAATAAT TAAAATTTTC CACTCATTAT AATTCTGAAT TCCAAATGTC GAATTCCGAA | 240 |
| | AACCAAACTC CAAATTCCAA AAACGCAACT CCAAAATTAA AAGCATTTCC CTACCATTCG | 300 |
| 30 | GGAAATGCTT TTTACATACT GGATTACTCT GTCATTAATG ATTTTACAAC GGGAAACCAT | 360 |
| | GTCGtCATGT ATGACCAAAG TAGCGTCGCT AtCATAAGGt GGTTCGGATC TTTATTGGAT | 420 |
| | AATnAT | 426 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 645: | 120 |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 3241 base pairs (B) TYPE: nucleic acid | |
| 40 | (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645: | • |
| 45 | nTTATTTACC CACAACATGT TGCGACATTA GGTAAATGGG TACCTTATTT ACTTGGTATT | |
| | | 60 |
| - | GTTATGTTAG GTATGGGATT AACAATTACA CCTAATGATT TCAAAATGGT CTTTAAAGCA | 120 |
| 50 | CCTAGAGCAG TAATTATTGG TGTCTGTCTA CAATTCAGTA TTATGCCCAC ATTAGCATTT | 180 |
| | ATAATTGCAA AGTCTTTTCA TTTACCACCT GATATTGCTG TTGGCGTAAT ATTAGTTGGA | 240 |
| | TGTTGTCCGG GTGGGACATC AAGTAATGTA ATGAGTTATT TAGCCAAAGC TAACGTAGCA | 300 |

| | ATATATCTAT | TTGCAAATGA | ATGGTTGGAA | GTATCTTTCG | TGAGTATGTT | GTGGTCAGTT | 420 |
|------|------------|------------|------------|------------|------------|------------|------|
| | GTTCAAGTTG | TATTAATTCC | AATTGCTTTA | GGTATTGTTT | TGCAAATTAT | TAATCGTAAA | 480 |
| 5 | ATTGCTGAAA | AAGCTTCTAC | AGCTTTGCCA | ATTATATCAG | TTGTTGCTAT | TTCATTAATT | 540 |
| | TTAGCAATAG | TTGTAGGTGG | CAGTAAGCAC | CAAATCTTAA | CTACAGGATT | ATTAATATTT | 600 |
| | TTAGTAGTTA | TTTŢACATAA | CGTATTAGGG | TATACGATTG | GATATTGGTT | AGCTCGTCTT | 660 |
| 10 | TTAAAATTAG | ATCGACAAGA | TCAAAAAGCA | GTCAGTATTG | AAGTTGGAAT | GCAGAACTCT | 720 |
| | GGTTTAGCTG | TGTCATTAGC | aGCATTGCAT | TTTAATCCAA | TTGCAGCAGT | ACCAGGCGCA | 780 |
| 15 | GTGTTTAGTT | TCATTCATAA | TATAACAGGG | CCTATTTTAG | CAAAGTATTG | GTCAAAAAAG | 840 |
| | TTATAATTGC | ACTAATAGAA | TGAAGTGGTC | ATCGGACTAT | GTTAAGCTTT | GATAAAGAGA | 900 |
| | AAAAATAGAG | GAGTAAATAT | ATGTATAGAG | CAGTTATATT | TGATTTCGAT | GGAACAATAA | 960 |
| 20 | TAGATACGGA | ACAACATTTA | TTTAATGTTA | TTAATAAACA | TTTAGAGATG | CATAATGCCG | 1020 |
| | ATCCTATAAG | CATTGATTTT | TATCGTTCTT | CTATTGGAGG | AGCAGCTACA | GATTTGCATG | 1080 |
| | ACCATTTAAT | TAAAGCGATT | GGTTCGGAAA | ATAAAGATAA | ACTTTATGAA | GAACATCATC | 1140 |
| 25 | TTACTAGTAC | AACATTACCG | ATGATTGATA | CGATTANATC | ATTGATGGCA | TTTTTAAAGC | 1200 |
| ٠. ي | AACGTCACAT | TCCTATGGCA | ATTGCCACAA | GTAGTGTGAA | AGCGGAAATA | ATGCCCACCT | 1260 |
| 30 | TTAAAGCATT | AGGTCTAGAC | GATTATATAG | AGGTAGTTGT | TGGTAGAGAm | GATGTTGAAC | 1320 |
| 30 | AAGTTAAACC | TGACCCTGAA | TTATATTTAT | CTGCAGTACA | ACAATTAAAT | TATATGCCGA | 1380 |
| | CACAATGTTT | GGCTATTGAA | GATTCTGTAA | ATGGTGCAAC | AGCCGCGATT | GCAGCTGGAT | 1440 |
| 35 | TAGATGTTAT | TGTTAATACG | AATAAAATGA | CAAGCGCACA | GGACTTTTCT | AATGTAGATT | 1500 |
| | ATGTAGCAAA | AGATATTGAT | TACGATCAAA | TTGTAGCGCG | TTTCTTTACG | AAATAGGAGG | 1560 |
| • | CGTATCATGA | TGGGTTACAT | TATATTGTTT | TTTCTAGCTG | GTCCAGTAAT | TTTAGGCGTT | 1620 |
| 40 | GGAAATTTGG | TGATTGGTCC | TATATTTAAC | AAACAGACAC | CATTTCGCGT | GCAAGTAAGA | 1680 |
| | TCTTTTGTTG | kTGGkTCmAT | Grtttactta | ATACTCGCAA | CAATTGGCTA | TTTTTTACTA | 1740 |
| | TTACAAGGTA | AACTTTAACG | AGAAAACCAC | CTTACCTCAT | TAAATGGACG | ACCATATGTA | 1800 |
| 45 | TGTGAAATGG | TAGAACGTTC | ATGTTTATGT | ATGAGATAGG | GTGGTTTAAA | TAGTTACATA | 1860 |
| | TATTTTAATA | ATAACGTCAC | GATGATAAGT | ACAATTAAGA | TAATATCTAT | GCCTACCATA | 1920 |
| 50 | ATTGTAGCTC | TTGTTGCATT | ACTTCCTTGT | TCTTTTGCTG | ATTTCATAGC | ACGGTAGTTT | 1980 |
| 7. | GGCACAAAGC | TAATAATTAG | TAAGATTAAT | ACAATTACAC | CAATTAATGC | TGTTGTCATG | 2040 |
| | ATGAACGACC | TCCTTTATTT | TTTTCAATCA | ATTCCCAAAT | AAACGTAGCA | ATCACACCGA | 2100 |

| | CAATAATTAA | TGCAATCGGT | AAAGTCGTAC | CGAGTTTAAT | CTTGCGCTCT | GGAGAATTAA | 2220 |
|----|------------|--------------|-------------|------------|-------------|-------------|------|
| ٠. | TAATAGTAAA | TACTGTAAGA | CAAATGAGTA | TGAAAGCAAG | TGTTGCAATA | ATAGTTCTTC | 2280 |
| 5 | CAACTAAATA | TAGGATGTCA | GGTTTTTCCA | TACCGATATA | ATTTATGATG | AAAAATGCTA | 2340 |
| | CAGCAAAGAG | TACCGATATT | TTTGTAGCAC | GTAGCAGTAT | TTGTTTTAAC | ATTGATATAC | 2400 |
| | TCCTTTTTAA | TATTATTAAA | ATTATATCAT | AATTACCAAG | AATAGCTGAA | GTTGTATGTG | 2460 |
| 10 | ACTCAACGGT | ACTTGAGCAA | CTTTTTTAAT | TTTTTAGAAA | AATCACAAAA | TAATTGTTTG | 2520 |
| | CAAAGTTGCA | AAAGCCTGCT | ATAGTAGTTC | TGTAAACGAT | TGCATGGTAT | GCAAATATTA | 2580 |
| | ATGTACCAAA | ATCGATAATT | TATAGTATAA | TTACGGCAAT | AAGTTTTTTT | ATGGATTTAT | 2640 |
| 15 | TTAGTATCAA | TCAGAGATGG | GGTAAGAAGT | TATGGAGAAC | AATGAACTAC | AAAGGGGATT | 2700 |
| | GAGTGCCCGT | CAAATTCAAA | TGATTGCACT | TGGTGGTACG | ATTGGCGTGG | GGCTTTTCAT | 2760 |
| 20 | GGGTGCGACA | AGTACAATTA | AATGGACAGG | CCCATCAGTT | ATCCTTGCAT | ATTTAATTGC | 2820 |
| | GGGTATCTTT | TTATTTTTAA | TCATGAGAGC | AATGGGGGAA | ATGATTTATT- | TAAACCCTAC- | 2880 |
| | AACAGGATCA | TTTGCAACAT | TTGCAAGTGA | TTATATACAT | CCTGCAGCAG | GTTATATGAC | 2940 |
| 25 | AGCATGGAGT | AATATATTCC | AATGGATTGT | AGTTGGTATG | AGTGAGGTCA | TCGCAGTAGG | 3000 |
| | AGAATATATG | AAGTTTTGGT | TCCCGGAATT | GCCAACTTGG | ATTCCTGGTG | TTATTGCTAT | 3060 |
| | TTTATTATTA | ATGGCAGCGA | ATTTATTCTC | GGTAAAAGCG | TTTGGAGAAT | TTGAATTTTG | 3120 |
| 30 | GTTTGCTTTA | ATTAAAGTTG | TAACAATTAT | TTTAATGATT | ATTGCTGGTT | TTGGTCTTAT | 3180 |
| | nnTCTnTGGT | TTTGGAAATG | GTGGCCATGC | GGTAGGTATT | TCTAATCTAT | GGACAAATGG | 3240 |
| | С | | * • | | | • | 3241 |
| 35 | (2) INFORM | ATION FOR SE | Q ID NO: 64 | 16: | | | |
| | (i) SE | EQUENCE CHAR | ACTERISTICS | 3: | • | | |

- (A) LENGTH: 1311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

| AGGCGTCAAC | TCAGATGGTT | TAATAATTGC | CGTATTACCT | GCTGCAATAG | CACCGATTAA | 60 |
|------------|------------|------------|------------|------------|------------|-----|
| AGGTtCGAaC | ACTAGTEGAA | AAGGATAGTT | AAATGGTGCA | ATGATCAAAA | CTGTTCCATA | 120 |
| AGGTTCTTTT | TTGATATAGC | TTTTTGTTGG | TATAAATAA | AAAGGTGTGT | CTACATTATT | 180 |
| TGTTTTAGTC | CAGTTTTTAA | GTTCcTTACG | GGCAATTTTG | ATACTTYTCA | AAGTTATGCC | 240 |

| | AATATCGCTC | TCGTATGATT | TAATAGCTTT | GCTTAACTTC | TTTAATTGCT | CTTTTCTAAA | 360 |
|----|------------|------------|------------|------------|------------|------------|------|
| | ACTAATATCT | TTAGTTTGTT | GTGTATŤGAA | AAAAGCTTTA | CTGTCATAAA | ATTTTTGCTC | 420 |
| 5 | AATGATATTC | ATAATGAAAA | GAACCTCCTT | ATATGATTAT | TTTGGAAAAA | GCGATTAATT | 480 |
| | GATTTGAATG | TTGTGGCCGT | TAATTTTAAA | TGGTCTTTCG | AATTATATAT | GTTGAAAGTT | 540 |
| | GAAAATAGAG | CGATGAATCG | TGTACATAAT | AATATTTATA | ACTITAATCA | TAACGAAAAA | 600 |
| 10 | GGTAGGAAGA | AAACAAAAAT | TTATACTCAA | CATCGCAAAT | ATTTTAAGAA | AATGTAAAGA | 660 |
| | CAAAAGGGGA | ATTGTATAGA | AATCACTAAT | CTGTGGGTTA | GGGTAGCTAA | AGGAATAAAA | 720 |
| 15 | ACTACTATTG | AAAAAGGGTT | GTAAATTAGT | CAAACGTAAA | TAAAAAACAG | TTCATTGAAA | 780 |
| | GTGAAATAAA | TTCTACTTTA | ATGAACTGTT | AGTTAAATAC | AACATGTCTA | TAATTAGACA | 840 |
| | GTAATATAGT | ATTATTTTGT | TAATGCTTCA | GTGATTTGAG | GTACGATTTG | TTTTTTTCGA | 900 |
| 20 | GAAACGACAC | CAGATAAGAA | GGCCATGTCA | TCTTCTAATT | GAACATTGAA | TGtTCGCCAA | 960 |
| | CTTTATCTTT | TTCAGCACCT | ACAACTAAAA | TTTTAGAATC | ACTATTAATG | ATGTCAGTAA | 1020 |
| | CAACAAGTAC | AAATAAGTCA | TATTTTTTTT | GTGCACTTAC | AGCTAACATT | TCTTTTTCTA | 1080 |
| 25 | ratettett | ACGATTTAAC | ACTTCGTCAA | GGTCAACAGC | ATTAACTTGT | GCAATACGAG | 1140 |
| | TCACATAGTC | ACCCATAGTA | AATGATTTAG | CATCCATGTT | TAATAAGAAT | TCAACTGATT | 1200 |
| | TATCAGTTGT | TGAAGCACCT | GCTTTLAACA | TATCTAAGCC | GTACTTTTGA | ATATCAACTT | 1260 |
| 30 | TAGCAATATC | TTTNAATTCT | tCAGCTGCTT | TAACATCTTG | TTGTGTACAT | G | 1311 |
| | | | | | | | |

17.

(2) INFORMATION FOR SEQ ID NO: 647:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1498 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

| CATATACTTT | TICATITCIT | TACGAGATAC | TTTACCAGAG | GATTTAGACT | TCATACGCTG | 60 |
|------------|------------|------------|------------|------------|------------|-----|
| ATCCATATGT | GCTTGCGTTT | CAGaATGTCC | ACAAACACAA | CGATATACCG | CTTCTTTCCC | 120 |
| TTTACCAAAC | AACGTTAATT | TCTTTTTACA | GTTTGGACAT | CTTGCATTTG | TTTTGCGCTG | 180 |
| TACATTCTTT | TTCGTCTTAC | AAGATGGATC | TTGGCACACA | AGCATCTGAC | CATTTTTAGT | 240 |
| TTTAACTTTA | ATCATGAATT | TACCACACGT | TGGGCATTCT | GTGGTTGTTA | AATTATCGTG | 300 |
| TTTATATTTA | CGATCACTAT | TTTTAATCCC | ATTTACAACA | TCTTTCGTAA | AATCTTTCAT | 360 |

| | CCATTGTGCA | GTTAAAAGTG | GCGACGTTAA | TTCTTCTGGT | GCTAATTCTA | ATATTTGTTT | 480 |
|------|-------------|-------------|-------------|------------|------------|------------|------|
| | ACCTTTTGAC | GTTACTTTAA | TTTTACCGTC | TCTTGATTCA | ATGGCATTCA | TATTAAATAA | 540 |
| 5 | TTTATCGATA | ATGTCGGCCC | TTGTTGCAAC | TGTGCCGATA | CCACCTGTTT | GTTTTAAAGT | 600 |
| | TTGCGCATAT | TTTTTATCCT | TCAATTGAAT | AAAGTTCTGA | GGGTTCTCCA | TCGCTTTTAA | 660 |
| 10 " | TAACGAACCT | TCATTAAAAT | ATTCTGGAGG | TGTTGTTTCA | TGTTCTCTAA | TATTTGTTTT | 720 |
| 10 | TGAAATCTTC | ACTTCATCGC | CTTCTGAAAA | AGGCTGTTGC | ATCTCTGTAA | TAGATTCACC | 780 |
| | TTGTCTAATA | GATTTAAAAC | CTAAAACAGT | TGTTACATTC | TCTTTCAAAA | CAAATGTGTG | 840 |
| 15 | CCCTGCAACC | TCTAAAGTTA | CAGTTATCGC | GTCATACTCG | TGCGGAGGCA | TTAAAGCTTC | 900 |
| | TAAAAAACGC | TCGACAATCA | TATCGTATAA | CTTTAATTCT | СТАТТАСТТА | AGTCTGACAT | 960 |
| • | GACAGGTCTC | ACTTCTGTAG | GAATAATTGC | ATGGTGATCA | GATACTTTTT | GATTATTAAA | 1020 |
| 20 | TATCGACATT | TTTGATGAAA | ATGTTTTAGA | CATTAATGGG | CGTGCTTGGT | CTTTATATGT | 1080 |
| | TGTTGCCATC | GTCACCTGAA | TACGTTCTTT | CATAGTATCT | ACCATATCAG | TTGTTAAATA | 1140 |
| | GTTTGAATCT | GTTCTTGGAT | AGGTTACGAC | TTTATGTCTC | TCATATAAGC | TTTGAAGTGT | 1200 |
| 25 | ATTCAATGTT | TCTTTAGGTC | CAATTTTATA | ACGTCTATAC | ATATCTTGTT | GTAAATCTGT | 1260 |
| | TAAATTGTAC | AGTGATTGCG | GATACGACTT | CTTATGTTTA | GTAGCAACAG | ATTTAATCTT | 1320 |
| 30 | ACCATCGACA | TTTTTCAAAT | TATTAACCAT | CTGTTCTAAA | GTTTCTTTAw | TGGtATATCG | 1380 |
| | CTGATTTGaw | TCTAGCTGAA | AATCAAACCC | TTTTACCGTT | AATGATAATG | TAAAGTATTG | 1440 |
| `., | TTGTGGnTTG | AACTGATTAA | TCTCTTGTTG | GTCGTGTAAT | TTACTAAATT | GAAACGGn | 1498 |
| 35 | (2) INFORMA | TION FOR SE | Q ID NO: 64 | 8: | | * | |

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1044 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

| TAAAACAATT | CGTTTTATTA | ATACAGTTTG | TAAAAGTATT | CTCTTAGTAC | TAATAGCTAA | 60 |
|------------|------------|------------|------------|------------|------------|--------|
| TGTAATGATA | GAAAATACTA | GTGTTATTAA | AGATTTGAAT | AAAATAAAAG | AAACTGAGAA | 120 |
| ATATTGGAAT | GTATTAGATG | ATTATTACAC | GATTGAATTT | GCACCTTATC | ACGAAACAAA | 180 |
| ACAAAGTTTG | ATTGATAATA | TGGTGCGATC | AGAACAATTA | GTAAAGGCTA | GTGAAGCAGA | 240 |
| AAATAATGCG | ATTTTATTCA | AACCAAAGGG | TGACTCCGTT | GACAATGACA | ACTTTTCGCC | 300 |

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|----|---|---------------|------------|------------|------|
| | TCAACCTGAT ATTCCGATAA AAAATCAA | AA AAATAATGTO | GAAGTAATTA | TTCCACAAAA | 420 |
| | GTTTCATGCA ATGCGTAATG AAATCAAT | CA AGCATATCAT | TCATGGTTTG | AATTTGTACA | 480 |
| 5 | AAATAAAAAT AATAAAGAGA ATAAGTTA | IC TATACAGTTI | ATCAACAAAA | ATGATTGTCG | 540 |
| | AATTTTTCA TTTGATGCAC GAGATAGT | CG CCATTTGTCA | TTTATAGAGG | CGCCAATCAT | 600 |
| | TGTGAATGTT CAGGCATCAG ATTTATCG | AA TGATTTLLAT | TATGCCATGA | TCaGTCaAGG | 660 |
| 10 | CGGGTATTTA TTCAAAAATT ATGACGCG | CT AGTAAAAAAT | ATTGGAAAAG | TATCCATCTT | 720 |
| | GATGGGGAAA TCCAGTGGAA TAACCAAT | TA TAAAGATAGO | GTGATGGAAA | TGTATCATGA | 780 |
| 15 | AAACAATTTG AAATTAACAG TACTCAAC | TT TTCACAAATC | ATTATCGCAA | TCATTTTAAT | 840 |
| ,, | AATTATTATT TTATTTGATG TGAAATAT | ra ttttgaacag | CATCGAAAAT | TACTCGTAAT | 900 |
| | CAAAAAGCTA TATGGTTATT CAACATTA | AG AGCCAATTAC | CAATACTTAT | TAATAAATAA | 960 |
| 20 | TATAGTTGTT ATTTTTATTG GAATATTG | AC GAATGTAATT | TTACATTCTC | ACTATATAAT | 1020 |
| | GATGTTATTT GCAACGATTC TTGT | | | | 1044 |
| | (2) INFORMATION FOR SEQ ID NO: | 649: | | | |
| 25 | (i) SEQUENCE CHARACTERIST | | | | |
| | (A) LENGTH: 399 base (B) TYPE: nucleic ac | id | | | |
| | (C) STRANDEDNESS: do (D) TOPOLOGY: linear | uble | | | |
| 30 | | | • | | |
| | (xi) SEQUENCE DESCRIPTION | : SEQ ID NO: | 649: | - | |
| 35 | GAACATATTG GGTTATGCAA GGnGGTCA | CT CTTCACACTI | ATAAACAACA | TTTTAATAAT | 60 |
| | GTAAAGTTTA ACCAGCTAAC ACTTTTGT | IA GCTGGTTTT | ATTTTCCTTC | AATTTTTAAA | 120 |
| | TGGTTAAGTC CCCTTCTATA TCTTATAA | GA CAATCATTAI | AATCAATTCA | ATTAATACAT | 180 |
| 40 | TAACAACCAC AACTAATAAA TATAGTAA | CT TCAAAATCCA | TATTTATGTC | TAAAGATAAT | 240 |
| | CTCAATGTTG TTCACGTCAA TAAAATTA | rc cctaggttti | TAAAAATTGT | ACATGTTTAA | 300 |
| | ACAATCAAAA GTGTACATTA TTAAATTA | IC ATTTCCAGTI | AGATTTAGAA | AACATTCACA | 360 |
| 45 | CCACGCATGG ACCAACGTAT TCGTCTTC | AT TCATTTTAG | | | 399 |
| | (2) INFORMATION FOR SEQ ID NO: | 650: | | | |
| 50 | (i) SEQUENCE CHARACTERIST (A) LENGTH: 747 base (B) TYPE: nucleic ac (C) STRANDEDNESS: do (D) TOPOLOGY: linear | pairs id | | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650: | |
|------|---|-----|
| | GTACTAGGTT CTANGATTCC CTACTGTAGT CATAGATATT TTCCAAACAG AGCCTGACAA | 6 |
| 5 | CTTTTCATTT TTAATAGTGA TCACTATATT AATCGCTATT GCAATTTATG CATGTCGATT | 120 |
| , | TGTTTGGGTT TATTTCTGGT ACAAAGATTT TTATTTCCCG AAAAATATAC AATCTTATCT | 18 |
| ı | AGACGAGGAA CATGATTCAC ATGAAACACC ACCTTCTCGA GTGCGTTACG CATTTATTAT | 24 |
| 10 | GACCATGTGT GGTATTCACG GTACAATTTC ACTTTCAATG GCACTTACAT TACCATTTAT | 300 |
| **** | CATTACAAAA GGACAAGCAT TCGAATACCG TAATGATTTA TTGTTTATTG CATCTTTCAT | 360 |
| 15 | GGTATTAATT AGTTTAATCT TAGCGCAAAT TGTTTTACCT TTAATTACAC CATCTGCCGA | 420 |
| | AGATACTACT TTTAAAGGTA TGACTTATCA ATCTGCCAAA ATTTTCATTG TTCAAAAAGT | 480 |
| | GATCCAGCAT TTTAAAAACG AAAGTAAAAA AGACAAAAAC GATACAAATT ATCGCCCAGT | 540 |
| 20 | ATTAAACCAA TACTATGGAG AATTGTTATT TTTATTAAAT TCAGAACCTG ATAATCAAAA | 600 |
| | TACTAAAGAA CTCAAACGTT TAGAAGATAT TGCAAAAGTA ATCGAAACAT CTACACTTGA | 660 |
| ٠. | GCGTTTAATT GATAAAGGTA AGGCAACATA TCAGGATATT AATAATTACC GCAATATTGT | 720 |
| 25 | CGAATTAACA GAGACACCC GTACTGC | 747 |
| | (2) INFORMATION FOR SEQ ID NO: 651: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 30 | (A) LENGTH: 1373 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651: | |
| | ATACAATACT CTTTTATTAT TCAATAAGCC ACTTCCTATA GCAAATGTTT AACTTTAAAT | 60 |
| 10 | ATTTTTCGAT GCTAACAAAA AATCACACTA TCATCTTTTA AAATGAAAGT GTGATTACAA | 120 |
| | GCAAATCTGT AAAATTTATA AAGCAGAAAC AATTCAACTT TATCATTATG ACATTTCAAT | 180 |
| | TAAACCTTCT ACATTATAGT TCCAAGCATC TTACACATGA ATGCAAGTAT TTAACGATTT | 240 |
| 15 | AATTGTGACA TAGCCTGTTG ATATTGTGTT TCATTGATAT AATTTTGTTG CTTCATTTTT | 300 |
| | TCTAAGTTCG TGCTTACACG TTGCGTAAAA TTCTCTGACA TATTATTGAT ATTATATACG | 360 |

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CTAGGTGCAT TGACTTTACT AGCTAAAATA GCGCTTTGTA AAACTGTTAT GTGAGACATT

GTTGTACTAT TTTTATTCAC GGTTGTTCCA AAGTAATGGT TTGCTGCGCC CTCAAGCGTA

TATTGATTAT CCCCAAAGTA AATATTATTT AAATAAAAGC TTAAAATTTC GTTCTTATTA

420

480

| | TCATTATCAT | TTAATAAAA | TTTGACAACT | TGTTGTGTAA | TGGTACTACC | ACCTTGCACA | 660 |
|----|------------|------------|------------|------------|------------|------------|------|
| | TCTCTGTCGC | TAATCGTTGA | AAATAAAGCT | CTAGTTGTAC | CTTTCAAATC | GAATCCATGA | 720 |
| 5 | TGATTGTAGA | ATCGTTCATC | TTCCATTGAA | ATAAAGGCAC | CTTTAACATA | CTCTGGCATG | 780 |
| • | TTATCAGCTG | ACACAAAACT | ACTITIATIT | TCAATTTTTC | TTAGTTCATC | CACATTATCG | 840 |
| 10 | CGTGTAGATA | AAAAATACAT | GATACCAATA | AACAATGCGA | TAATGATTAG | AATGGTTAAT | 900 |
| | AATATTTTTA | ATAGTATTCG | TTTACTTTTT | TTCTTTTTCG | GCGGTTTGCC | AACTGGTTGA | 960 |
| | TAATACGTAT | TATAGTGAGG | TTCGTGTTTC | ATATGCTCAA | AATGTTCATT | TGAGTTTGAG | 1020 |
| 15 | TACCTATCGC | TTCTTTTCAT | GCGTTTGCTC | CTTCTTTTAA | AACTCACTTA | GLATATACCT | 1080 |
| | TGaGTTTACC | AGTÁCTATCA | CAAATAGGCT | ACACTTTTTG | GGAAAATCAG | TCCAAGGGCT | 1140 |
| | TACAATCGTA | TACGCCATCA | TACTTACTTT | TTTGTTTTTT | GAAAAAATTA | TAGATAAATC | 1200 |
| 20 | ATTGCAATTT | TAAATATTAA | TCATGTCAAA | TATTGTTATA | TTTTATAAAA | ATAAAAGACC | 1260 |
| | ATCCCTATTA | AATGCCAATA | GAGACGAĆCT | TTTATTTGTT | ATTCATTTAT | TAAAACTAAA | 1320 |
| | ATCCATATTT | CATTTCAAAC | GAAAATATAT | AAATTTTAAC | AATCGTTAAC | CAC | 1373 |
| 25 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 652:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 859 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652: 35

| GGCAGATA | AT T | TAGTCATTG | TTGAATCGCC | TGCAAAAGCA | AnAACCATTG | AAAAGTATTT | 60 |
|----------|------|-----------|------------|------------|------------|------------|-----|
| aggtaaga | AA T | ATAAAGTTA | TAGCTTCAAT | GGGACACGTC | AGAGACTTAC | CAAGAAGTCA | 120 |
| AATGGGTG | TC G | ACACTGAAG | ATAATTACGA | ACCAAAATAT | ATAACAATAC | GCGGAAAAGG | 180 |
| TCCTGTTG | TA A | AAGAATTGA | AAAAACATGC | AAAAAAAGCG | AAAAACGTCT | TTCTCGCAAG | 240 |
| TGACCCCG | AC C | GTGAAGGTG | AAGCAATTGC | TTGGCATTTA | TCAAAAATTT | TAGAGCTTGA | 300 |
| AGATTCTA | AA G | AAAATCGCG | TTGTTTTCAA | CGAAATAACT | AAAGACGCTG | TTAAAGAAAG | 360 |
| TTTTAAAA | AT C | CTAGAGAAA | TTGAAATGAA | CTTAGTCGAT | GCACAACAAG | CGCGTCGAAT | 420 |
| ATTAGATA | GA T | TAGTTGGCT | ATAACATCTC | GCCAGTTCTT | TGGAAAAAG | TAAAAAAAGG | 480 |
| GTTGTCAG | CG G | GTCGAGTTC | AATCTGTTAG | CmTTCGTTTA | GTCATTGACC | GTGAAAATGA | 540 |
| nATTCGAA | AC T | TTAAACCAG | Angaatattg | GACTATTGAA | GGAGAATTTA | GATACAAAAA | 600 |

| • | CACCAGATION GAGAAAANTA CAGCTGCATT AGATGGAGAT CAATTCGAAA TTACAAACGT | 720 |
|--------|---|---------|
| . 7. | GACTAAAAAA GAAAAAACGC GTAATCCAGC AAACCCATTT ACAACTTCTA CATTACAACA | 780 |
| 5 | AGAGGCGGCA CGTAAATTAA ACTTTMAAGC AAGAAAAACA ATGATGGTCG CACAACAATT | 840 |
| | ATATGAAGGT ATAGATTTG | 859 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 653: | |
| ₩ | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 747 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653: | |
| 20 | TTCAACTTCG TTTGGAAATC ATGTTCCTCA ATTGTTGGAC TTAAACGAAT TTCTTTAACA | · 60 |
| | TIGATAATTT TITGTTTCTT TITCATTTCT TITTCTTTTT TCTGTTGTTC GAATTTGAAT | 120 |
| | TTACCGTAAT CCATAATTCT TGCAACTGGT GGTTTCGCAT TCGGTGCAAC GACCACTAAG | 180 |
| 25 | TCTAAATCTA CACGTTCAGC CATTTCTAAA GCTTCACGCT TTGATTTAAC ACCAATTTGT | 240 |
| .: | TCACCATCTT GACCGATTAA ACGTAATTCT TTTGCACGAA TTTTGTCATT GATTTGAGTT | 300 |
| 30 | TGATCTTTTG CTATGGTTGA CACCTCCAAA ATTTTTACGA AATTTGCACC AAGCAAAAAG | 360 |
| | GAAGAGCAGG TATAAAATAC CCGCTCTTCC TTATACACAG TTATGTGTAA TGTGATTAAC | 420 |
| | CTGCCAACTG CTTTATGCGT CGCTACAGGT GAGAAGCGGG TGCTTCTACT TGGTTCGTTT | 480 |
| 35 | CGTATTCAAC GTTATTAATC ATATCAACAA TTCACATTTA AGTCAACACT ATAACTGTAA | 540 |
| | TTATTTTAT TTTAACCTTT TATTTCATCC ATTGACACGT CTTGACGTAA ATCTACTTGT | 600 |
| | TCTAATGGAA TTTTTTCGT TTTATATCGA AGCTTATGAT AAATAAAGAA TGCTAAAAAT | 660 |
| 10 | ACTGGAATTC CCATATACGT AATTAAGAAG CGACTAAAAT TAAAATCTCC TGTnTTAATA | 720 |
| | AAGTCAACAT CTTGCCCAAn AAnTACT | 747 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 654: | . 4 |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 501 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | , |
| 60 | (D) TOPOLOGI: TIMEAR | * |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

55

| | TTGTGCTTCT TTTTTAGCTT CTTGAACCTC TTGTGCCTCT TGTGATGTAT CACTYAAATT | 120 |
|------------|---|-----|
| | ATTTGCACTT GCTTCTTCTT TTATCGCTGC TTGTTGTGCT TTCAATGCCA CTGCTTTTGT | 180 |
| 5 | TTCTTYATTT GATACAGCCA CACTITTATC CGCTTCTGCT TGTGCTTCTC TTTTAGCTTC | 240 |
| | TTGAATCTCT TGTGCTTCTT GTGATGTATC ACTTAAATTA TTTGCACTTG CTTCTTCTTT | 300 |
| | TATCGCTGCT TGTTGTGCCT TTAATGCCGC TTGCTCATTT TTAGATTTGT TTAAAAATCC | 360 |
| 0 | TTCAACACGT TCTTTTGTAT AGGCAACCGT TTCTTCAAGT TGCGTTTTTC TTTCTTCAAA | 420 |
| | CTTTTGCGAC AGTTCTTGTn CTTTGACTTT nAAATCATCT GCTTTTTGAT AAACTTTATT | 480 |
| 5 | TTAAAATACC AACCTAAAGC C | 501 |
| | (2) INFORMATION FOR SEQ ID NO: 655: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| _ | (A) LENGTH: 830 base pairs | |
| 20 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
|) 5 | | |
| . , | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655: | |
| - ' | CACCITGICA TAATTAATTT TITGATTITT CATTITACTG ATAATAGGIT CAGCATTAAT | 60 |
| 80 | CATGATTTAA CCTCCCACAT TTAATCATTA ACTTCTATTA TATATGATTC ATATTAAATG | 120 |
| | TCAGTCAAAA AAGTTAGAAA TTCATTTTAA TGCATTTATA TTTCGAAAAT CCCTTATGTA | 180 |
| | TCTAAAAGCA TTTTTTAAAC TTGAATTTTA AAACACTAAA CAACACATAC GTCTCTGTGT | 240 |
| 15 | CATTTCATT TTTTGTATGT CATATATATG TTTACTTCAT TTAAATCAAT TTCATCTTAT | 300 |
| | AATTTATCGT GTATTTTACA AAAGATTGAC TTCAATTCAT CGTAAAAGTT ATACTTTTGC | 360 |
| ÷ | CATTTTTAA TGTAACATGG TGTTAGTAAT AAAAATAATA CATTGAGGTG TTTTACATGA | 42Ó |
| 10 | CAGCATTATT CCCTTATATC GCTTTTGAAA ATTCAAAAGA AGCCCTTGCA TATTACGAAG | 480 |
| | AAGTATTTGG TGCAACTGAC GTTAAACGTT TAGAAGTTGG CGAAGAACAA GCGTCACATT | 540 |
| 15 | TTGGTATGAC TAAGGAAGAA GCGCAAGAAG CAACTATGCA TGCTGAATTT GAAGTGCTTG | 600 |
| 15 | GCGTAAAAGT GTTATGTTCT GATTCTTTTG GTCGCGCTGA CAAAATTAAT AATGGCATAT | 660 |
| | CATTATTAAT TGATTATGAT GTTAACAATA AGGAAGATGC TGATAAAGTT GAAGCATTCT | 720 |
| 60 | ATGAGCAAAT TAAAGATCAT TCTTCAATTG AAATAGAATT ACCGTTTGCT GACCAATTCT | 780 |
| | GGGGTGGCAA AATGGGCGTC TTTACCGATA AATACGGTGT TCGTTGGATG | 830 |

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(2) INFORMATION FOR SEQ ID NO: 656:

(A) LENGTH: 539 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656: | |
|----|--|-----|
| 10 | GTATCCATGG GCCCGTTNCG CACAACATTT GGNACAATTA GGTACACGNG TTGTCaTCGG | 60 |
| | TCGTTTCGGT ATAATTITAT CGAATGAAGG CGGTGCGTTA CAAACAATGA AACTACCATA | 120 |
| • | CGAATATTAC ATTGGTGGTA AATTAGGTTC TGGTCAACAA TGGTATTCAT GGATTCATAT | 180 |
| 15 | CAATGATTTA ATTCAAGCTA TTTTATTTTT AATAAATAAC GAGTCAGCTA GTGGTCCGTT | 240 |
| | TAATTTAACT GCACCTATAC CTGAACGTCA AAATTTATTT GGCTACACTT TAGCAAGAGC | 300 |
| | TATGCATAAG CCTCATGAAA CTTGGGCACC AAGTCTTGCA ATGCGTCTCA TACTTGGTCA | 360 |
| 20 | AATGTCAACA GTAGTATTGG ATACTCAAAA AGTATTACCT AATAAAATTC AAGCATTGGG | 420 |
| | ATTCCAATTT AAATATAGTA ATTTAAAAAT GGNACTTGAA GATTTAATTA AAGAATAATC | 480 |
| 25 | AATACCATTA ATGAGCATTA GAAACAACAT ATGTACTAAA TGTAATGTCT AGAGCGACT | 539 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 657: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 30 | (A) LENGTH: 1106 base pairs (B) TYPE: nucleic acid | |
| • | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657: | |
| | ATCAAGTTGA ATATCATCCA TATTTAACCC AACATAAATT GAYATTATAT TTGGCAGCAC | 60 |
| | AACGTATCGT GATGGAATCT TGGTCACCAT TGATGAATGC ACAAATTTTA AATGATGAGA | 120 |
| 40 | CAATTAAAGA CATTGCTCAA GAATTAGGAA AGTCACCTGC CCAAGTTGTT TTAAGATGGA | 180 |
| | ATGTGCAGCA TGCTGTGGTT ACAATCCCTA AATCGGTGAC ACCAAACAGA ATCTCTGAAA | 240 |
| 45 | ATTTCCAAAT ATTTGATTTC GAATTATCAG ATGAACAAAT GACGCGAATT GATGGTTTAA | 300 |
| 45 | ATCAAGATAA GAGAATTGGA CCTGATCCAA AAAAATTTGA AGGCTAGATT AAAATCGCTC | 360 |
| | AACTGATGAA AAGGTTAGAT GAATTGTCAG GGCTTGGGAC ATTAAGTTCT TAGGCAATGT | 420 |
| 50 | AAAAAAGCTG ATTTCTATTA ATTATTTGAT AGAAATCAGC TTTTTTGATA TGTATTTTAT | |
| | AATGTACAGC TCGTTGAGCT GCTATTTTCC TTATATTAAG TGCCATTAAT ACAAAACCTA | 480 |
| | GCTCTCGTTT AACTTTATTT ACTCCTCGAA CTGACGTTCG AGTTAAACCC AAAATAGCCT | 540 |
| | The second state of the se | 600 |

| | CTGGTTCAGA AAGCTTTTGA TTAATTTGGA CTTTAAAGTA TTCCCAATTA TAATTCTTCA | 720 |
|-----------------|--|------|
| ٠ | TGATTLTCTT ATTGGATTTT GAATTTGGTT TCATGCATTG TTGCCTCAAA GAACATGCTG | 780 |
| 5 | AACAGTCATC GCATTCATAT AGTTTGAAGT CTCGTTTAAA ACCATATCTA TCATTACGGT | 840 |
| | ATGCATATCT TTTAAAACCT ATTCTTTTGT TATTAGGACA TATAAATTCA TCATTAAGTT | 900 |
| 10 | CGTCATATTT CCAATTTTGA GTGTCGAAAA TGTCACTTTT AAACTTTCTA GTTTTATCLT | 960 |
| ,,, | TAATAAACAT GCCATACGTA ATAAGTGGCG TTTTATTAAA ATCATCTATA ATGGCCATAT | 1020 |
| | AGTTTTGGCT CACTACCCAT AACCTGGCAT CAGCTACCAA ATGAACCGAA GGGATTTTTG | 1080 |
| 15 | GAATCCATTG GTTGAAAAAA TGGGAA | 1106 |
| | (2) INFORMATION FOR SEQ ID NO: 658: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658: | |
| | TTTTAACTTT ACTCTTTGAT TTAAAGAGTG ATAAATGTTT ACAGTTTAAT TAAAACTGCA | 60 |
| 30 | TAAGAACTIC TAGCTTTCT CTTTCGTTCA AAGAGAAGCA GCTGTTCGCA GTTTAATCAA | 120 |
| | AACCACATAA AGCTTTTAAC TITACTCTTT GATTTAAAGA GTGATAAATG TITACAGTTT | 180 |
| | AATTAAAACT GCATAAGAAC TTCTAGCTTT TCTCTTTCGT TCAAAGAGAA GCAGCTGTTC | 240 |
| 35 _, | GCAGTTTAAT CAAAACCACA TAAAGCTTTT AACTTTACTC TTTGATTTAA AGAGTGACAA | 300 |
| | ATGTTTACAG TTTAATTAAA ACTGCATAAG AACTTCTAGC TTTTCTCTTT CGTTCAAAGA | 360 |
| | GAAGTTCTAA TACCACCATA TCGTGCGATC GGGAACGGTA | 400 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 659: | |
| 4 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1899 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · . |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659: | |
| | ATAATTACAA TGGCTACTGC AATTATTGTT GGAATTATAT ATTTCAGTTT AGTCATCATT | 60 |
| | TATGCTCCCT TGATTTCAAA TTCATATCAT TAGTTTACCA TATTGAAGAT GATATAATAA | 120 |

| | AACTTTAACT | GAGCTTCATG | GGGCACCAGG | TTTTGAAGAA | GAAGTAAAAA | ATTATATGAC | 24 |
|----|------------|------------|------------|------------|------------|------------|--------|
| | TCAGCAAATG | GCGCCGTACG | TAGATGAATT | TATTGAAAAT | CGTATGGĞTG | GATTTTTTGG | 30 |
| 5 | TGTGAAAAA | TCTAAAAATC | CAAATGCAAA | ACGTGTAATG | ATTGCAGCAC | ATATGGaTGA | 36 |
| | AATCGGATTT | ATGATTACAA | ATATCACTAA | AAATGGAATG | ATTCAATTCA | CAAATTTAGG | 42 |
| | TGGTGTTGCA | AATGATATTT | GGCAAGGACA | ACGCTTAGTA | ATTAAAAATA | GAAATGGCGA | 48 |
| 10 | TAAAATTATC | GGTGTTGTTT | CTAATATACC | TAAACATTTT | CGTACTGGTA | GTGAAGGTGC | 54 |
| | ACCGGAAATT | AAAGATTTAA | CATTAGATAT | AGGTGCTCAA | AATGAAGATG | AGGTGCGTGA | 60 |
| 15 | gCGCGGAATA | GATATAGGAG | ATACAATTGT | ACCTCACACG | CCATTCACAC | AGTTATCTGA | 66 |
| | ACATCGATAT | AGTGCTAAAG | CATGGGATAA | TCGTTATGGT | TGTGTCTTGG | CAATTGAAAT | 72 |
| | ACTAGAATTA | TTAAAAGATA | TAGAATTAGA | TGTAGACTTG | TATGTTGGCG | CAAATGTTCA | 78 |
| 20 | AGAAGAGGTT | GGATTACGAG | GTGCGAAAGC | ATCTGCAGAG | ATGATAGACC | CAGACGTTGC | 84 |
| | ATTTGTAGTT | GATTGTTCAC | CTGCCAATGA | CGTTAAAGGA | AACCAACCAT | TATCTGGTGA | 90 |
| | ACTTGGTAAA | GGGACGTTAA | TTCGCATAAA | AGACGGTACA | ATGATTITAA | AGCCTGTATT | 960 |
| 25 | TAGAGACTAT | TTATTAAAGT | TAGTAGAAGC | ACATGACATT | GAACATCAAT | ACTATATGTC | 1026 |
| | ACCAGGTGGA | ACAGATGGTG | GAGAAATTCA | TAAAGCTAAT | ATTGGTATTC | CGACTGCAGT | 1086 |
| | TATTGGTGTA | TGTGCACGAT | ATATTCATAG | TACAGACTCA | GTATTTGATA | TAAGAGACTA | . 1140 |
| 30 | TTTTGCAGCT | AGATCTTTAC | TTTCAGAAGC | CATTTGTAAT | TTAGATAATA | ATCAAATAGA | 1200 |
| | AACATTACAA | TATAAATAAT | CGGGTAATAA | CAACTATTAT | CTCTAAATAG | ТТАТАТАТА | 1260 |
| 35 | TCATTAATTA | AGGAGACATA | AAAATGAAAC | AACTTGAATC | AGAACAACAA | TTTGAATCTT | 1320 |
| | TAAAACAAGG | TGCTACAGTA | TTTGAATTCA | CTGCAGGCTG | GTGTCCAGAT | TGTAGAGTGA | 1380 |
| | TAGAACCAGA | TTTACCGGAA | TTAGAAGCGA | GATATCCTAT | GTTTGACTTC | GTATCAGTAG | 1440 |
| 40 | ACCGTGATAA | ATTTATGGAT | ATTTGTATTG | AAAATGGTAT | TATGGGTATT | CCAAGTTTTC | 1500 |
| | TAGTATATAA | AAATGGAGAA | CTGCTTGGAA | GTTATATTGG | AAAAGAACGA | AAATCAATTG | 1560 |
| | AACAGATAGA | TGCATTTTTA | GCTCAATACG | TGTAATTTAG | ACTAGAGAAA | AACGGGGTAA | 1620 |
| 45 | TACTCGTTTT | TCTCTGTTAC | TATGTGTTGA | TTTATTGTAA | ACTATTATAA | GGTGCGAAAT | 1680 |
| | TAGGAGTGTT | ACATATGAAT | ACCTTTCAAA | TGAGAGATAA | ATTAAAGGAA | CGTTTAAGCC | 1740 |
| | ATTTAGACGT | TGATTTTAAA | TTTAATCGTG | AAGAAGAAAC | TTTGCGTATT | TATCGAACAG | 1800 |
| 50 | ATAATAACAA | AGGTATCACG | ATTAAACTTA | ACGCTATAGT | CGCAAAATAT | GAAGATAAAA | 1860 |
| | AAGAAAAAT | TGTAGATGAA | ATTGTTTATT | ACGTTGATG | | | 1899 |

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 3774 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660:

| GTATAATATC | CTTTCAATCT | GTTTTCATAT | TTTATATATT | TTTTAAATAT | AAGTGCTAAA | 60 |
|------------|------------|------------|------------|------------|------------|------|
| TGTTTTAACT | AAAGCATAGA | TTGACAAGAT | GTTATACAGA | ATTTCAAATT | CTATCCAATA | 120 |
| TTGTTCGAAG | TGTAGTATCA | CTGGATTGGT | ATTAAACAAT | GTAAAGGAGA | GATTGCAAAT | 180 |
| GCCGTATAAT | TACAAGAAAC | AAAATGGAGA | GTTAATGTCT | GTAATGAGCC | AAGGTGAAAA | 240 |
| GTTTATTCAT | CAATCACCCG | TTAATGATGA | ACTTAGTGCA | TTGATTAAGT | TATTAATTTC | 300 |
| TAAAATTAAC | GGTTGTCATT | ATTGTGTTGA | TATCCATAAA | AAAGAATTAA | AGGAATTGGG | 360 |
| TGTAaCACAA | ATGAAAATTG | ATGAAGTCTT | GAGTTTTAGA | CATTTAGATT | TATTTACTGA | 420 |
| TCAAGAAAAA | GTGACGCTTG | AATTTGCAGA | AATGTTAAAT | TCAATCAAAĞ | ACTTTAAGAA | 480 |
| GTTTGAAATT | ATTGACCGGC | TAAAATCATT | TTATGATGAA | GAACAAATTA | TTGATCTTGT | 540 |
| CTTTGTTGTA | AACCAAATTA | ACGGTTGGAA | CAGATTAAAT | ATTATTAGTG | ATAGACTATA | 600 |
| ATTGTTCATA | TAAATGCAGA | GTTTCATCTC | GAACGCTATA | TCATAACAAA | TCATGCCACT | 660 |
| ATACAGGTCA | AATCTTGTAT | AGTGGCATTT | TAATTTATCC | CTTTGAATAC | TGTTATTTAA | 720 |
| CGAATATCGG | TCCACCTGGT | CCAACAGGGA | TACCTAATAG | GAACCAAATG | ATGACAAATA | 780 |
| CTGTCCATAC | AATACTTAGC | GCGATTGAAT | ACGGCATTAA | ACTAGAAAGT | AAGGCTCCGA | 840 |
| GTTTCATGCG | TTTATCGTAT | TTTTGTGCAT | AAGTTAATAA | TAAAGGTAAG | TACGGCATCA | 900 |
| TCGGTGTAAT | TGGATTGGTA | ATTGAATCGC | CTACACGGTA | AATGACTTGT | GTGAATGCGG | 960 |
| GATGAAAGCC | GATAAGGATT | AACATTGGTA | CGAATATCGG | TCCTAAAATA | CCCCATTTAG | 1020 |
| CCGATGCGCT | TCCGATTAAC | ATGTTGACCA | TTGCACTCAG | TACAATAATA | CCTAGTATCA | 1080 |
| ATACAATACC | GTTTTGATGT | TCTAATAATT | TGGCACCTTT | AACAGCAGCG | ATAATTCCTA | 1140 |
| AATTACTCCA | CTTTAAATAC | GCAAGTAGCT | GTGCTGCAAA | AAACACAATA | ACGATAAATG | 1200 |
| TTCCCATTGA | TCCTACAGCA | TCGCCGAACA | TTTTACCTAA | GTCTTTTGTA | TTTTTAATTT | 1260 |
| CTTTGCTTAA | AATCCCATAA | ACTAATCCAG | GTACTAAAAA | TACGACAAGA | ATAATTAATC | 1320 |
| CGACACCGTT | AATTAATGGC | GCATCGTCTA | GTAAGCTGCC | TGTTTTAGCA | TTTCTTAAAA | 1380 |
| AGCTATGTTC | AGGAATGGCT | GTAATAATTA | TAAAATAAT | TGTGACTATG | AAACTGATAT | 1440 |

| | | • | | | | | |
|----|------------|------------|------------|------------|--------------|------------|------|
| 9 | CATCATGCAT | TAAACTGTCA | TCATATTTTC | CTAATCTAGG | AATAATGAGC | TTAGTTGTAA | 1560 |
| | CTAGCAATAT | CGTAGGAAGT | AATACAACGA | CACTCGCTGC | GATAAAGTAC | CAGTTCATAG | 1620 |
| 5 | CAACGTTTGT | TTTAATAGAA | TCTGAAACGA | TACGTGTTGC | CGGTTCTGTA | AATGAATAGA | 1680 |
| | CCAAAGCATC | TTGCATACCA | ACAACTATAT | TTGCTGCAAA | TCCTCCAACA | GCGGAAGCAT | 1740 |
| | ATGCCATCGT | TAGTCCAGCG | ATAGGGTGAT | AGCCAATTTI | AATAAAAAGC | ATTGCTGCAA | 1800 |
| 10 | GCGGCGGCAA | GATAATTGTC | GCAGCATCGC | CGGCTGTACT | ' ACCTAAAATA | CCAATTAATA | 1860 |
| | TAATAGTCGG | TAAAATTAAG | AAACGTGGTG | CGCGATTCAC | AACAGAAATC | ATTAACTTAT | 1920 |
| 15 | CGAAGTATCC | TGTTTTCTCT | GCAACACCAA | TACCAATCAT | CACTGCTAGT | ACTAAGCCTA | 1980 |
| | ATGCTGGGAA | CTCTGAGAAA | TTTTTAATCG | TATCATTCAT | TATCATCGTA | AATCCATCAT | 2040 |
| | | | | | • | ACAGATACAT | 2100 |
| 20 | | | | | | AAGAATAAGA | 2160 |
| | | • | • | | | CGATTGACGA | 2220 |
| | | | | | | TAAATATTTA | 2280 |
| 25 | | • | | | | AACTAATATT | 2340 |
| | | | | | | ACTGCCTGAA | 2400 |
| | | | - | | | TAAGTTTAAG | 2460 |
| 30 | | TAGGAGTGAC | | | | | 2520 |
| | | AGGTATCGGT | | | | | 2580 |
| | | AGACATAGCT | | • ' | • | • | 2640 |
| 35 | | GAAGGCGTAT | | | | • | 2700 |
| | * | AAAGGAACAG | | | | | 2760 |
| 40 | | TGATAGAATT | | | | | 2820 |
| | | TGGGACATTT | | | | | |
| | GTGGCTCTAT | | | | | | 2880 |
| 45 | | TGCGAAAGGT | | | • | | 2940 |
| | | CATTCGAGCC | | • | | • | 3000 |
| | | AGGTACGAGT | | | | • | 3060 |
| 50 | · | | | | | | 3120 |
| | | GCTGGGACGT | | | | | 3180 |
| | MOUNTCIGA | CGACAGTTCA | LICATAACTG | GAGAGACGAT | TCGAATTGAT | GGTGGTGTGA | 3240 |

| AATTATTAA | AATCGATATC | CAGTGGAAAA | GAATTTGGCA | TGAAGTAGGC | AATGTATGCA | 336 |
|------------|------------|------------|------------|------------|------------|------|
| TATTGTCGCA | ATGAAAGACA | TTTAAAGCGG | AGATTAATTA | ATCTTTGAAA | ATCACATATT | 342 |
| GTTCATTTGA | AGTGTATTGC | TTAAAGCTTG | TTTTAACGTA | TTGTAGGTCG | TGCATCTAAT | 348 |
| TTATCAGAAT | CTCGAGTTCA | AACTTTTGGA | GTATCTTTAA | AATAAGCTGT | ATTTTGTCTA | 354 |
| TTCTAATAAA | TTAAGGAGAA | TTTTATGTTA | AAAGAAAAAG | AAAGTTTTAG | ATTGCTATAT | 360 |
| CAAGCTATAA | GAGAGATTGC | AGATAAAATT | GGAGATAATC | AGTTAGAAAC | TAATTCCGTT | 3660 |
| AGTTTATLAT | tATTGGACTT | TGATTTTGAA | CATGAAGTAT | TTGATGAATT | GTATCTTGTG | 3720 |
| ATTTLAAAAT | ATTTAAATAC | AGTAAGTATA | GAGAACATAA | GTCATAGTGA | GCTT | 3774 |
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(2) INFORMATION FOR SEQ ID NO: 661:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1078 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661:

| | TACIGGITIT | GGATTTTGGA | GGTAATACAG | TACCTAATAG | TAATRATGGT | GTCGTCAnAA | 60 |
|---|------------|------------|------------|------------|------------|------------|-----|
| | TTATATCTTT | CCGTGATGTT | CTTACTCATT | AGAACATCnG | CCTTCAGAGG | AATCATGATA | 120 |
| | CGAGGAATAA | GAAATTTAAA | TGTGAGCGAA | GŤCAATATAG | TATTTGCGAT | TATTTTTATT | 180 |
| | AACTCCATTA | TTATTGTTAG | TTTGATTTTT | CGAGGATAAC | TTCAATTTTT | GCATTTTGAG | 240 |
| | GTTTTTTAAC | ATATCTATTT | GCATCAGTTG | ATGGCAACCT | TTTACTTAAA | TCTATTGTGT | 300 |
| | AGTTATTGTC | TGCACCTGTT | ATTTTAATTT | GTCCTTTATT | ATAAGAATTA | TTATATAATT | 360 |
| | TTTTACTTTT | AATTAATGTT | TGACGAATAC | GAAAATCTAA | TTCTTTTAAA | GTTAAAACAG | 420 |
| | GCTTATTGCC | TTCATAAACT | GGAAATCCGC | CAGTAAACGT | TTCTGCTTTA | TCTTTATATG | 480 |
| | TTACATTCAG | TTTATAGTGT | TTATCGTTAG | ATGTTGCTGC | AGGAGTAACA | CCACCAGTAA | 540 |
| | ACGTTTCTTG | AGATAATGCA | AAAGaATCAA | TGGTTTCTTG | GTCTTTTATG | Суааааатат | 600 |
| | CAACGCTTTT | ATTTCTTAAT | TGGTTGATAT | TGCCCCAACT | TTCAGGTCCA | TAAACTTGAA | 660 |
| | TATGACTATA | CCAAGaAAAC | TGTAACAACG | TTGCATGAAT | CGTACCGTTA | TCTTTTTGCC | 720 |
| | ATAACGTACT | GTTAGAGAAG | GTTAAATATT | TTTGCGAGTA | ATATTTAGTT | AACTCATTAA | 780 |
| | CGTTAGTTTC | GTTTTGATTT | ATATAAtAAG | CTTTCGCTTC | AGATGAAGAA | TTGATAKGTG | 840 |
| • | TATTAGGAAA | TTGTGTAGAT | GCTGTACCTA | ATAGTAACAA | TGTTGTTGAT | AAAATAATTT | 900 |

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| ATAAAAAGGG | GTTAATTAGA | TAATTGAAAT | TATCCGCATT | TACAAAAGGT | AATAGGTTAG | 1020 |
|------------|------------|------------|------------|------------|------------|------|
| TTAGATTTTT | CGAGTATGAC | TCAATTTCTG | CATTACGAGG | ATTTTTAACA | TAACGGTT | 1078 |

(2) INFORMATION FOR SEQ ID NO: 662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662:

| | AACTTGCTTT | TTAGTATCTA | CGTTAATATT | AATAGCTTTA | ATTTCACTTG | TATTAATTAA | 60 |
|---|------------|------------|------------|------------|------------|------------|------|
| | ATCAGCTGTG | TAAATACCTG | CTTTCAAATC | GATAACTTTC | TTTGTTCCAT | TTTTAAAGTA | 120 |
| | AACAGTATAT | TTCGCTTGCT | TCGATAGTCT | TAAATCTATA | TCACTAATAC | CTCTGTCTGA | 180 |
| | TTTTAAAACT | GATTTAACTC | TATCCTCTAA | ATCTTTATAA | CTAATATTTT | GATTCTTATT | 240 |
| | AAATGTTAAG | CTTGATAAAA | TATTTTGGCT | TGTACCGTTC | ACAGTGaTTG | CATATGGAAC | 300 |
| | ATGGACTTTA | GAATATCCAT | GGTGTAACGA | ACTTGATGAT | TTATCTAATG | GCTTAGCTGC | 360 |
| | GGCAGACGCT | TCATTATTAT | TAAAGTTTGC | ACCTGTTGAT | GCTAAAACAC | CTAATGCTAA | 420 |
| | AGTTGTTGTA | ATCAATGACT | TAAATTTCAT | AAATTATCTC | TCCTTTTTTG | TGTAATTCGT | 480 |
| | ATTTGCAACT | TAATTATAGC | CAGACTTTCT | CTATTTTTG | AATTAACTGA | АТАТТААТАА | 540 |
| | TAAATTATCT | TTAACAATAA | TTTTTTAACA | CTGTTAAAAG | TTCTTTTAAT | TTTGATTAAC | 600 |
| | TAATTAATTT | ACAATACCTA | AAATGTTGTT | TGGTTTTGTT | TATACCAAGC | TTCAAACTTA | 660 |
| • | AATGTCATAA | CAACATTCAT | TTCTTAATTC | CTATTAGATT | TGTCGATTAT | ATTTACAGCA | 720 |
| | TCTTTATACT | CAAAAAACAT | TTACTTAAAA | ATATAAATTC | GATTTAATAA | TTAATTTAAA | .780 |
| | TTTAGTTAAT | CAATTTTGCA | TCTATTTTGT | TGTAAGCTAT | ATAAAAGGAG | TGATAATGAT | 840 |
| | GGTGAAAAAA | ACAAAATCCA | ATTCACTAAA | AAAAGTTGCA | ACACTTGCAT | TAGCAAATTT | 900 |
| | ATTATTAGTT | GGTGCACTTA | CTGaCAATAG | TGCCAAAGCC | GAATCTAAGA | AAGATGATAC | 960 |
| | TGATTTGAAG | TTAGTTAGTC | ATAACGTTTA | TATGTTATCG | ACCGTTTTGT | ATCCAAACTG | 1020 |
| | GGGGCAATAT | AAACGCGCTG | ATTTAATCGG | ACAATCTTCT | ТАТАТТАААА | ATAATGATGT | 1080 |
| | CGTAATATTC | AATGAAGCAT | TTGATAATGG | TGCATCAGAC | AAATTATTAA | GTAATGTGAA | 1140 |
| | AAAAGAATAT | CCTTATCAAA | CACCTGTACT | CGGCCGTTCT | CAATCAGGGT | GGGACAAAAC | 1200 |
| | TGAAGGTAGC | TACTCATCAA | CTGTTGCAGA | AGATGGTGGC | GTAGCGATTG | TAAGTAAATA | 1260 |

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| | CAACAAAGGC TTTGTTTATA CAAAAATAGA GAAAAATGGT AAGAACGTTC ACGTTATCGG | 1380 |
|----|--|------|
| | TACACATACA CAATCTGA | 1398 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 663: | |
| | | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1200 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663: | |
| | TTGTAATTGG AACGTACGAA CTTTTCTAGG TAAGAAACGT CGAATCTCGT CCTCATTATA | 60 |
| | ACCAACTTGT AGTCGTTTAT TATCTAAAAT AATTGGACGA CGTAATAAGC CAGGATTATC | 120 |
| 20 | TTGAATGATT GAATATAAGT CTTGTAATGG TAGTGAATCA ATATCAACAT TTAATTTTTG | 180 |
| | GTATGTTTTA GAACGTGTAG AAATGATTTC ATCAGTACCG TCTTCAGTCA TTTTTAATAT | 240 |
| | TTGCTTAATT TCATCAATTG TTAAATGTTC AGAAAAAATA TTACGCTCCG TATACGGAAT | 300 |
| 25 | GTCCATGTTC LTGKTAACCA TGCTTTCGCT TTTACGGCAA GATGTGCAAC TTGGLGAAGT | 360 |
| | AAATAATGET ACCATACATC TCACTCTCCT ATTTGAATGA ATAAAATTCA TTGCTTAAAA | 420 |
| | TTTAGTTATA GATCAAGAAA AAACATTTT TTCTAAAATT CTTAATCGTT ACTATTTATT | 480 |
| 30 | ATAACTATCT AACATTAAAA TTAAATGAGA AAAACCTAAT TTTTCAGATA AGTTTCTACA | 540 |
| | CTTATAAAAA AGATTATTAA TCCCTTTGTT AGTAGTAAGT TATACGTATA TTCTAACACA | 600 |
| | TCTTACATTT TTAAGAAATA CTGTTATAAT GATAATTATT AAAATATTAC TAAGAAAGTA | 660 |
| 35 | GGCATTTAAA TGGAGACATT ATTTTCAGGC ATCCAACCTA GTGGAATTCC TACTATTGGA | 720 |
| | AATTATATTG GCGCACTAAA ACAATTTGTT GATGTGCAAA ATGACTATGA TTGTTATTTC | 780 |
| | TGTATCGTAG ATCAACATGC AATTACAATG CCACAAGATC GTTTAAAATT ACGTAAACAG | 840 |
| 40 | ACCAGACAAT TAGCAGCGAT TTATTTAGCT TCTGGTATAG ATCCAGACAA AGCAACATTG | 900 |
| - | TTCATACAAT CTGAAGTCcC TGCACACGTA CAAGCAGGAT GGATGTTAAC TACGATTGCT | 960 |
| 45 | TCTGTTGGAG AATTAGAGCG TATGACGCAA TACAAAGATA AAGCTCAGAA AGCAGTTGAA | 1020 |
| 75 | GGTATACCTG CTGGTCTATT AACATATCCA CCTTTAATGG CAGCTGATAT TGTTCTTTAC | 1080 |
| | | |

AATACTAATA TCGTTCCAGT TGGAGATGAC CAAAAGCAGC ATATCGAATT GACTCGTAAC

CTTGTAGATA GATTTAATAG TCGCTATAAT GATGTGCTTG TGAACCTGAA ATTCGTATGC

(2) INFORMATION FOR SEQ ID NO: 664:

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| 5 | (A) LENGTH: 787 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|---|----------------------|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664: | |
| 10 | TGTACCTTTT GCTTTAATAA ATACTGTTTC TTTATCATAA TTAGGTTCAG TTAAGAAATT | 60 |
| | AAATTGTAAG CTTTGAGTAA TATTTTTTTG ACTATCACTT GTTGTAGCTG TACGTGTATA | 120 |
| | CATTITAGTA TCACCATCAA GATTCTTCTC AGAAACTTGT TTGATTTCAG AATTAATCTT | 180 |
| 15 | TGCAAATGAA GTAGCTGGTA ATACAGTGAA AGTAGTCGAT AGTGCTAASG WACAAATTGT | 240 |
| | GATATTITTA CATAGTTGTT TAATCATTAG TAATCCGCCC TTTCAATATT ATCCTTCTTT | 300 |
| | ATAAGGTTTA TTGTCATCAG AATATTTATC AACGACTTTA ACTGTTTTAT TTTTCCAATC | 360 |
| 20 | AACTTCATAA GTGACAATTA ATCTTTGACC ATCTTTATTT TtcTCTAAAA TTGGAGGTGC | |
| | ATAATGTATY CCAGGTCTGT TTTTCAAAAT ATCTTGATTT CGTGTGTATG TTACTTCAAA | 420 |
| | TTGCGTTTTC TCATTTGACT TTTCATTAGA TAAATAAGTT AAAAATTCTG GATTAAAGCC | 2 / 480 <u>- 2 /</u> |
| 25 | | 5 4 0 |
| | ACTICITACT AATGCTGGGT ATCTATATTT TGAAGCAAAG CTTAGTTCAG GGTTTTCTAC | .600 |
| 30 | AGTAGCAATT CTCGTATTTC TATAGAATAA TAATTCATCA TTTCTATTTT TCACTTCTCC | |
| 30 | ACCATACTTC AAGTCATTCG CAATAACTGA CCAGTGTACA TGGCCAGTTn ATTTATTTTT | 720 |
| | ACCGCTGGCA ATTGTGTCAT AATTTGCTGC ATCATCAACT AATCGTTTTG GAAGTAGCTA | 780 |
| 35 | TTTGCTG | 787 |
| | (2) INFORMATION FOR SEQ ID NO: 665: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 533 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
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| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665: | |
| | TTATCTGTCA TTAACCACTG GTACATGTGA ACCCGGCNTN AATCAATATA TATATTTAAA | 60 |
| | AGCAAAGGCG CGCCATGTGC CTTTtTTnTA tTTTGTATAT CTGTATCAAA ATCGATTTGA | 120 |
| 50 | TTAAAATCCG CTTTATTTTA TCATCTATTC AAATGATTTT AGTGCGCTTA TTTTACTATG | |
| | GCATTATTGC CTAACCTGTT TGAGATATAT TAATATTTGA TGATTCGTAT TCAAAGTTTT | 180 |
| | | 240 |
| 55 | CATTTAACAT GTATTTAGTA TCATGATAGC TGCTTCATTG ATGATATACT ACCTACTTTT | 300 |

| | CAGAGGCAAT ATTGAACAAT TCTTCATCAT GACTATTTTC CATCACATAA CTATGCTTAG | 420 |
|----|---|-------|
| 5 | CGAACGCTAA CATATCTTTA TCATTATTCG CATCTCCGAA GGCCATGAGC TCTGAAGGAG | 480 |
| 5 | ACATTTCCCA TITATCTAAC AATCGTTTTA ATGCCTGnCC TTTAGTCATG TTT | 533 |
| | (2) INFORMATION FOR SEQ ID NO: 666: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
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| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666: | |
| | GACTTCTCTT GCACTAAAAA TTGCTCAAAT TGCTCGCTGT CATAACCAGG CGGTGTTTCC | 60 |
| 20 | AACCATACAT ATATGCCACC TTTAGCATGA ACAAATGGCA AATCAGCTTT TGCAAGCATG | 120 |
| | GCTTCGAATC GGTCACGACG TGTTTTAÄAT ACATTGCTTT GTTCTTCTAA AAAATCATCA | 180 |
| 25 | TAATGGATTC AAAGCATATA TTGCGGTCAT CTTGTAAATG CACCAAACAT CCCAGCATTT | 240 |
| | GTGTGCGTTT GGTACTTTTT CAAAGCTTGA AATCATATCT TTATTACCAA CTGCCAAAAC | 300 |
| | CGACTCTGAA AACCTGGACA TGTTGATGAA CCTTTNAGAC AAGGGAAGAA ATTTGCAATC | 360 🐺 |
| 30 | GCAACATCTT TGCCCATTTT nCCGAAGCAA GTGnGACTAG | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 667: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667: | |
| | TCTCCAATGC TACTCAAATT AAAAAGGTTT TAAATATTGT TAATTCTGAT CCAGAGCGAA | 60 |
| 45 | AGATTGTTAT CGTTTCTGCT CCAGGTAAAA GACATGATAA TGATATTAAA ACAACTGATT | 120 |
| | TGTTAATCAG ATTATATGAA AAGGTCATTA ATCATCTTGA TTATCATGAT AAAAAAAGAG | 180 |
| | AAATTATTCA GCGTTATGAT GATATTGTAA AAGAATTGCA AATGGATGAA AGTATTTTAC | 240 |
| 50 | GGACGATAGA TGTGACTTTG GAACATTATA TAAATCAATT AAAAAATGAA CCAAAGAGAC | 300 |
| | TATTAGATGC ATTACTTTCT TGTGGTGAAG ATTTTAATGC GCaAYTGALA GCYTTATATA | 360 |
| | ATAALAGTCA GGTLACCAAC AAMATWTATA TCCcCGAAGG AAGCGGGTAT TT | 412 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
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| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668: | |
| | TTACTCGTTA AAGATATTGT AAAAGATGAA GTGACAGAAT ATGACATTCA TCAAATGTTA | . 60 |
| | CCGCATCCGA TTAATATGGT AAGGGTTAGA CTTTTTGGTG TGAAATTAAA AGAGATTATA | 120 |
| 15 | GCTAAAAGTA ATAAACAAGA nTATATGTAT GAACATGCAC AAGGTTTGGG TTTCAGAGGG | 180 |
| | AATATATTTG GAGGATATAT TCTTTATAAT TTAGGGTACA TTCATTCTAC AGGGCGTTAC | 240 |
| | TATCTGAATG GAGAAGAAAT CGAGGACGAC AAGGAATATG TACTAGGTAC GATAGATATG | 300 |
| 20 | TATACGTTCG GTCnTATTnC CCAACATTGA AGGATTACCA AAGAGTATTT AATGCCAGAG | 360 |
| | TTTTTCAGAG GTATATTTAA nGAAAATTAT TGGCTATTTA | 400 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 669: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1236 base pairs | |
| 30 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
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| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669: | |
| 35 | TGTTCGATAT TTTTAAATTT ATCTTTTAAA TACAACAACT GTTTCCGTAA TGATTTAACT | 60 |
| | GTTTTATGAC TAATGCCATT GAATATTTCT AGCGTTTTAT TTAACTTATC GATAATCGCA | 120 |
| 40 | TGTAAATCCT TCAAAATGTC TTTTGTTTCA AAAGTAAATA CATTATGGAA GCGATGAATA | 180 |
| 40 | TCATCATCAT AAACATCAGA ATCATTGATA ATCGTAAATA TCGTTGAGAA CAATTGCTCA | 240 |
| | TTTAACTCAT GAATCTCATT CATACTAGCC TTCAAGCCAA AAATATCAAT TGGTGCAATA | 300 |
| 45 | TCTAATTTTT CCAAAATTCG CTGCTTTTCC AGTTGATCAA TTGCCTTTAA CAATTTTTCA | 360 |
| | TTTTCGTTTT TACCAATCAA ACCAAGCTGA TATTTAATAT CAGCATAACT CAACTCATTT | 420 |
| • | GTCACTTGAT TTAAGGCATA GTCTGGTAAG CGATGTGCTT CATCCACTAT ACAATCATCA | 480 |
| 50 | AACAATTGAT ATATTGAATT TTCAACATCA GAATGAATTA AATGTGCATG ATTTGTAATA | 540 |
| | CCAATTTGAA TGTTCTGTGC ATTTCGCTTA ATAAAATTAT AATAATGAAC ATCGTGACGT | 600 |
| | GCCGGTACAT ATGTTTCAAT TTTCTGGTCA AAATACATCT TTTGACCACC TTTTAAATTT | 660 |
| | | |

| | ATATTCACtT | CGTAATTACT | TGTGTCATCT | TTTAAAATTT | GACTAATAAG | CCCCAATGAA | 780 |
|----|-------------|--------------|--------------|------------|------------|------------|------|
| _ | ATGTAATCaC | TTTTACTTTT | AATCAATAGT | GCATTAATTT | TAAAATTCAA | CGCTTCATTC | 840 |
| 5 | ATTGCTGGAA | TATCTTTTTC | TAACAATTGA | CTTTGCAGTA | ATTTAGTATT | GGTAGAAATC | 900 |
| | ATGACATGCT | TCCCAGTTTC | AATATTATAC | ATCAAGGCCG | CAAGTAAATA | TGCTAATGAT | 960 |
| 10 | TTACCACTGC | CTAGTGATGC | TTCAATCATT | GCTTTTTCAC | TATGCATGAG | CTGATCTAAT | 1020 |
| | ATAGTTTCCG | СТАААТАТАА | TTGTTGCGGT | CGATATGTTA | AGCCAAGTTG | ATCTACAGCT | 1080 |
| | TTGCTATATA | AAGACTTCAA | GCTGCCATTA | TAATTTGTTG | TCGGCTTTTT | AAAATCAACT | 1140 |
| 15 | TGCTTACGAT | AGATAATCTG | TTCGAACTTT | TCGTACGATT | TATCCAATGG | CTTTGCATCA | 1200 |
| | TATTGCCTAA | CCATCTCAAA | GAAAATATCA | TACAAA | • | • | 1236 |
| | (2) INFORMA | ATION FOR SE | EQ ID NO: 67 | 70 : | | - | |
| 20 | (i) SE | COUENCE CHAR | ACTEDISTIC | 2. | | | |

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670:

ACASAATTAT TGACCAATAT GACTCGTGGA CTGATATGTT TAAAGCACTA CTGCATGAAA 60 CATTTAAAGC ATATGCGTT CTATTTATAG ATGCGCAGTT TGAGCCGTTA AGAAAAATGG 120 AAGCGCCTAT GTTTAAAAAG ATTTTGAAAA AACATCAGTT GCTTGATGAT GCTTTTAGAG 180 CAACACAACA ACGTACTCAA AATCAAGGCT TGAATGCGAT GATACAAACA GATACAAATG 240 " TTCATTTATT CTTACATGAT GAAAATATGC GTCAATTAGT LTCGTATGAT GGTAAGCAYT 300 TTAMATTAAA TAAAACAGAT AAGACATATA TAAAGGAAGA AATTATAAAT ATTGCGGAAA 360 ATCAACCKGA ATTATTTTCT aATAATGTAG TGACAAGACC ATTAATGGAA GAATGGTTAT 420 TTGAACACGG TGGCATTTGT TGGAGGACCG AGTGAAATTA AGTACTGGGC TGAACTAAAA 480 GATGTATTTG AACTATTTGA TGTTGAAATG CCLATCGTGA TGCCAAGGCT TAGAATTACT 540 TATTTAAATG ACCGTATAGA AAAATTACTT TCGAAATACA ATATTCCATT AGAAAAAGTG 600 TTAGTCGATG GTGTTGAAGG AGAAAGAAGT AAGTTTATTA GAGAACAAGC ATCACATCAA 660 TTTATTGAAA AGGTAGAAGG TATGATTGAA CAACAGCGTC GTCTAAACAA AGACTTATTA 720 GATGAAGTGG CGGGGAATCA AAATAATATT AACCTTGTGA ATAAAAATAA TGAAATTCAT 780 ATACAACAGT ATGATTATTT GTTAAAACGT TATCTTTTAA ACATTGAAAG AGYAAACGAC 840

960

GAAAGAATAT GGAATCCACT TCAAATTTTG AATGATTTTG GGACAGATGT GTTCAAGCCC

| 5 | TCCACCTATC CACCACTTTC TTACACTTTT GATCATATTA TTATAAAACC TTAATATACC | 1020 |
|----|---|------|
| | AAGGGTTTAG CCCGATTTAT CTTAATGATA AATCGGGCAT TTTTTTGTTT TTTAAAATAA | 1080 |
| | ATTTCACAAA TTTTGTATAA ATAGTGGTGG ATAGTGGGGA GATGTGGTAA ATTATATATA | 1140 |
| 10 | AGGTGAGGTG ATAAAAAATG TTCATGGGAG AATACGATCA TCAATTAGAT ACAAAAGGAC | 1200 |
| 9 | GTATGATTAT ACCGTCCAAG TTTCGTTATG ACTTAAATGA GCGTTTTATT ATCACAAGAG | 1260 |
| | GCCTTGATAA ATGTTTATTC GGTTACACTC TAGACGAATG GCAACAGATT GAAGAGAAAA | 1320 |
| 15 | TGAAAACCTT ACCTATGACA AAAAAAGACG CACGTAAGTT TATGCGTATG TTCTTCTCTG | 1380 |
| | GTGCTGTTGA AGTAGAACTT GATAAGCAAG GGCGTATTAA CATCCCTCAA AACTTGAGGA | 1440 |
| | AATACGCTAA TTTAACTAAA GAATGTACAG TAATCGGTGT TTCAAATCGT ATTGAGATTT | 1500 |
| 20 | GGGATAGAGA AACTTGGAAT GATTTCTATG AAGAATCTGA AGAAAGTTTC GAAGATATTG | 1560 |
| - | CTGAAGATTT AATAGATTTT GATTTTTAAA ATGGAGGAAT TGAAGEGTTT CATCATATCA | 1620 |
| 25 | GCGTTATGTT AAACGAAACC ATTGATTATT TAAATGTAAA AGAAAATGGT GTGTACATTG | 1680 |
| - | ACTGTACGCT AGGTGGAGCG GGACANGCCC TTTATTTACT AAATCAATTA AATGACGACG | 1740 |
| | GAAGATTAAT AGCAATCGAT CAAGACCAAA CTGCAATTGA TAATGCTAAA nGGGTATTAA | 1800 |
| 30 | AGGATCATTT GCATAAAnG | 1819 |
| | (2) INFORMATION FOR SEQ ID NO: 671: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 609 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
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| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671: | |
| | ACCAATTATT GGACAGGAAT TAGCAAAAAA TGCAATGCTT GCATTAATCT ATGCATCGAT | 60 |
| 45 | AGGTATCATC ATCTATGTAT CATTACGATT TGAATGGCGC ATGGGTCTTT CATCTGTATT | 120 |
| | GGCATTATTA CATGATGTAT TCATTATAGT AGCGATTTTC AGTTTATTTA GAATTGAAGT | 180 |
| | AGATTTAACA TTTATCGCCG CTGTATTAAC AATTGTCGGT TATTCAATTA ATGATACAAT | 240 |
| 50 | CGTAACGTTT GACCGTGTAC GTGAAAACTT ACAAAAGGTT AAAGTGATTA CGACAACAGA | 300 |
| | ACAAATTGAT GATATCGTTA ATAGATCAAT tAGACAGACA ATGACACGTT CAATTAATAC | 360 |
| | AGTATTAACA CTTATTGTAG TAGTAGTTCC TATACTATTC TTCCCTCCTC CTACCATA | |

| TGCCGTTCCG | CTATGGGGAA | TAATGAAAAA | ACGTCAGTTG | AAAAAATCGC | CGAAACACAA | 540 |
|------------|------------|------------|------------|------------|------------|-----|
| ATTAGTTGTA | TATAAAgAAA | AGAAATCGAA | CGATGAAAAG | ATTTTAGTTT | AAAAtGaATT | 600 |
| AAGCGGTAT | | | | | | 609 |

(2) INFORMATION FOR SEQ ID NO: 672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672:

| CTTAAAACAG | CAATTTGAAC | GTTTACAAAA | TGAACAAATC | TTTGTTTATG | TTTGTCATGG | 60 |
|------------|------------|------------|------------|------------|------------|------|
| TAATCACGAT | CCTTTATCAT | CAAAGATTTC | ATCÁAACTGG | CCAGATAATG | Tentigrati | 120 |
| TTCAAATAAA | GTTGAGACGT | ATGAAGCAAT | TACTAAATCT | GGTGAAACAA | TTTATATTCA | 180 |
| CGGATTTAGT | TATGAAAATA | GAGCAAGTTA | TGAGAACAAG | ATTGATGAAT | ATCCATCAAG | 240 |
| TCAAGGCCAA | AAAGGCATAC | ATATTGGTGT | CTTGCATGGT | ACGTATAGTA | AATCTTCAGT | 300 |
| TAACGAAAGA | TATACCGAGT | TCATTTTAGA | AGATTTAAAC | AGTAAATTGT | ATCATTATTG | 360 |
| GGCTTTAGGT | CATATACATG | AACGTCAACA | ATTAAGTGAT | ATGCCTGTAA | TTAACTATTC | 420 |
| AGGTAATATT | CAAGGTAGAC | ATTTTAATGA | GCAaGGTGAA | aAAGGTTGCT | TATTAATCGm | 480 |
| GGGTGACCAC | TTAAAATTAA | AGACTAAATT | TTATCCTACA | CAGTATATTA | GATTTGAAGA | 5.40 |
| AGCAACTATT | GAAACGGATA | AGACATCTAA | GCAAGGTTTA | TACGAGGTCÁ | TTCAAAACTT | 600 |
| TAAAGAACAA | GTGAGAGAAG | AAGGAAAAGC | CTTTTATCGT | TTAACGCTTG | TTATTAATAG | 660 |
| TGAGACATTA | ATTTCACCTC | AAGATTTATT | ACAAGTTGAA | GAAATGATTA | CAGATTATGA | 720 |
| AGAAAACGAA | AATCAATTTG | TATATATTGA | TGAGTTAAAA | ATACAATATG | CACAAAATGA | 780 |
| TGAGTCACCT | TTAGTTAATG | AATTTTCAGC | GGAATTÄTTA | GTCGATCAAA | CTGTTTTTGA | 840 |
| TAAAGCGATG | TCAGATTTAT | ATTTAAATCC | AAGGGCATCT | AAGTTCCTAG | ACGATTATGG | 900 |
| AACATTCGAC | CATACAGCAT | TAGTTAATCG | TGCTGAAGAA | ATATTAAAAG | CTGAAATGAG | 960 |
| AGGTGAACAA | AATGATAATT | AAATCACTTG | AAATTTATGG | TTACGGTCAA | TTTGTTCAaC | 1020 |
| GTAAAATTGa | ATTTAATAAA | AACYTCaCTG | AAATTTTTGG | TGAAAATGAA | GCGGGTAAAT | 1080 |
| CGACGATTCA | AGCATTCATC | CATTCGATAT | TATTTGGATT | TCCAACTAAA | AAGTCTAAAG | 1140 |
| AGCCAAGACT | AGAACCACGT | CTAGGTAACC | AATACGGTGG | TAAATTAGTA | CTTATTCTTG | 1200 |

| | TATATTTACC | TAATGGTGCT | GTGCGTGATG | ATGCTTGGTT | ACAAAAGAAA | CTTAATTATA | 1320 |
|---------|--|--------------|------------|-------------|------------|------------|------|
| | TTTCTAAAAA | GACATATCAA | GGTATCTTTT | CATTTGATGT | ACTAGGGCTT | CAAGACATTC | 1380 |
| 5 | ATAGAAATCT | ' AAATGAAAAA | CAATTGCAAG | ATTATTTATT | ACAAGCmGGG | GCTTTAGGAT | 1440 |
| | | | • | | | ТТАТАТААА | 1500 |
| 10 | aATCAGGTAA | AAATCCGATC | ATTAATCAAC | AAATTGAGCA | ATTAAAACAA | CTAGAAAGTC | 1560 |
| | | | • | | | GATCGAGATA | 1620 |
| a say y | | 4 4 | 1 | | -1.1 0 - | AAAATGCATG | 1680 |
| 15 | | | | | | TCTCTAGAAC | 1740 |
| ŗ | | | | CAGAAAAAGG | * | | 1800 |
| | CACGAGCGCA | TAAGCAATCG | TTAGWAAGAG | ATATTGGTTT | AAGAAATGAG | CGTTTAGCTC | 1860 |
| 20 | AACTTAAAGA | AGAAGCGACT | CAATTAGAGC | CAGTTAAACA | ATCTGATATT | GACGCCTTCA | 1920 |
| | TTAGTTTGAA | TCAACAAGAA | AATGAAATTA | AAAATAAAGA | ATTTGAACTT | ACTGCAATCG | 1980 |
| | AAAAGGATAT | TGCGAATAAA | CAACGTGATA | AAGATGAATT | GCAATCAAAT | ATTGGTTGGT | 2040 |
| 25 | CTGAAACGCA | TCATGACGTA | GATAGTTCAG | AGGCAATGAA | AAGTTATGTC | AGTGAGCAAA | 2100 |
| | TCAAGAATAA | ACAAGAACAA | GCTGCATACA | TTAAACAATT. | AGAACGTAGT | TTAGAAGAAA | 2160 |
| 30 | ATAAAATCGA | AGATAATGCG | GTTCATAGCG | AACTAGATTC | TGTTGAAGAA | AAATAGTTCC | 2220 |
| , | TG | | | | | | 2222 |
| | and the second of the second o | | | | | • | |

(2) INFORMATION FOR SEQ ID NO: 673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673:

| TTGCAGGT | AT CATTTTTTA | ATGCCATATG | GATTATGTTT | TCTACCGTTT | TATAAGCAAA | . , 60 |
|----------|---------------|------------|------------|------------|------------|--------|
| AAAAGAAA | AA ACAGACATTT | AAAAAATACA | TGGTTTACAC | TACGATTGGT | TTGTCAATTT | 120 |
| GTCTAGGC | TT ATCTCTAGTT | TTGGTTCACA | CTACGAAAAT | TTATATGGAC | GAAGGTGGCG | 180 |
| TAAGATAC | TA TTACGGTAGT | TTTGTAATGA | AACAAGCGGG | CGGTTATGCT | TATTTAGCTT | 240 |
| TAGCGGTA | CT TTCAACGTTG | TTAATTGTTG | CGAAAAAAGC | TACAAATAAA | AATAAAGAAA | 300 |
| TCGAAACC | GT CGACAATACA | AATATAACGG | AAAGATAATT | AAGGGAGTGC | TCATTCAGGA | 360 |

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(2) INFORMATION FOR SEQ ID NO: 674:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 927 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|--|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674: | |
| | CCACTTTGTG GATTTTCTTT ATATTCTCCA CGCTTGLACT ACAACTTCTT TCGTTTCTGT | 60 |
| 15 | TTCATCACCG ACTGCCGCAT TCGTTAGCAC ATGTAATAAC TCTTTTGCGG TTAATACATT | 120 |
| | CTCATCTATA ATCTTATCTT TTTGTTCTTG TATATATTGC TTGATGTGCG GCTTTTTCAA | 180 |
| | TAACCTACAC GCTGTCACAT GTGCGCTATT TGCGTTATAT CCTGYTTTTA TGGCACTTTG | 240 |
| 20 | TGTTACATTC AGTGTTCTAA TATACTCATT CACAAAACGT GCTTGCTTTG CAGTTAACTC | 300 |
| | ACTCATTTTA TCACCCCCAC AATTTTATCT AATATGGTTT CATACCATAA TATTACAGAT | 360 |
| | TGTTCTGAAC AATCTAAGGC ACTACTAATA TCTTGATAAC TAAGTCCTTG TATAAGGGAG | 420 |
| 25 | TCAAAAATAT AAAACTCTTT ATCGGTCGCT AATCTGTCAA CAATCATTTC TATGTGATTC | 480 |
| | TITATAATAT GATCATTGAC ATTATCGTCT GTCATCAATT CGTCAGAATC TTCATCACCT | 540 |
| 30 | ATTAAAAAGA AATCATCAGT ATTTATTTCA TCATCGCCCC GTTAACTAGC TTTGAAGTCT | 600 |
| | TTAGCACACT TGCATATACC GGCTGTCGTG CTGGCKAGAT ACTAGCATTG AAGTGGTCTG | 660 |
| | ATATTGATTT TGAAAACAAC ACGATTAGTA TTACTAAAAC ATATTACAAT CCAAATAATA | 720 |
| 35 | ACAAGAAGAA ATATCAGATA CTTCCCCCTA AAACTGAAAG TTCTATCGGT AAGATTTCCG | 780 |
| | TTGACCCAAA TGTAATAAAG GLGLTGCGLG ATTATAAGAT AAACGTTCAA AATAATTGGA | 840 |
| | AAAACGAATT ATATAATGAT AACCATTGTA ATGAAAAAAC TATCAATGTG GATACAAACC | 900 |
| 40 | ATTATGTCAC GTACCAGCAT ACTCAAA | 927 |
| | (2) INFORMATION FOR SEQ ID NO: 675: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1100 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675: | |
| | GATGTTAANA TAAGTACATC ATTTTGACTC CCAAATATTG GCTTTAGACC TTGAAATGCT | 60 |
| 55 | | |

| 16 | CTCATAATGG | CATCAGGTAC | cAGGGGTTGG | GaccAGGTGT | TAATAACAAC | GGTTGATGAT | | 180 |
|----|------------|------------|-------------|------------|------------|------------|-----|------|
| | AATACATTTA | TATGCCTCCT | ATAAATAAGA | TTTCACTATT | TTAGCAAATT | TTCTGAAAAT | | 240 |
| 5 | TTAAAAGCCT | AAAAAgtGAT | AACGCTATAT | TGTCGAACAA | ACGTTATCAC | TTAACGATTT | • | 300 |
| | TATTTGGCCT | GAATGATGGG | ATAGATTTTT | ATGTCCACAT | TATTTCTTAC | AGCATTTGAA | | 360 |
| 10 | ATCATGCAAT | TATTATCTGC | AATTGTTATC | AATTTTGGTA | ATCGCTTTTC | TAATTGTGCT | 4 | 420 |
| | ATTTGATCAC | TTGGAATTTG | AATTTGAGGA | TGGTGCACAA | TTTTTGACAT | ACTGAATTTT | | 480 |
| | CCGTTATTTA | AACAAGCTGT | TCCAATCGAT | TGTTGTkCAA | TTGAAATATC | TGTGAACTTT | | 540 |
| 15 | GCACGTTCAA | GAGTAGCTGC | TAATGAGATG | ATATAACATG | ATGAAGCGGC | TGATACTAAC | | 600 |
| | ATTTCATCGG | GATTTGTTCC | TATACCAACA | CCACCTAAAG | AAGCAGGTAT | AGAAATATTC | | 660 |
| | TCTGAAAGTA | TGTCGCCTTG | AACGTTTCCG | ACATTGTTAC | GACCACCTTG | CCAAGAAGTT | | 720 |
| 20 | TGGACTTTAA | AGTCATGTTG | ATGCAATTGC | TTTAACCTCC | AATATAATTG | TGATAGTTTA | | 780 |
| | ATTTTAGAAT | AGTTTATCAA | AGTTTAACAG | AAAGGTGACT | TATCAATGAC | TCTGAATAAA | | 840 |
| | CTGAAAGATG | AATTACAAAT | TGTTTCGCAC | CGTGGATTGC | CGAGTGATTT | TCCTGAAAAT | | 900 |
| 25 | ACAATGGTCG | GTTATCGAGA | GGTAATGGGG | CTCAATGTTG | CTATGTTAGA | AATAGATGTT | | 960 |
| | CATTTGACCA | AAGACCAACA | TTTTGTTGTG | ATACATGATG | AAACAATTGa | TAGAACATCG | . 1 | 020 |
| 30 | GaTGGtArGG | GGCGTAwTGc | TGaTTACACA. | TTATCGCAAT | TAAAATCATT | TGATTTTGGT | . 1 | 1080 |
| | AGTTATAAAG | ATGTTGCTTT | | | • | | 1 | 100 |
| | | | • | | | • | | |

(2) INFORMATION FOR SEQ ID NO: 676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676:

| ATTAATTTCA | TATGGAAATA | GTTGAACTAA | CTGCGCTGTA | TAAGCTTCAA | CAGTTTGATG | 60 |
|------------|------------|------------|------------|------------|------------|-----|
| AATTAACGAT | TGATCTTCAA | TATATCCGTA | GAACAAATCT | TCAGTACAAA | CTACTTTACC | 120 |
| TTTATCAGGT | TTAATTGCAC | CTGCCAACAA | TTGACCTACC | AACGCTTTGG | AAGATTCAGG | 180 |
| TTCACCAATT | ATACCTAATG | CTTCTCCTTG | ATAAATATGT | AAACTAATAT | TGTTTAAATC | 240 |
| GATATCTTCA | GCATCATATC | CAAAAGGTAA | ATACCATTTC | TTATTCTGTT | TATTCCTATA | 300 |
| GTAGTGTGTT | ACTTTTAGTA | ACTTTAÄÄAC | AATTGAACTT | CCCATCTATT | TTCATCCTTC | 360 |

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CCCCACGCAA AAATACCTTT TAATCTTnCT ACTTTAAAAT

| | 127 INFORMATION FOR SEQ ID NO: 677: | |
|------------|--|------|
| 5 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1451 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677: | |
| | GTCAAGTTTT CGGCTAGATT TTAAACGCTC ATCACTATGT AGAATGAAAC TTTCGAAAAA | 60 |
| 15 | • | |
| | CTGTAAATCA TCATAACCTT TTACATAAAC ATAACCTTCG CCACCAATTG CTTGAATTAA | 120 |
| | ACATTGGGCG GCCATTTGAA TTTCTAAAGA TTGTTTTTCT AGCCTATTAA AGATACCTAT | 180 |
| 20 | TAGTTGTGT TTTAAGATTT TTGACATCTT TATCCTCCAA TCTACTTATA AAATATTGTA | 240 |
| | ATTAATGACT ACATATTATG CAACGGCTTA AATTGTATAA AAATGTATAC GTTTGCATTT | 300 |
| 25 | AGTATAACTA TCGCATTTTT CAAAAAATAC ACATTTAATC TGCAGTATTT CAATGCATTG | 360 |
| | ACGCTATTTT TTTGATATAA TTACTTTGAA AAATACGTGC GTAAGCACTC AAGGAGGAAC | 420 |
| | TTTCATGCCT TTAGTTTCAA TGAAAGAAAT GTTAATTGAT GCAAAAGAAA ATGGTTATGC | 480 |
| 3 <i>0</i> | GGTAGGTCAA TACAATATTA ATAACCTAGA ATTCACTCAA GCAATTTTAG AAGCGTCACA | 540 |
| | AGAAGAAAAT GCACCTGTAA TTTTAGGTGT TTCTGAAGGT GCTGCTCGTT ACATGAGCGG | 600 |
| | TTTCTACACA ATTGTTAAAA TGGTTGAAGG GTTAATGCAT GACTTAAACA TCACTATTCC | 660 |
| 35 | TGTAGCAATC CATTTAGACC ATGGTTCAAG CTTTGAAAAA TGTAAAGAAG CTATCGATGC | 720 |
| | TGGTTTCACA TCAGTAATGA TCGATGCTTC ACACAGCCCA TTCGAAGAAA ACGTAGCAAC | 780 |
| | AACTAAAAAA GTTGTTGAAT ACGCTCATGA AAAAGGTGTT TCTGTAGAAG CTGAATTAGG | 840 |
| 40 | TACTGTTGGT GGACAAGAAG ATGATGTTGT AGCAGACGGC ATCATTTATG CTGATCCTAA | 900 |
| | AGAATGTCAA GAACTAGTTG AAAAAACTGG TATTGATGCA TTAGCGCCAC ATLAGGTTCA | 960 |
| | GTTCATGGTC CATACAAAGG TGAACCAAAA TTAGGATTTA AAGAAATGGA AGAAATCGGT | 1020 |
| 45 | TTATCTACAG GTTTACCATT AGTATTACAC GGTGGTACTG GTATCCCGAC TAAAGATATC | 1080 |
| | CAAAAAGCAA TTCCATTTGG TACAGCTAAA ATTAACGTAA ACACTGAAAA CCAAATCGCT | 1140 |
| | TCAGCAAAAG CAGTTCGTGA CGTTTTAAAT AACGACAAAG AAGTTTACGA TCCTCGTAAA | |
| 50 | | 1200 |
| | TACTTAGGAC CTGCACGTGA AGCCATCAAA GAAACMGTTA AAGGLAAAAT TAAAGAGTTC | 1260 |
| | GGTACTTCTA ACCGCGCTAA ATAATTAATA TTTAGTCTTT AAGTTATTAA TAACGTAGGG | 1320 |

| | AATAAATAAA ACAGTTTGAT TTTAAAATGA AAGCGTAAAA ATGGTAAAAT ATATCAAAAT | 1440 |
|---------------|--|------|
| | TGATTGTGAT A | 1451 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 678: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 668 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | in the second of | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678: | - |
| | NGTATTGAAG CGGTTAAACA AACACCTAAT GCAACTGACG AAGAAAAGCA GGCTGCTGTT | 60 |
| | AATCAAATCA ATCAACTTAA AGATCAAGCA ATTAATCAAA TTAATCAAAA CCAAACAAAT | 120 |
| 20 | GATCAGGTAG ACACAACTAC AAATCAAGCG GTAAATGCTA TAGATAATGT TGAAGCTGAA | 180 |
| ~ · · · · · · | GTAGTAATTA AAACAAAGGC AATTGCAGAT ATTGAAAAAG CTGTTAAAGA AAAGCAACAG | 240 |
| | CAAATTGATA ATAGTCTTGA TTCAACAGAT AATGAGAAAG AAGTTGCTTC ACAAGCATTA | 300 |
| 25 | GCTAAAGAAA AAGAAAAAGC ACTTGCAGCT ATTGACCAAG CTCAAACGAA TAGTCAGGTG | 360 |
| | AATCAAGCAG CAACAAATGG TGTATCAGCG ATTAAAATTA TTCAACCTGA AACAAAAGTT | .420 |
| | AAACCAGCTG CACGTGAAAA AATCAATCAA AAAGCGAATG AATTACGTGC TAAGATTAAT | 480 |
| 30 | CAGGATAAAG AAGCAACAGC AGAAGAAAGA CAAGTAGCAC TAGATAAAAT CAATGAATTT | |
| ٠. | GTAAATCAAG CCATGACAGA TATTACGAAT AATAGAACAA ATCAACAAGT TGATGATACA | 600 |
| 35 | ACAGTCAGCG CTGATAGCET GCTTTAGTGA CGCCTGACCA TATTGTTAGA GCGCTGCTAG | 660 |
| | AGATGCGT | 668 |
| | (2) INFORMATION FOR SEQ ID NO: 679: | |
| 40 | (i) SEQUENCE CHARACTER CONTROL | |
| 40 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 1906 base pairs(B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | - |
| 45 | (D) TOPOLOGY: Timear | |
| | | ٠, |
| : | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679: | |
| 50 | GATCCAAATT TAAAAGGAAA AATAGCCTTT AACGAATTTA CGAAACAAAT TGAATGTTTA | 60 |
| | GGGAAAGTGC CATGGAATAC TAATTTTAAG ACACGTCAAT GGCAAGACGG TGATGATAGC | 120 |
| | AGTTTAAGAA GTTATATCGA AAAGATTTAT GACATACACC ATTCAGGTAA AACAAAAGAT | 180 |

| | ATCGTGGGAT | GGACATAAAC | GCCTTGAAAA | GTTATTTATC | AAATACTTAG | GTGTTGAAGA | 300 |
|----|-------------|-------------|-------------|------------|-------------|------------|------|
| | CcTGaAGTGA | ATAGAACAAC | TACCAAAAAA | GCATTGACTG | CTGGAATCGC | TAGAGTAATG | 360 |
| 5 | GAGCCTGGAT | GTAAATTTGA | CTATATGCTT | ACACTTTATG | GTCCTCAAGG | TGTAGGTAAA | 420 |
| | TCTGCTTTGC | TAAAAAAATT | AGGTGGTGCA | TGGTTTTCTG | ACAGTTTAGT | TTCTGTTACA | 480 |
| | GGTAAAGAAG | CTTATGAGGC | CTTACAAGGC | GTTTGGCTAA | TGGAAATGGC | AGAACTTGCA | 540 |
| 10 | GCTACAAGAA | AAGCTGAAGT | TGAAGCTATT | AAGCATTTCA | TATCTAAACA | AGTTGACCGA | 600 |
| | TTTCGTGTTG | CTTATGGGCA | TTATATTGAA | GATTTTCCAA | GGCAATGTAT | TTTCATTGGT | 660 |
| 15 | ACAACTAATA | AAGTTGATTT | CTTAAGAGAT | GAAACTGGTG | GAAGACGTTT | TTGGCCAATG | 720 |
| | ACTGTAAATC | CAGAGAGAGT | TGAAGTGAAC | TGGTCTAAAC | TAACCAAAGA | TGAGATTGAC | 780 |
| | CAAATTTGGG | CAGAAGCTAA | ACACTATTAT | GAACAAGGAG | AAGATTTATT | CCTTAACCCT | 840 |
| 20 | GAACTAGAAG | ÄAGAAATGCG | TTCAATACAA | AGCAAACATA | CTGAGGAATC | TCCATATACA | 900 |
| | GGCATTATTG | ATGAATATCT | TAACACACCm | ATTCCtAGCa | ATTGGGATGA | CTTAACTATC | 960 |
| | TTTGAACGAA | GACGATTTTA | TCaAGGTGAT | GTTGATATGT | TACCAACAGG | AAATGTaGAT | 1020 |
| ?5 | TACGTTAAAA | GAAATAAAGT | CTGTGCGCTT | GAAGTGTTTG | TTGAATGTTT | TGGTAAAGAT | 1080 |
| | AAGGGAGATA | GTAGAGGATC | TATGGAAATT | AGAAAGATTT | CAAACATCTT | AAGACAATTA | 1140 |
| | GACAATTGGT | CTGTATATGA | TGGTAATAAA | AGTGGGAAAA | TTCGATTTGG | AAAAGATTAT | 1200 |
| 30 | GGTGTACAGA | TAGCTTATGT | AAGAGATGAA | AGTTTAGAGG | ATTTAATATA | AGAAATATTG | 1260 |
| | AATAAATATG | CATTTTAGAG | TGTTGTATCA | GATGTTGCAT | CATTTTTTGA | GTGATGCAAC | 1320 |
| 35 | ACGGGAGTGT | AAAAAGTAAT | CGTAGGTGTT | GTATCATTTT | TGGTGATGCA | ACATTGATGC | 1380 |
| | AACAAATGAT | ACAACACCTC | TTTCCTTTCT | AGCTGTAGGG | TTCAACCCTG | TTTGTTTCCA | 1440 |
| • | ATGTTGCATC | AAATTCACTA | TAAAGTTTAA | AAAGTAGTGT | TAGGGAGTAA | AGGGGTATAG | 1500 |
| 10 | GGGTAACCCT | CTAACAGCTA | TTTTTAAAAG | TTTGGCAAGA | ATTGATACAA | CATCGGAACA | 1560 |
| | CAAATATAAA | TTTTGTATAC | AAGGTGAATA | AATGAAAGAA | TCGACATTAG | TTTATAAAAA | 1620 |
| | agtgaaagag | ATAACAAAGC | TAAACGGTTT | ATGTTTAAAA | TGGGTCGCAC | CTGGAACAAG | 1680 |
| 15 | AGGTGTGCCA | GATAGAATTA | TTATTATGCC | AGAAGGAAAA | ACATATTTTG | TAGAAATGAA | 1740 |
| | GCAAGAAAAA | GGAAAGTTGC | ATCCTTTACA | Araatatgtg | CATAGACAAT | TTGAAAATAG | 1800 |
| | AGaTCATAAA | GTATATGTGT | TATGGAATAA | AGAACAAGTA | àa tacttita | TCAGAWTGGT | 1860 |
| 50 | AGTGAACATT | TGGCGATTGA | CTTTCAAACC | ACATAGCTnT | CCAAAG | | 1906 |
| | (2) INFORMA | TION FOR SE | Q ID NO: 68 | O: | | | |

| 5 | (A) LENGTH: 948 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|-----------|--|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680: | |
| | | |
| 10 | AATTATTTGA ATAAATTAGC AATTAAAGAG TTGATTTGTC AGTTTAAGYA TTTGAGTGCA | 6 |
| | TTTGAAAAAG ATGTCATGTA TTTAATGTGT GAACAATATA AGCCGAGAGA AATTGCTCAA | 120 |
| | TTGATGCATG TAAAAGAGAA AGTGATTTAT AATGCCATAC AACGATGTTA AAATAAAATA | 180 |
| 15 | AAACGTTATT TCAAAATGAT TTGAAAAGCG CCTTAGGACG TGAATTGAAT | 240 |
| | TACTTACTGA TGGTTTGACA TTTGTTATAA ATTTTATGTA TAGTATACTG GTATTATAAT | 300 |
| • | GAATAAAGGT GAATTATTGT GAGAAAAATA CCTTTAAATT GTGAAGCTTG TGGCAATAGA | 360 |
| 20 | AATTATAATG TTCCTAAGCA AGAAGGCTCG GCAACAAGAT TAACCTTAAA GAAATATTGT | 420 |
| • | CCAAAATGTA ACGCGCACAC AATTCATAAA GAATCGAAAT AAATACATTC GAAATAATAC | 480 |
| 25 | TITGATAATA TGTTCAAAGG ATTTGGAGGT TGAGCAGATG GCTAAAAAAG AAAGTTTCTT | |
| 23 | TAAAGGCGTT AAGTCTGAAA TGGAAAAAAC AAGTTGGCCG ACGAAAGAAG AGCTATTTAA | 540 |
| | ATATACTGTA ATTGTAGTTT CTACTGTTAT ATTCTTCTTA GTCTTTTTCT ATGCCTTAGA | 600 |
| 30 | TTTAGGAATT ACAGCATTGA AAAATTTATT ATTTGGTTAG AGGAGTGAAG ACATGTCTGA | 660 |
| | | 720 |
| | AGAAGTTGGC GCAAAGCLTG GTATGCAGTG CATACATATT CTGGATATGA AAATAAAGTT | 780 |
| 35 | AAAAAGAATT TAGAAAAAAG AGTAGAATCT ATGAATATGA CTGAACAAAT CTTTAGAGTA | 840 |
| | GTCATACCGG AAGGAAGAAG GAAACCTCCA GTAANAAGNT GGCCAAGCCT AAAACCGCCT | 900 |
| | GTTAAAAAA ACCATTCCCC TGGGnTANGG TTTTAAGTGG GAATTTAA | 948 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 681: | |
| 45 · | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 863 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681: | |
| 50 | ACANATAATA ACAAAGCGCT TGCTAGTACC TCTTAAAAAG ATGATGCTAG CAAGCGCTTk | 60 |
| | TCTATACTAT ATATTATTT TCTAAAATTT TAACACCCTC TTGAGTGCCT ACAATAACTT | 120 |
| | GATCTGCCAT ATCTAAGAAG TATCCTGTCT CAAACACACC TGTCAGATGA ATTAAATACT | |
| <i>65</i> | The state of the s | 180 |

| | TATCAGTTAT AAATGCGACA TCTTCGTTTA CACGACGTTC TACTTTTATA TCAGCGTATG | 300 |
|------------|---|-----|
| | ATTCAATTTT ACGTAATATG TGATACCAGT TAAATTTATC CACCTCTACT GGTAACTTAA | 360 |
| 5 | ACGTCTCACC TAAGTATTGA ACTATTTTCG TTTCATCGAC AACCACAACA AAACGCGATG | 420 |
| | CCATTTCATC TATAACTTTC TCTCTGAACA GCGCACCACC GCCACCTTTA ATTATATTTA | 480 |
| | AAGATGGATC TACTTCATCA GCACCATCAA TTGCTAAGTC GATATGATCA ACATCATTGA | 540 |
| 10 | TTTCACATAT TTTAATACCT AATTCTTTTG CTAAAAATGC AATTTTATTA GAAGTGCATA | 600 |
| | CACCTGTAAT ATTGTAACCA CGTTCTTTAA TTAGTTGCGC CATTTGAGGT AAGAGTAATT | 660 |
| 15 | CCATTGTACT TCCTGTACCA ATTCCCAGCG TCATGTCACC ATTGATTKGA CTTAAAACAT | 720 |
| | CATTTAATGT CATTAACTTG AGTGCTTTGA CATCTTTCAT GAAGGTAGCC TCCCATATTT | 780 |
| | ALGTANTCTA TTCANTTCAT ATTTTACATG ACTCGTATAA ATTAACATAC CCTTATnGCT | 840 |
| 20 | AACCATTTGT GTTAAACATA TCG | 863 |
| | (2) INFORMATION FOR SEQ ID NO: 682: | |
| ? 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 480 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682: | |
| | TTCATTTTTG TTGTTCAGCA ATTTTGGTCC GAATTTCAAT TCATCAGATG ATAGCTCTAT | 60 |
| 35 | TAATTCTGTA GAATATTCTG CEACAACAAT TTCATAAATA TGGCCTTTTT CTTCCATTAT | 120 |
| | TATTTCATCA ATTATTTCAT AATTCAATTG TTGTAATGTT TGTCTTAAAT TTTCAGTTTG | 180 |
| | GATATTACTT TGTAAAATCA ACCTTGGATG TTGACTTAAC TTATCTTGCC CATCTTTAA | 240 |
| i o | AATTTTAGCA ATAAGTGGTC CGCCCATACC ACAAATTGTG ATATTATCGA TTACGTCCTC | 300 |
| | AGGTTGAATA ACACTTAAGC CATCCCCTAA ACGTACATCA ATTCTATCTA CTAATTGGTT | 360 |
| | TGCAGCTACA TTTTTCACAG CAGCTTGAAA AGGGCCTTGA ATAACTTCTC CAGCAATACC | 420 |
| 15 | GATTCGCATA AATGGTTTTG AATTGCATAG ATTGGCAAAT AAGCATGATC TGAGCCAATA | 480 |
| | (2) INFORMATION FOR SEQ ID NO: 683: | |
| 6 0 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 689 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (XI) SEQUENCE DESCRIPTION: SEQ ID No: 883. | | | | | | | | |
|-----|--|------|--|--|--|--|--|--|--|
| | CTGCAAAAA TATTGGTATA ATAAGAGGGA ACAGTGAA CAAGTTAATA ACTTGTGGAT | 60 | | | | | | | |
| 5 | AACTGGAAAG TTGATAACAA TTTGGAGGAC CAAACGACAT GAAAATCACC ATTTTAGCTG | 120 | | | | | | | |
| | TAGGGAAACT AAAAGAGAAA TATTGGAAGC AAGCCATAGC AGAATATGAA AAACGTTTAG | 180 | | | | | | | |
| | GCCCATACAC CAAGATAGAC ATCATAGAAG TTCCAGACGA AAAAGCACCA GAAAATATGA | 240 | | | | | | | |
| 10 | GTGACAAAGA AATTGAGCAA GTAAAAGAAA AAGAAGGCCA ACGAATACTA GCCAAAATCa | 300 | | | | | | | |
| *1) | AACCACAATC CACAGTCATT ACATTAGAAA TACAAGGAAA GATGCTATCT TCCGAAGTTT | 360 | | | | | | | |
| 15 | GGCCCAAGAA TTGAACCAAC GCATGACCCA AGGGCAAAGC GACTTTGTTT TCGTCATTGG | 420 | | | | | | | |
| 15 | CGGATCAAAC GGCCTGCACA AGGACGTCTT ACAACGCATA ACTACGCACT ATCATTCAGC | 480 | | | | | | | |
| | AAAATGACAT TCCCACATCA AATGATGCGG GTTGTGTTAA TTGAACAAGT GTACAGAGCA | 540 | | | | | | | |
| 20 | TTTAAGATTA TGCGAGGAGA GGCGTATCAT AAGTAAAACT AAAAAATTCT GTATGAGGAG | 600 | | | | | | | |
| | ATAATAATTT GGaGGGTGTT AAATGGKGGa CATTAAATCC mCGTTCATTC mATATATAAG | _660 | | | | | | | |
| | ATATATCACG GTAATTGCGC ATATAACTT | 689 | | | | | | | |
| 25 | (2) INFORMATION FOR SEQ ID NO: 684: | | | | | | | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 858 base pairs | | | | | | | | |
| 30 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | | | | | | | |
| | (D) TOPOLOGY: linear | | | | | | | | |
| | | | | | | | | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684: | | | | | | | | |
| • | TTATTAAATT GGTATGTGTT CATTATACAT ATGACAAATA TGAATGTAAA CCGATAATTT | 60 | | | | | | | |
| | AGATTTTTTG GAATAACCTG AAAATTCAAG TTATAGCGTT GCTTATATTT TAAAAGGTGG | 120 | | | | | | | |
| 40 | TGATAATGAG ACTTTTTGAA AAATAAAATT CAAAATACTT ATAGCATAAT CAATATGCAC | 180 | | | | | | | |
| | ATTAAATAAA TGTACTCTTT TAATGCGTTG ATAACTGTAT TTGTAATTTA GAGAAGGGGT | 240 | | | | | | | |
| | GTTCACTATG CTGATGTGTT AAAAAATAAA ATAAAAAGGA CACCTCGATG CTATAAATAT | 300 | | | | | | | |
| 45 | TAGCATCGAG ACGCCCAGTT AATGTCTATT AAATTGAATA TAGTCTCGGA CATGAATCAA | 360 | | | | | | | |
| | TOGGGTTAGGG COTTONATOT TATATTGACA GTAGTTGACT GAATGAAAAT GACTTTGTAG | 420 | | | | | | | |

CTAGCTTTTT TCAATCCTTG TCGGTGCAAC ACATAGAGAA ATTGGATTCC TAATTTCTAC

AAACAATACA AGTTGCGGAA TAAGTCCCAA TATAGAAGGT GACAGTAAGC CAACTTACAA

TAATGTGCAA GTTGGTCGGG CCTCAATACA GAGATTTTCG AAAAGAAATT CTACATATTA

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| GCCACCTTGT | TTATTTAAAT | CGATAACACG | GTTTGCGATT | GTATTGATAA | ATTCAAAGTC | 720 |
|------------|------------|------------|------------|------------|------------|-----|
| ATATGAAGTA | AAGATAATAG | AACCTTTGAA | TGATTTAAGT | CCATCATTAA | CAGCAGTAAT | 780 |
| ACTTTCTAAG | TCTAAGGGTT | GTGGGTCATC | AAGTAAAAGA | CGTTGCCCTG | ATAACATCAT | 840 |
| TTACTAGCAn | CACGACTT | | | | | 858 |

(2) INFORMATION FOR SEQ ID NO: 685:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685:

TTAGTATTTT CAGGNTGGAA ATTGATGTTT GAAATTCACT GAAATGGGCC AGAACCTGAA 60 ATGAAACTTT ACCAACAATT TGGtCTTCAT CAATGAGGCC AAACGCACGG CTATCTTTAC 120 TTACTTCACG ATTATCTCCA AGCACTAAAT ATTTACCTTT TGGAATGACA TTTGATTTAG 180 GATTCGCATT CGGTAAATCT TTAACTTGGA AAGTCCCAGT AATGTAATCA CCTTGTTTAT 240 GTTTTAAATT GTAGTTTAAA TATGGTTCAT CITGTTTTTT ACCATTGACA TATAATGTAT 300 CATTITIGTA TICTACTITA TCACCAGGAA CACCGATGAC ACGITTAACA TAGTCATCAT 360 TTTTGTTTGC ATGGAAGACA ACTACATTAC CTTTTTCCAA ACCACCTGTT TTATATCCAA 420 CAATGTTTAC AGCTACTCGC TCGCCATCTT TCAAAGTTGG ATCCATTGAT TCACCTTTAA 480 TTGTATATGG CGTAACAATA AATTTACCTA CTATAAATAA AATGACAAAA GCGACTGCAA 540 TTGAAATAAT CCATTCCAAT ATTTCTTTTT TCAATTTTGA CACCTCTTTT TAAGATTTGA 600 ACTGAACAGT CCATTTTGAA AAAGGATAGT ATCGTAAACL AACATTACCA ATAATALCCT 660 TTTTATCGAT TAAACCAAAT TGTCTTGAAT CGTGCTTGTk ATTATCTTGA TCATTTAGCA 720 CAACAAAATT GTTTGGCGGA ATAATATCAC CATCTAATTC TTTAAAATTG CGCAAACTAA 780 AATCTTTAAT TITTCTGTTC TTGGCATAAG ATGCGTCAAC CGGTCGGTCA TCACGGTATA 840 ATTGTCCCTG ACGAAACGCC ATTGATTGAC CAGGTTTGGC AATAATTCGA CTAGTATATA 900 TCTCGTTACC ACGCCTATAT GTAATGATAT CACCATTATT CAATTGATTA AATGTAACTT 960 TAATTTIATT TACAATAACA CGATCCCCTT TGTTAAGGGT TGGTGACATA TCATTATTCG 1020 GAATGACATG ACCAACTATT ACAAAAGTTT GTACGAACAG TACAATGATA ATAGCAAGTA 1080 TCAATGAAAT CAAATATTTT ACAACTTTTT TCACGATGTC ACTCCTTTTT CGATCCCATA 1140

| | AAAGTTA | | ~ | | | , | 1747 |
|----|------------|------------|------------|------------|------------|------------|------|
| | TGATGAAACG | ACAAATCATC | AATCCCTTTC | TTTGGTTGAA | GATAATTATT | CTTACATTAT | 1740 |
| 15 | AACAATATAA | ATCCAGGTAA | ATAACCAAAC | TGTCGAAATA | TCTCAAACCA | TTCTTCTACT | 1680 |
| | TGAATGTTAA | TTAAAATATA | GAGTGCTAAA | GGAAATACTG | GAATTATAGC | TCTAATATAT | 1620 |
| 10 | AATGTTCCAG | AAATTAATCC | AAGCCAACTA | ATCAATATAC | CTAAAATAGG | TCCATAAGCT | 1560 |
| | TGTTTAATTC | GCTGCATCCT | CTCAGTGTTC | ACCAATCGTT | TACAGATCAA | ATAGACTGTA | 1500 |
| | AACAATGGGA | TTAATCCTTG | GCGATCAATA | AAACTAATCA | AGCGTTGAAC | AGCAGTACGT | 1440 |
| 5 | GATAGACTCG | CTACAAAATT | TATTAATGTA | TTTGGCGTAA | AAGGAAAACA | AAGTAAAATA | 1380 |
| | ATTGTTGAAA | CTAACTTTGA | TGATGCCAAA | ACAATGAAAT | AATATTTAGG | TCTAATATGA | 1320 |
| | ATCCCTCTTA | AAGGATGCGT | TAAAATTGTA | GTAATTTCCT | TACCTAAATA | ACCTAAAATA | 1260 |

(2) INFORMATION FOR SEQ ID NO: 686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 686:

| CGTAAAGATT ACTATTTAGG | AGGGTGACTA | TGAAAAAGAA | ATTAGGTATG | TTACTTCTTG | 60 |
|-----------------------|------------|------------|------------|------------|-----|
| TACCAGCCGT AACTTTATCA | TTAGCCGCAT | GTGGGAATGA | TGATGGAAAA | GATAAAGATG | 120 |
| GCAAGGTAAC AATTWAACGa | CaGTTaTCCm | TTGCAATCAT | TTgCAGAGCA | AATTGGTGGA | 180 |
| AAACACGTGA AGGTATCATC | AATCTATCCA | GCAGGGACAG | ATTTACATAG | CTATGAACCA | 240 |
| ACACAAAAAG ATATATTAAG | TGCAAGCAAG | TCAGACTTGT | TTATGTATAC | AGGGGATAAT | 300 |
| TTAGATCCGG TTGCTAAGAA | AGTTGCATCT | ACTATCAAAG | ATAAAGATAA | AAAACTGTCT | 360 |
| TTAGAGGATA AATTAGATAA | AGCAAAGCTT | TTAACTGATC | AACACGAGCA | TGGTGAAGAG | 420 |
| CATGAACATG AGGGACATGA | TCATGAGAAA | GAAGAACATC | ATCATCATCA | TGGTGGATAT | 480 |
| GATCCACACG TATGGTTAGA | TCCTAAAATT | AACCAAACTT | TCGCTAAAGA | AATTAAAGAT | 540 |
| GAATTAGTGA AAAAAGATCO | AAAACATAAA | GATGACTATG | AGAAAAACTA | CnaAAATTAA | 600 |
| ACGACGATCT TAAGAAAATT | GATAACGATA | TGAAGCAAGT | TACAA | | 645 |

(2) INFORMATION FOR SEQ ID NO: 687:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 956 base pairs

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(C) STRANDEDNESS: double (D) TOPOLOGY: linear

| 3 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687: | |
|--------------|--|-----|
| | TTTGTTACTG CTTCTAAAAT AATATCCTTT AATTGTTTAA CATGTTGGAT TGTCATATGA | 60 |
| 10 | GGTGATGGTA CATTAAAAGG ATTTAATTCA TCTATTTGTG CATATTGATT TATGACATCT | 120 |
| | TGATGCATTG AAATAGGGTT GATATCATTT GTTACTACTT TATTAGATTG GTCTTGTGAC | 180 |
| | ATACTAATGG TGCCACCAGT ATGAATAACA AGTAGATGTT TCATATATTT CCTCCTATAT | 240 |
| 15 | TTAATTTACC TAATTATGAT AAAATATTAT TCATAAAACG ACAAGGAAGG GAAATGACGC | 300 |
| | ATGAAAGCCA TTAATATTGC ATTAGATGGT CCAGCTGCTG CCGGAAAAAG TACAATTGCG | 360 |
| | AAACGTGTAG CCAGCGAACT ATCAATGATT TATGTCGATA CAGGAGCAAT GTATCGTGCA | 420 |
| 20 | TTAACATACA AATATTLAAA ATTAAACAAA ACTGAGGACT TTGCAAAACT AGTTGACCAA | 480 |
| | ACAACATTAG ATTTAACTTA TAAAGCAGAT AAAGGTCAAT GTGTCATTTT AGATAACGAA | 540 |
| 25 | GATGTAACAG ACTITITAAG AAATAATGAT GTGACGCAAC ATGTTTCATA CGTTGCATCT | 600 |
| | AAAGAGCCAG TACGTTCATT CGCCGTTAAA AAACAAAAAG AGTTAGCTGC AGAAAAAGGT | 660 |
| | ATCGTAATGG ATGGTCGCGA TATCGGAACT GTAGTGCTAC CAGATGCAGA TTTAAAAGTA | 720 |
| 30 | TATATGATTG CATCAGTTGA AGAGCGAGCA GAAAGAAGAT ATAAAGATAA TCAATTAAGA | 780 |
| | GGTATCGAAT CAAATTTTGA AGATTTAAAA CGTGATATTG AAGCTCGTGA TCAATATGAC | 840 |
| | ATGAACCGTG AAATATCACC ATTAAGAAAA GCAGATGATG CAGTGACATT AGATACGACm | 900 |
| <i>35</i> ′- | GGCMAGTCGA TTGAAGAAGT TACTGACGAN ATTTTAGCGA TGGTGAGTNC AATTNA | 956 |
| | (2) INFORMATION FOR SEQ ID NO: 688: | 4 |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1166 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | • |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688: | |
| | AAAAGGGAGG AAAGAGAACA GTTAAATATG AATACAAAAT AATTTTGTTT TCGGACAGCA | 60 |
| 50 | GGGGTATTAG ACGCGATTGA CAATGTCTGT TIAATTAAAC GTAATGTTTA TTTAAGCGAT | 120 |
| | GAATATTAGG TGAAAAGTTT TTGAATTTGA ATGTAATTGA GGTTTATTGA TTAGACATTT | 180 |
| | TATTCAATTC CCTCTTATTA TATAAATCTA AAAATAACAC CACATCCCCC AACATCTCCC | 240 |

| • . • | TAATGCGGAA TGGTTTTTT ATTTTCCGCT AATTGAAATA AAAATGACGT TTTAA | TATAT 36 | 0 |
|--------------|--|---|---------|
| | TATGGGCTAG GTGGTTTGTA AGAAAGGGTT AGTTATTAAT GTTTTATGAA TTAAG | GAAAT 42 | 0 |
| 5 | TTGAGTTTAA GGTTTAATCA ATTGTGATTT TGTTGATGAA GCGTTTAGTT AGAGT | ATTTT 48 | 0 |
| | CGCCACCACT AGTTACTCCT TCTCCCACTT TACCCGAGAC TGGAGAAGAG CTATC | IGAAG 54 | 0 |
| | AATAAATAGA TACTTTTGG CCATTTTGTA GTAAACCAAG ACCTTTTAAC TKCTC | GGTTA 60 | 0 |
| 10 | GAGAATTCCA TGTATTTTTA GCATCTAGCT TTTTGTTAAA GTCAYCGTAG ACATT | TTCCT 660 | o |
| • | TAGTTAAATC AATTIGTTTT AATCCTTTAA AGTCTATAGA TTGTGTTAGA TGGCC | rccat 72 | 0 |
| 15 | CATCATTIC: AGGAGCAGAA ACGCIGCIAG AATAICCAIT GCITAAIAAA TAAGI | AACGT 78 | 0 |
| | TGATTGTTTC GTACTCGTTA CTTAAAATAA TATCAGAATC ATGTAAGAAT CTTTA | ACTTT 84 | 0 |
| | TTTCCATAAT TGACCATCTG TCATTTTTC TTCTGCTTTA GCCGTTTTAA CAACT | | |
| 20 | TGTATCTAAT CCTAAGTATG AAGAATGTAA GCCTGTTCCT AATGTTGTTA ATACT | | |
| | ACTTGCTACT AATGTTTTAC CTAAAAALLT TGTATTCATT TTTATTGCTC CTTLT | · | 1- |
| • | ATTGTAAACG TTTACAATGA AAATATAATA ATAATTTTTT AAAAGAACAA TTAAC | | |
| 2 5 . | ATCAAAAATG TATTAACTAT CTATTAACTA AAAAATAGAA TAATTTTTTA ACATAC | ,,, | |
| | | | _ |
| | | 7.77 | |
| 1: 4 | GTTGTTTTGA ATTATAAAAA CTAAAG | 1160 | |
| 30 | | 7.77 | |
| 30 | GTTGTTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: | 7.77 | |
| 3 0 | GTTGTTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1083 base pairs | 7.77 | |
| 30 | GTTGTTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: | 7.77 | |
| 30 35 | GTTGTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1083 base pairs (B) TYPE: nucleic acid | 7.77 | |
| | GTTGTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1083 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 7.77 | |
| | GTTGTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1083 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 7.77 | |
| | GTTGTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1083 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 7.77 | |
| | GTTGTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1083 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 116 | 5 |
| 35 | GTTGTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1083 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689: | 1160 CGAGC 60 | 6 |
| 35 40 | GTTGTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1083 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689: AGCACTGAAG GATGGCTAGT TGTCATAGCA TATGCGGTCA TTGGTATAGT TATAAG | 1160 CGAGC 60 ITTTG 120 | 6 |
| 35 | GTTGTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1083 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689: AGCACTGAAG GATGGCTAGT TGTCATAGCA TATGCGGTCA TTGGTATAGT TATAAGGTTTCTTATA TGTTGTCTAT TAAAATTTTT AACAAACAAG AACTAKAATT GTCGAT | 1166 CGAGC 66 CTTTG 126 CATCT 186 | 0 0 |
| 35 40 | GTTGTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1083 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689: AGCACTGAAG GATGGCTAGT TGTCATAGCA TATGCGGTCA TTGGTATAGT TATAAC GTTTCTTATA TGTTGTCTAT TAAAATTTTT AACAAACAAG AACTAKAATT GTCGATGTGTATAGT TATTAAC GTGATGATAG TATTTGAAAT AATATTTAGA GCAGGTGATA AATCTTTACG ATTGTC | 1166 CGAGC 66 FTTTG 126 CATCT 186 FTGAT 246 | 6 0 0 |
| 35 40 | GTTGTTTGA ATTATAAAAA CTAAAG (2) INFORMATION FOR SEQ ID NO: 689: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1083 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689: AGCACTGAAG GATGGCTAGT TGTCATAGCA TATGCGGTCA TTGGTATAGT TATAAG GTTTCTTATA TGTTGTCTAT TAAAATTTTT AACAAACAAG AACTAKAATT GTCGAG GTGATGATAG TATTTGAAAT AATATTTAGA GCAGGTGATA AATCTTTACG ATTGTG GTTCTTTKG GTGTGGAATG AAATGTGGGG GATAAGTATA GGTGACATAT CTATAG | CGAGC 66 ITTTG 126 CATCT 186 ITGAT 246 GGATT 306 | 5 0 0 0 |

1606

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GAAGTTCGAC ACTTTTGGAT TCAGTTCAAA TACTTTGACC GAGGTAAATA CTATTTATTC

| | TGATACTGAG ATAATCATTA CATGGTCGTG ACCTTTAAAT AAAAGGCTGA CAATATAAGA | 600 |
|-----------|---|------|
| | CATAACGAGT ATACCTAGTG AATATGAAAT ATACTTCGCG TTTGTCAGTT CATTATGGAA | 660 |
| 5 | ATAAGGCGTG ATTAACCATA ATCCAATATA GAATATTAAA ACACTGATAT ACATCATATT | 720 |
| | AATTTCAAAC AAGTCATTTA GTTTATTGTT ATTACTAAAA ACAATTGCAG CATTAATCAC | 780 |
| 10 | ACCTARAGCG ATATTGATTA ATAGATGCGT ATACGATARA CGGARACCGA TAGATGTTAR | 840 |
| ,, | TTTATGATTA ATATAATTTT CAGTAATGAT CCAATATACA CCGAAAAGAC TAATTAAAAT | 900 |
| | CATAAATTGG AATATATAAA TGTAACTAAA ATGATCAATG CTAAATGATG ACGAAGCTAA | 960 |
| 15 | ACCAACCAGT ACCTCGCCAr AGWTALAATT GTTAGTAACG AAAAACGTCT ACTAAATGCA | 1020 |
| | TCATATTAAC AGGTNTAATA CAAGTATTTC TGAAATGGAA TAAGNCTGTC GCTGCATGAT | 1080 |
| | ACG · | 1083 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 690: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 627 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| <i>30</i> | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690: | - |
| 30 | TTAATCATCT GGATGTATTT AGTATTNAGA ATAATAANAA AACGATCATG TTGTATLTGA | 60 |
| | GTAGCGATTG GTTTGCGGAA TTAGGCTTTA CTTTCTTTAA TTACCACTAT ACAGCAAAGT | 120 |
| 35 | TGATTAAATC ATCCTATAAT TTGAAATGTC TACTATTAAA ATTGACATAT CGATACCTTG | 180 |
| | ATAATCAGCC TCTTAATGAC GCTGATAYTA GAAAATTACA GGATATTATT AAAATCATTG | 240 |
| | CAAAAGAAGC AAGTATGGAT AAAAAGATTG CACAAAATCA ATATCGATAT GCGTATTATG | 300 |
| 40 | GTGATTTGCG TGATGAGCTC GAATATATTT ATCAAAATGT AAATCAACGA TTGACATTAA | 360 |
| | AAAGTGTCGC TGATAAATTA TTTGTCTCAA AGTCAAATTT GTCATCACAA TTCCACTTAC | 420 |
| | TTATGGGCAT GGGTTTTAAA AAATATATTG ATACTTTGAA AATMGGTAAA TCGATTGAAA | 480 |
| 45 | TTCTACTTAC TACTGATAGT ACTATTAGCA ACATAAGTGA NCATTTAGGT TTTAGTAGTA | 540 |
| | GCTCCACTTA CTCTAAAATG TTTAAAAGTT ATATGGATAT CACACCGAAT GAATATCGTA | 600 |
| 50 | ATTTATCAAA ATATAATAAn TGTTTAC | 627 |
| | (2) INFORMATION FOR SEC ID NO. 601. | |

1607

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 641 base pairs

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691: | |
|-----|---|---------|
| - | TTGAACGTAA TGCTAGCAAA TGACTITGTG CCATAAAATA TTCTTCCCAT TTGATTCTTT | , 6(|
| 10 | CCAAGATGTT CACCTTCCAT ACTTAAAATT TAGTAACATT TTCTAATAAT ATAAGATTAA | 120 |
| 10 | TCACAAAAA TAAAATTTGC AATTAAAATA ATCCATTATG TCGTGAAATA AGATTTCAGT | . 180 |
| | TTATCAAAAG TTTTACTTCC AAAACCTTTT ACTTTTTTCA AATCGTCAAT TTCTTGAAAT | 240 |
| 15 | GCACCTTGTT GGTTGCGATA TTCAACAATT GCATTAGCTT TAGCTTGCCC AACTCCAGGA | 300 |
| | ACAGACATCA ATTCTGATAC AGATGCCGTA TITAAATTTA CTTTAGTATT ATTTGTGTTC | 360 |
| | CCATTTTTT CGTGCACACT GTTTACTTCA ATTTGTGGTT CAACATTCTT TTGTCCTTTA | 420 |
| 20 | TGAGGTATGA AAATCATTTT TTGATCTGTT AATTTTTCAG ACAAATTAAT TTGACTTACA | 480 |
| | TCTGCATCCT CCAATAATTG TGCTTTATCA AGTAAATCAA CTACTCTATC CTTAGATGTC | 540 |
| | ATTTTATAAA CATTAGGATG TTTAACAGCA CCTTTTACAT CGACATATAC AGGACCCTTA | 600 |
| 25 | TTTTTGGAAT TATCTCCATC TTTGACCTGG ACATCTTCTA C | 641 |
| | (2) INFORMATION FOR SEQ ID NO: 692: | |
| .30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 631 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692: | |
| | TATTAAAGDA CTTGATGAAC CAAATCATAA AAAGCDATAT ATGTTATTTG CAGCTGGCAT | . 60 |
| 40 | TGTGTTnGCA ACTATTTAC TTATTTCGGC ACATTTATAC AGCAGAAAGA GAGGTAACCA | 120 |
| | AGTTTGAGAA TCATAAAGTA TTTAACCATT TTAGTGATAA GCGTCGTTAT CTTAACCAGC | 180 |
| * | TGTCAATCTT CCAGTTCTCA AGAATCAACT AAATCCGGCG AATTCAGAAT CGTACCAACA | 240 |
| 45 | ACTGTTGCAT TGACAATGAC ATTGGACAAA TTGGATTTAC CAATTGTCGG CAAACCCACG | 300 |
| | TCATATAAGA CATTGCCTAA TCGTTATAAA GATGTACCGG AAATTGGTCA ACCAATGGAG | 360 |
| | CCGAATGTTG AAGCTGTTAA AAAGTTAAAA CCAACACATG TTTTGAGTGT GTCAACGATT | 420 |
| 50 | AAAGATGAAA TGCAACCATT TTACAAACAA TTAAATATGA AAGGCTACTT TTATGATTTT | 480 |
| | GATAGTTTAA AAGGGATGCA AAAGTCGATT ACACAATTAG GTGATCAATT TAATCGTAAA | 540 |
| | | |

631

GCAGCTAAAC AAAAGAAACA TCCCAAAGTA T

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| | (2) INFORMATION FOR SEQ ID NO: 693: | |
|----|---|------|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1111 base pairs (B) TYPE: nucleic acid | |
| 10 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | - |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693: | |
| 15 | AATTTAACTA TGTTTTCCAC ATTGTTTCAT GTCACGAAAA GGACAACGCG CGACTATAAG | 60 |
| | TATCAACTAT TTCCACAAGT TTTATTGGTG TTTTTATTAT TCATCGATAC GCTTCATTTT | 120 |
| | CATCTCTCCA ACACAAAAAA GAAGCTAAGC AACTTATGTT GCCTAACTCC TCTATACTAT | 180 |
| 20 | CCATATTTTA CTATTATCCA TATTTCATTG AATTATCTAA TGTTGGCTTC TATTTTTTCA | 240 |
| | ATATTTCTAC CGTCAATGAC GTCACTCATG CGATTTGTTT GTAATTTTTT ATTAAGTTCA | 300 |
| | AACGTATAAT AGCCGCCATC TTTCATTATC ACTTTTATCT TACTATCTTT AGGAAACTTT | 360 |
| 25 | TTATACAGAT CAAAATTTTG AATTAAATAC TGTCTCAATT TAAAGTCGAG TTCTTTAAGT | 420 |
| | GAAATCTCTT CTTTATAAAT GTAGTGTACT CTACCGTACG TAGCAATACC GTCACCTTCA | 480 |
| | TCTCTCTTGA TTTGAAATCT TGGTGCGTTT ATATAATCAT AATAAGCGTC TTGATTTTTC | 540 |
| 30 | TTAGTGACAC CACCATATGA AAACACTGTG CCATTACGGT TTTCCGCTTC TTTAACAACA | 600 |
| | AATATGTCTA ATCCCGGATT TTTACGTGCT TTAAATCTTT CAATATCTTT ACCAAATATC | 660 |
| 35 | TGTACTCTTG TGAATTITCT ATTTTTATCA AAGATAAGGT AATGCTTGCC ACCTTTGCTA | 720 |
| .5 | TAACGATAAC CAGTAACATT TITAAGTTCC TTACTTGCGC CACTATAGTA ATCTCTTAAG | 780 |
| | TCAAAGATAT CTTTTGTCAC ATTTTCATAT TTTGCTTTAT GTTCACTCGC ATTTACAGTT | 840 |
| 10 | TGATGCAATG ACGTTATTGT TCCTGTTGCT AAAATACCTA ATGCTAAACT TGCTTTCGCA | 900 |
| | | , |
| | ATTGCTGTCA TTTTCATAGT TGTATGCTCC ATTCGTAATT ATTAGATTTG TTCGCTTACG | 960 |
| 15 | TCTATTGAAT CATACAGCTT TATTATAGTT AGCGTATTTG ACCTTTCACA TTAAACCATG | 1020 |
| | TTTAATAATC ATTGAATCAT TATTAAGTAA ATTAAGGALC TATAATGTTC GTTAAATAAA | 1080 |
| | CTGAnCCCGT TGTGCTTCAC ACCCGnTnGA T | 1111 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 694: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 426 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694: | |
|----|---|-----|
| 5 | TTATGGATGG ATTAAGAGGT CGTGTTGAAA AAATCAACGA TAACTCTGTT ATTGTTGACT | 60 |
| | TAACAATTAT GGAAAATTTT AATGACCTTG ATTTACCGGA AAAAACTGTT ATCAATCATA | 120 |
| | AACGATATAA GATTGTTGAA TAAGAAGGTA AGTTATAATG AATAAAATCT CGAAGGCTTT | 180 |
| 10 | AACTTGGTTT ATTATAAGTT TCATTATATT TCATCTCATA TTATTTATTA TGTGGGGCGA | 240 |
| | ACACCAAGAA TACTGGTATT TATATACAGG TATAATGCTA ATTGCTGGTA TCAGTTATGT | 300 |
| 15 | ATTTTATCAA AGAGATATTG AATCTAAGCG GTTGCTTACA TCAATTGGTG TTGGTATTAT | 360 |
| | TACGGCAATT ATTTTAATTA TGCLTCAACT TTTATKCTCA CTTATAACTT CTAATTTAAG | 420 |
| | TTATAG | 426 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 695: | 8. |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 737 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 25 | (D) TOPOLOGY: linear | |
| ٠. | | • |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695: | |
| | AAAAGGGGNG TAAGGTTTAG CTCAAGTACG AGAAGTCTTT GGTGATGAAG CAATTGATGA | 60 |
| | AAATGGTGAG ATGAATCGTC GTTATATGGG TGATCTAGTG TTTAATCATC CAGAAAAACG | 120 |
| 35 | CTTAGAATTA AATGCTATCA TACATCCTAT CGTGCGAGAT ATTATGGAAG AAGAAAAGCA | 180 |
| | AGAATATTTA AAACAAGGAT ATAATGTAAT CATGGATATT CCATTATTAT TTGAAAATGA | 240 |
| | ATTGGAAAAT GCAGTAGACG AAGTGTGGGT TGTATACACT TCTGAAAGTA TACAAATGGA | 300 |
| 40 | TCGTTTAATG CAACGTAATA ATTTGTCATT AGAAGATGCG AAAGCACGTG TCTATAGCCA | 360 |
| | AATTTCTATT GATAAAAAA GCCGAATGGC CGATCATGTT ATCGATAATT TAGGGGATAA | 420 |
| | ACTTGAATTA AAACAAAACC TTGAGAGATT GTTAGAAGAA GAAGGTTATA TTGAAAAGCC | 480 |
| 45 | GAATTACGGA GAAGAAGATT AATATTACAC TATAAATAAG TCATTACTTT ACGTACGCGT | 540 |
| | TGATGTATGT AAGTAATGAC TATTTTTTAT AAAAAAGATA AATAAATCAA CGGAAAACGC | 600 |
| | TTTCAAATTT CATATAATAT GCTATACTAA TTCCATAAAG TATAACACAT AAAGATCAAG | 660 |
| 50 | GGGTGCTTTT AATGTCAACG AATATTGCAA TTAATGGTAT GGGTAGAATT GGAAGAATGG | 720 |

1610

737

TATTACGTAT TGCATTA

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 432 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696: | |
| 10 | AACGATAAGA ACAAAAGATA TATTACAAAG CGTTTATTTA AAACGTTATT TATTACGCGC | 60 |
| | GATGATGGCA GGATTTATTA TCGGGATTAT TACGGTCTTC GTATTATCAG TTAAAGCAAC | 120 |
| 15 | ACACGAACCA GATTTACCGC CAGGCATTGT GAATATGGCC AGTGCCATTA CATTCAGCTT | 180 |
| | TGCGTTAGTA CTCATTTTAT TTACAAACTC CGAACTACTA ACCAGTAACT TCATGTACTT | 240 |
| | TACTGTAGGC CTGTATTMTA AAGTAATTAA ACCAACTAGA GTATTGAAAA TATTTTTATT | 300 |
| 20 | ATGCTTTGCA GGAAATATTT TAGGTGCTGC TATTTYATTT AGTTTCATGC GTTTTTCAAA | 360 |
| | TGTAATGACG CCAGATAWGE TAAAYCAGTT ATCAGCAGTT ATAGAGCATA AAACGTTGTC | 420 |
| | TACTGGTTTT GT | 432 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 697: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 782 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697: | |
| 35 | CTTTTATACG AAAGTTAANA TCAAATATAA CATTAATGTT TGATGGGGAT TTTGCGGGTA | 60 |
| | GTGAmGCAAC ACTTAAAACA GGTCAAAATT TGTTACAGCA AGGGCTAAAT GTATTTGTTA | 120 |
| 40 | TACAATTGCC ATCAGGCATG GATCCGGATG AATACATTGG TAAGTATGGC AACGATGCAT | 180 |
| | TTACTGCTTT TGTAAAAAAT GACAAAAAGT CATTTGCACA TTATAAAGTG AGTATATTAA | 240 |
| | AAGATGAAAT TGCACATAAT GACCTTTCAT ATGAACGTTA TTTGAAAGAA CTAAGTCATG | 300 |
| 45 | ATATTTCGCT TATGAAATCA TCGATTTTGC AACAAAAGGC TTTAAATGAT GTTGCACCAT | 360 |
| | TTTTCAATGT TAGTCCTGAG CAATTAGCTA ACGAAATACA ATTCAATCAA GCACCAGCCA | 420 |
| 50 | ATTATTATCC AGAAGATGAG TATGGCGGTT ACATTGAACC TGAGCCAATT GGTATGGCAC | 480 |
| 50 | AATTTGACAA TTTGAGCCGT CAAGAAAAG CGGACNAGCA TTTTTAAAAC ATTTAATGAG | 540 |
| | AGATAAAGAT ACATTTTTAA ATTATTATGA AAGTGTTGAT AAGGATAACT TCACAAATCA | 600 |

| | TATCAGTGAT GCTGTGCAGT ATGTTAATTC AAATGAGTTG AGAGAAACAC | TAATTAGCTT | 720 |
|----|---|------------|------|
| | AGAACAATAT AATTTGAATG ACGAACCATA TGAAAATGAA ATTGATGATT | ATGTCAATGT | 780 |
| 5 | TA | | 782 |
| | (2) INFORMATION FOR SEQ ID NO: 698: | • | |
| 10 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 714 base pairs(B) TYPE: nucleic acid | | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * | 2 |
| 15 | | ٠ | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698: | | |
| | AAATCATTGG CAAAATATAC GAATTGCATT TAAATCGTCA ATTTACATAT | ATTTTTGCGT | 60 |
| 20 | AGTAATCAAT CGTTATCATT GTTATTTATC GTTACATTAT TTCGAGTATC | AGTATGTATT | 120 |
| | TCGGGCTTCGTTTGATAACGACATTCTTTGTGACATCGCTTCATCAGTG | TAACAACAAA | 180 |
| | TACAATGATT TCGTGATGTT AGTTACCCAT TTTATGTGTT GCATAAAATA | TGTTGTTATA | 240 |
| 25 | AAACATTTTA AATCATTTTA TATAAACAAT CTATATATTT TTGGCATTTC | CAAAATATCA | 300 |
| | CTTGTTATAT TAAAAACCGA CAAGACATTT TATCTTATCG GTTGAAATTT | GTTATTGTTA | 3,60 |
| | TTTGTAATGT TTTTAGGTTT CTTTTTAATA TAATATATTT CAGTGAAAAT | ACATGATTGA | 420 |
| 30 | TTGTGATTTC ACTGAAACAT GGTTAATTGC GTTGTTGATG AATAACTTTA | GCATAAATAT | 480 |
| | AGGAAGTTAT TTTGTACATC GCCATATATA GAAACGAAAT TATAATGACA | GCTAGTACGT | 540 |
| 35 | AACTTGTTAA AAATATATGA TGGTTATTAA TACCTATCAT ATTTAGTAAC | GTATATACAA | 600 |
| | TGTTACTAGA AATTAATGTG TGAATCAGTG CTACTGTTAT TGGTATLGCG | AACAAGAAAG | 660 |
| | TCATTTGATT TCGTGTTATC TTTGCTATTC TTCCATTATC TAAACCAAGT | TTTT | 714 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 699: | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 361 base pairs (B) TYPE: nucleic acid | - | |
| 45 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · · | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699: | | |
| 50 | ACTGAGAGCA ATAATTTAGT AACTTCTACT CAAGGAATTA TTAAAGAAGC | ATTGCATAAA | 60 |
| | TTGGGATTTG nnTTTAATTA AAGAACCTTT AAGAATGTTA CAAGTGCGTA | TCCCTGTACG | 120 |

| | TGGACCAACA AAAGGGGGCG TGCGTTTCCA CCCAGATGTT GATGAAGAAG AAGTAAAAGC | 240 | |
|----|---|-----|-------|
| | ATTATCAATG TGGATGACTT TGAAATGTGG CATTGTGAAA CTTACCATAC GGTGGTGGTT | 300 | |
| 5 | AAGGGTGGTG ATCGTTTGTG GATCCACGTC AAANGAGCAT TCCATGAAGT TGGAACGTTT | 360 | |
| | A | 361 | |
| 10 | (2) INFORMATION FOR SEQ ID NO: 700: | | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 943 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | (with anatomical productions and to the same | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700: | | |
| 20 | GTCCTTAATT GGTATCCACC TTTAGCACCG CGTACACTTC GAATTAACCC CGCATTTCTT | 60 | |
| | AAAGGACCTA CAAGCTGTTC TAAATATAAA TCACTCAAAT TATTTTCTTC AGCAATTGAC | 120 | |
| | TTTAATGATA TACATCCTTG CCCCTCTTTT TTAGCAAGAG AAATCATCAA TGTAAGTCCA | 180 | |
| 25 | TATCTCCCTT TAGTAGAAAT TTTCATTGTA TAACCTCACT TAATTCGAAT ATTGATATTC | 240 | |
| | CCATTTTAGC ATTTTTGAG TTAAGATAGT ATAAGAAAGG TGTGACAAAT GTGAGTACAG | 300 | |
| | AACCATTAGC ATCGAGAATG CGCCCAAAAA ATATAGATGA AATCATTTCC CAACAACATT | 360 | • |
| 30 | TAGTTGGACC AAGAGGCATT ATCAGAAGAA TGGTTGATAC AAAAAAATTA ACTTCAATGA | 420 | Par 1 |
| | TTTTTTATGG TCCACCTGGT ATAGGCAAAA CAAGTATTGC CAAAGCAATT TCGGGCAGTA | 480 | |
| | CGCAATATAA ATTCAGACAA TTGAATGCTG TAACTAACAC TAAAAAAGAT ATGCAACTTG | 540 | |
| 35 | TTGTTGAAGA AGCTAAAATG TCTGGTCAAG TTATCTTGTT ATTAGATGAA ATACATCGAC | 600 | |
| | TAGATAAAGC TAAACAAGAC TTTTTATTAC CTCATTTAGA AAATGGCAAA ATCGTCTTGA | 660 | .11 |
| 40 | TCGGTGCTAC AACTTCAAAT CCTTATCATG CTATCAATCC AGCGATTCGT TCAAGAGCGC | 720 | |
| •0 | AAATTTYCGA GTTATATCCT TTÄAATGACG AAGATGTGCG CCAAGCGTTA ACTCGTGCAA | 780 | |
| | TAGAAGATGA TGAGAATGGT TTGAAAMCAT ATCAACCCAA AATTGATGAA GATGCCATGA | 840 | |
| 15 | CCTACTITIC TACACAAAGC CAAGGTGATG TTCGTAGTGC GTTAAATGCA TTGGAATTAG | 900 | |
| | CTGTATTAAG CGCAGATAAT GACAAAGACG GTTATCGACA TGT | 943 | |
| | (2) INFORMATION FOR SEQ ID NO: 701: | | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 445 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | |

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701:

CATTAAGTGA AGTTGTTGAT ACACCCATGC ATCAAGTCAA TTGTTCTGTT GATTTAGATA

| Ð | • | |
|-------------|---|-----|
| | CAGAAAGCTT ATTAGGCTTT AAAACAATTA AAACAAATGC GGAAGGTCAA CAAGAAATTG | 120 |
| | TCTTTGTAGA TGGTCCAGTT ATTAAAGCTA TGAAAGAGGG GCATATTTTA TATATTGATG | 180 |
| 10 | AAATAAATAT GGCTAAACCT GAAACATTGC CTGTATTAAA TGGGGTCTTA GATTATCGTC | 240 |
| * * v | GTCAAATTAC GAATCCATAC ACTGGTGAAG TAATCAAAGC TGTACCAGGA TTTAACGTTA | 300 |
| | TAGCAGCGAT AAATGAAGGT TATGTTGGLA CTTTGCCAAT GAATGAAGCA CTAAAAAAAT | 360 |
| 15 | CGCYTTGTTG TTATTCACGT KGATTATATT GATGGGGACA TTTAAAAAAT GTGANTAAGG | 420 |
| | AGCAAGGTTT ATTACAAGAT GTTAA | 445 |
| | (2) INFORMATION FOR SEQ ID NO: 702: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | |
| - | (A) LENGTH: 752 base pairs | |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | 1 |
| | 15, 15152511 1Incut | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702: | |
| | · | |
| <i>30</i> , | TGCAAGATAA ACAAATTTGT CATTGTTTTG GTTGTAAAAA AGGTGGCAAT GTTTTTCAAT | 60 |
| | TTACTCAAGA AATTAAAGAC ATATCATTTG TTGAAGCGGT TAAAGAATTA GGTGATAGAS | 120 |
| | TTAATGTTGC TGTAGATATT GAGGCAACAC AATCTAACTC AAATGTTCAA ATTGCTTCkG | 180 |
| 35 · | AYGATTTACA AATGATTGAA ATGCATGAGT TAATACAAGA ATTTTATTAT TACGCTTTAA | 240 |
| | CAAAGACAGT CGAAGGCGAA CAAGCATTAA CGTACTTACA AGAACGTGGT TTTACAGATG | 300 |
| | CGCTTATTAA AGAGCGAGGC ATTGGCTTTG CACCCGATAG CTCACATTTT TGTCATGATT | 360 |
| 40 | TTCTTCAAAA AAAGGGTTAC GATATTGAAT TAGCATATGA AGCCGGATTA TTATCACGTA | 420 |
| - | ACGAAGAAAA TITCAGTTAT TACGATAGAT TTCGAAATCG TATTATGTTT CCTTTGAAAA | 480 |
| | ATGCGCAAGG AAGAATTGTT GGATATTCAG GTCGAACATA TACCGGTCAA GAACCAAAAT | 540 |
| 45 . | ACTTAAATAG TCCTGAAACA CCTATCTTTC AAAAAAGAAA GTTGTTATAC AACTTAGATA | 600 |
| | AAGCGCGTAA ATCAATTAGA AAATTAGATG AAATCGTATT ACTAGAAGGT TTTATGGATG | 660 |
| | TTATAAAATC TGATACTGCT GGCTTGAAAA ACGTTGTTGC AACAATGGGT ACACAGTTGT | 720 |
| 50 | CAGATGAACA TATTACTTTT ATACGAAAGT TA | 752 |
| | | |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 830 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|---|----------|
| | (3) TOPOLOGI: Tillear | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703: | |
| | nCGTTTTTGT nAAACnGCTT ATATGTATAA CTTTTCCCAA TTTATCATAA GTTTTGATAG | 60 |
| | AAGGAGTTGG ATCGCTAAAG AAAATATCTC TAAAGATATC ATCTTCAATG ATAGGAATAT | 120 |
| 15 | TATGTCLTTC GCLATAAGTA ATTATATTTT TCTTTTGCTC ATTCGTTAAA GAACGACCTG | 180 |
| | TCGGGTTATT AAACCTAGGT TCTATATAAA TCGCTTTATT TTTAAAATTA ATAAATCTAT | 240 |
| | CAATGATGGT ATCAATTTCA TTAATTTGAT TATAAGGAAC ATCAATATGT CTAAAATTCA | 300 |
| 20 | ATTGCTCAAA AACATTTGTA GAGTGAATAT ATGATGGTGT ATTCGAAATT ATTATGGCAT | 360 |
| | CTTGACCTAA AAACCCAATA GATAAAAGTT GAATGGCATG TAAAGCGCCT GAAGTGATCA | 420 |
| | TTACATTTTC TCTACCTACA TTTATACCTT GCTTTGACAT TCGTTCAACG ATAATATCTC | 480 |
| 25 | TTAACTTGAT ATAACCATAG CCATTATTAT AACCAAAAGA TAAGTCTTCA ATATGACTGG | 540 |
| | CTGTATTAGA CATGGCTTTT TTCAATTGAA TATGTGGCAT TAACGATATA CCCAATTCAC | 600 |
| | CTTTACTTAT ATGTATATAC GAATCATCTG TCTCAATTTT ATTAATTAAT TGCACCGTAT | 660 |
| <i>30</i> | ACTGACTTCT TTGTTGAGAG GACCATAACA TCATTTCAGA CCACTTATTT GTAATATGTG | 720 |
| | CTTCATTCAA ATAGTCATTA ACATATGKTC CACTACCTAC TTTAGTATAG ATAAATCCTT | 780 |
| | CAGCTTCTAA TAACTCAATA CTTTTAATAA TCGTTACTCT ATTTACGTTG | 830 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 704: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 659 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | <i>*</i> |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704: | |
| | AGTGGTGTTG GAAAAGCTAT TATGAAATTA TTACGTGAAC AACAAGTTTA ATAAAAAAAG | 60 |
| | AGGGGTCAAA TATGAAAGGA TTAATTATTA TTGGCAGTGC ACAAGTGAAT TCACATACAA | 120 |
| 50 | GTGCACTAGC AAGATACTTA ACTGAGCATT TTAAAACACA TGATATTGAA GCGGAAATAT | 180 |
| | TCGATTTAGC AGAAAAACCG TTAAATCAAT TAGATTTTTC AGGAACAACA CCGTCTATTC | 240 |

| | TATTAGGAAC GCCAAACTAT CATGGTTCAT ATTCTGGAAT ATTGAAAAAT GCATTAGATC | 360 |
|----|---|-----|
| | ATCTAAATAT GGATTATTTT AAAATGAAAC CTGTAGGCTT AATAGGAAAT AGTGGTGGTA | 420 |
| 5 | TTGTTAGTTC AGAGCCATTG TCACATTTAA GAGTAATCGT CAGAAGTTTA CTAGGCATTG | 480 |
| | CTGTACCAAC TCAAATAGCA ACACATGATT CTGATTTTGC TAAAAATGAA GATGGTTCAT | 540 |
| | ATTACTTAAA TGATAGTGAA TTCCAATTAC GAGCAAGATT ATTTGTCGAT CAAATTGTAT | 600 |
| 10 | CTTTTGTGAA TAATAGTCCA TATGAACATT TAAAATAATA TTAANAAATA TGTAAATNT | 659 |
| | (2) INFORMATION FOR SEQ ID NO: 705: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | ٠, |
| 20 | (xi-)SEQUENCE-DESCRIPTION:-SEQ-ID-NO:-705: | |
| | ncaccatata gtaactggca ccaactacat taccgtcttt taaaaagatt tttttatagt | 60 |
| | | |
| 25 | TATTATCAAC ACTATTAAAT ATTTCAATAC CTTTAATTTC TGCATTTTCT ACAATTIGAC | 120 |
| | CAGCACTATA CAAGTCACAC CCAGAAACTT TTAATGACGT AAATGTTGTT GATCCCTTGT | 180 |
| | ATCCGTTCGT TTCTTTATTT GTTAAATGAT CAGCTAATAC TTTACCTTGT TCATATAGTG | 240 |
| 30 | GTGCAACGAG TCCATAAACT TTGCCGTTAT GTCTGCACAT TCACCAACTG CATATACATT | 300 |
| | GCTATCACTT GTTTGCATCA CATCATTGAC AACAATACCA CGATTACATC TAGACCTGAT | 360 |
| | CTTGGCACTC CTGGGAAGGC GGAACCACTG CATACAACTA | 400 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 706: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 380 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706: | |
| | TTAAAAATAC AGCTACAGGT AATTTTAATG ATTTTTCATC AATATCAAAT TTGGGATTAT | 60 |
| | GGTGTGGCGC TGTAATACCT TTAACCAGTC AGAAAGAATG CACCTGGTCG TACTTTCAAA | 120 |
| 50 | TAATGTGAAA AATCTTCTCC AATCATCATT AAATCTGATT CATTAAAGCG TACATGTAAG | 180 |
| | ጥርልተሞተርሞተር ርሞዋርሞሞክልነዋ አልርሞፕርርያዊል ፕርርሞሞሮሞርር ሞሞነልሞዋልሞርር ል ሮልርርርንልልም | 240 |

| | GCTTAATCCA TTTTGTCCAT ACATGATTCT GTATATCTGA AATCGAAAGT TCTnACTGTA | 360 |
|----|---|-------|
| | CCTTTACAAA ATGCCTTGnn | 380 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 707: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707: | |
| | CANAAAGGAT CAAAGTGATC GGTATAGTGA TAATTAGCTC CAAAGAAAGA ATATTCTAAA | 60 |
| | TCAAATCCAT ACCAAGCAGA AAGTATTAGC GAATATCAAT TTAAATGGTA CCGATTCAAA | 120 |
| 20 | TAAAGAAACA CGACATATAG AATTTTTACT TGATGATTTT AGTGAATCAT ATGAACCAGG | 180 |
| | AGATTGTATA GTAGCATTAC CGCAAAACGA CCCTGAATTG GTTGAAAAAC TAATATCCAT | 240 |
| | GTTAGGTTGG GATCCGCAAT CTCCGGTGCC AATTAATGAT CATGGTGATA CAGTTCCTAT | . 300 |
| 25 | TGTTGAAGCA CTAACATCAC ATTTTGAATT TACTAAATTA ACATTGCCAT TATTGAAAAA | 360 |
| | TGCAGATATC TATTTTGACA ATGAAGAATT ATCTGAnCGT | 400 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 708: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 447 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| · | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708: | |
| 40 | TAATGCTGGT ACGGGTCATG CAGCATTATG TGAGTTGAAC TACACAGTTT TACAACCTGA | 60 |
| | TGGTTCTATC GACATCGAAA AAGCGAAAGT GATTAACGAA GAGTTTGAGA TTTCAAAACA | 120 |
| | ATTCTGGGGT CACTTAGTGA AAAGCGGTAG CATCGAGAAC CCAAGAGAAT TTATCAATCC | 180 |
| 45 | ATTACCAÇAÇ ATCAGTTATG TTAGAGGTAA AAACAATGTT AAATTCTTAA AAGATCGTTA | 240 |
| | CGAAGCGATG AAAGCTTTCC CTATGTTCGA TAATATCGAA TATACTGAAG ACATCGAAGT | 300 |
| 50 | AATGAAAAA TGGATTCCAT TGATGATGAA AGGCCGTGAA GATAACCCTG GTATCATGGc | 360 |
| 50 | GGCAAGTAAA ATTGACGATG GTMCAGATGE AAMCTYCGGT GAATTAACAC GTAAAATGGC | 420 |
| | TARARGCATT GAAGCACATC CAAATGC | 447 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709:

| | (22) | ondonien bre | | 224 TD 110. | | | |
|-----------|------------|--------------|------------|-------------|------------|------------|------|
| 10 🕮 . | GTGTCTACCT | CTTTTTCTTC | TTCAATTGTT | AACTTTTCTT | TTTGAATAGT | AGTATTCGAT | 60 |
| | AATTCTTTAT | CGCTTATAAA | ATCATCTAGT | GGATGGCTTT | CTTTGAAACT | TTTATTTTCA | 120 |
| 15 | GTCATCAATC | ATCTCTCCAA | TAGTTGCTAT | TTTACATCAA | TCTTGATGAT | GTTTTTGATG | 180 |
| | TAACTTATTT | AATTCCATTT | CAATATCTAA | ACGTTCATAA | TCATCTTCGT | TGAGACGCTT | 240 |
| | TAAATCAGCG | ATTAATGTTC | GTTTGACCTC | ATCCAAAGTA | ATTCGTGTTT | GTTCTAACTT | 300 |
| 20 | TTGCTGTTCA | TTAATTGATT | TTTTGGGCAT | TTTTGCTAGA | CGTGTATATG | CATCAACCAA | 360 |
| - | ATTTAAAGCA | TTATCAATAT | GAGAATAAAA | AAAGCCTTCA | ACTTTATAAA | ATGATGCAGG | 420 |
| | TCTCTGTCTA | ACTGTCGTAT | AAATAGAACG | TGAAATTTGG | TATATATCAT | TAATCTGCCT | 480 |
| 25 | AAAATCTTTA | ATTGATCTTA | TATTGACATA | CGTTTTTAAA | ATACCTCTAA | GTTTTTGGTG | 540 |
| | TGTATGATTT | AACTGATTTC | GAATATAGCG | ATAGTCTTTT | CTAGTCAAAC | CAATTTCGTT | |
| | TAAATATTTG | CGTGAAGTGA | GTTTTTGTAT | CGGTAGGTAT | GTCATTAAAA | AGCCAACAAT | 660 |
| 30 | ACCAATAGAC | ATATCAATTA | AAAAAGATAC | ATCAAGTGCA | ATCATCCCAA | ATATGCTTGT | 720 |
| · · . | TAAAAACGCT | ACAGGAATTC | CCACTAACAC | CCCAAATATA | TGAGAAATAT | TATATCTCAC | 780 |
| 35 | TGTCATCTTC | CTTTATTTAG | CATTTTATAT | TGATCGAAAA | TCCGATAATT | TTTGATTTAG | 840 |
| | TTCTAACTCT | TCAAGTTGAT | GGCTTGTTAC | ATTTGATGCT | GGTGAGGCAC | CTTCAATTAC | 900 |
| • | ACCTTGAATA | AATCTCTCTA | TATCTGCGTC | ATCCCCTTGT | GCATATATCT | CTACATAGTC | 960 |
| 40 | ATCTACATTT | TGAACAGTAC | CGACAATGTT | ATAGTTCATT | GCAATGCGTT | GTGTAAAATA | 1020 |
| | TCTAAATCCG | ACGCCTTGAA | CGCGTCCGAA | TACTTGTAAA | TGTATATGtC | TCATTTTTAC | 1080 |
| | CACCTCATAA | TGTTATTATA | CGTAGTTTTA | CTTAAAAAAA | CTAATAATTA | CTATAGTTAC | 1140 |
| 45 | TACTTTGTTT | GTTTCAAGTC | GTCAAACTTG | ATTTTCAGAG | GATAAAGGTA | TAAAAATAAG | 1200 |
| | TATAGAGTTT | TTGAAGTATG | GAAGGGGTCT | TTAATAATGT | GGACAGTTAC | CAAAATTAGA | 1260 |
| | GCCGATTATG | AGGGATGGTG | GTTATTCAGT | GACTGGCCAG | AAAACATTGT | TGAAAAATAT | 1320 |
| 50 | CAATATCAAG | ATTTTGATGA | CATGTTTAAG | CACTATCAAC | AATTGATTAA | TCAATGTAAA | 1380 |
| | GTTCAGTTCG | ATAACTATGT | CACAGGCAAA | TATAATATTT | ATGCATTTTA | TAATAATTGT | 1440 |

(2) INFORMATION FOR SEQ ID NO: 710:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 519 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|------------------------|---|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710: | |
| | GCTGNAAAAT ATGTTAGAAG CAGATGCATG GGCAAAGCTG GGGTCCTTAT TTATTGTCAG | 60 |
| 15 · | GTAAAGATGT CTTCAATTCA ACTATTGGAA TATATGGTAT GGGAGATATT GGTAAAGCTT | 120 |
| .0 | TTGCAAGAAG GTTGCAAGGG TTTAATACTA ATATTCTTTA TCATAATCGA TCAAGACATA | 180 |
| | AAGATGCAGA GGCGGACTTT AATGCAACAT ATGTTTCTTT TGAAACGTTG TTAGCAGAAA | 240 |
| 20 | GTGATTTTAT CATCTGTACA GCGCCACTTA CAAAAGAAAC ACATCATAAA TTTAATGCTG | 300 |
| | AAGCATTTGA ACAAATGAAA AATGATGCAA TTTTTATTAA TATCGGTAGA GGACAAATTG | 360 |
| | TAGATGAAAC AGCATTAATC GATGCACTAG ACAATAAAGA AATTTTAGCA TGTGGTTTAG | 420 |
| 25 | ATGTATTAGC AAATGAACCG ATTGATCATA CACATCCATT AATGGGACGT GATAATGETC | 480 |
| | TGATTACACC aCACATTGGG TAGGCGCATT CAGTTAACn | 519 |
| | (2) INFORMATION FOR SEQ ID NO: 711: | |
| <i>30</i> <i>35</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1349 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711: | |
| 40 | CTATTACAGG TGGCGAACCA ATGTTTTCTA AAAAGTCTAT TAGAAATGTT GTTAAACCTC | 60 |
| | TATTAAAGTA TGCACATCAT CGAGGTATAT ATACACAAAT GAATTCAAAC CTAACATTGC | 120 |
| | CTCAAGATCG TTATTTAGAT ATTGCTGAAT ATATCGATGT TATGCATATC TCACACAACT | 180 |
| 45 | GGGGAACAAC TGATGAATTC GCAAATGTTG GCTTTGGCGC AATGAAGAAG CAACCACCGT | 240 |
| | TAAAAGCTAA GTTAAAATTA TATGAACAAA TGATTTCGAA TGCACGTACA TTATCAGAAC | 300 |
| | AAGGAATGTT TGTATCTGCG GAAACAATGC TCAATCAAAG TACGCTACCA CATTTACGAA | 360 |
| 50 | AAATACATCA AGAAGTCGTT CATGATATGA AATGTAGCAG ACACGAGATT CACCCTATGT | 420 |
| | ATCCAGCTGA CTTTGCAAGT CAATTAAATG TGTTAACTCT AGCGGAAATG AAAAAGACAA | 480 |

| * - | TGTTTCCATG CTTAAAGGAT GATGAAGATC AAAAGTTACT ATCACGTTTA AGAAATGCTA | 600 |
|-----|---|-------|
| | AAAATGTAAC GACTAGAAAT GACCCGGATG GCCGTAGTCG TTTAAATGTC AATGTATTTA | 660 |
| 5 | CAGGTAATGT AATCGTAACT GATTTCGGAG ATGAAACAGG TACAATTTCG AATATACAAA | 720 |
| | AAGATAAATT AACAGATGTA TTTGATAAAT GGTTATCCTC TGATCTTGCT AAATCATTAA | 780 |
| | ATTGTCATTG TTCCGAGTTT AGTTGTTTAG GGCCAAATGT TCTTGTTAAA AATATGTACT | 840 |
| 10 | ATCCGAATAT GGATTTTAAA GATAATGAGC GTCATATGCA CAAACAACCA CAAATTATAC | 900 |
| | AATTTTAAAA ACTCTTAATT ATGCGGAGAA GCACTTTATC GATAAGTAGT CTCCGCATAT | 960 |
| 15 | TTTAATGCTA TTATAAAATA AAAAACAATT AATTGCTGGC AGTACTCTAC TTAAATAATA | 1020 |
| 15 | AAGGGCATTT AATAGGACTA ATAGTCTATA ATAAAAGGGG TAAATTTTAA CTAAAAGCAT | 1080 |
| | AAACGTGCAT AATCAAAAAG ACAGATTGTA GGTGGAATAT TCGAaCATAA CAGTTCAATT | 1140 |
| 20 | CATCCTTAAC AATCTGTCTT TATATTTTTA GTCTCTAATA TGTTGCACTT GAGCTAAATA | 120,0 |
| | TTCAATTGTT gTTTACTTtC AaTGCGaCGt GCTTttCTtC GTtCAaCaCG TgwGGTGCTG | 1260 |
| | TATCATAAAA CCATTTTTCA ACATCATCTT CTGGATATAC ACCAGGTACA TGTTTAGGTT | 1320 |
| 25 | GCCTTCATCA TCTAACGCAA CAAATGTAA | 1349 |
| | (2) INFORMATION FOR SEQ ID NO: 712: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 377 base pairs (B) TYPE: nucleic acid (C) STRANDENNESS: double | |
| | (D) TOPOLOGY: linear | * |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712: | |
| | GAAATTAAAA AAGCAATTGG ACAAGATGCA ACAGTGTCAT TGTTTGATGA ATTTGATAAA | . 60 |
| 40 | AAATTATACA CTTACGGCGA TAACTGGGGT CGTGGTGGAG AAGTATTATA TCAAGCATTT | 120 |
| | GGTTTGAAAA TGCAACCAGA ACAACAAAAG TTAACTGCCA AAAnCAGGTn GGCCTGAATG | 180 |
| | GAACCAGGAG GAANTTGAAA ATATGCTGGG GATTACATTG TGAGTACAAG TGAAGGTAAA | 240 |
| 45 | CCTACACCAG GATACGAATC AACAAACATG TGGAAGAATT TGAAAGCTAC TAAAGAAGGA | 300 |
| | CATATTGTTA AAGTTGATGC TGGTACATAC TGGTACAACG TCCTTATACA TTAGATTTCA | 360 |
| | TGCGTAAAGA TTTAAAA | 377 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 713: | |

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 base pairs

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-------------|---|-----|
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713: | |
| | AATGAAnCGA AAAATGACTA TAAAAAGTTT AAAGTGTTTT CACTTATTTC AACACTTGTC | 60 |
| 10 | ATTGTCATTT TAGCAATTAT AAGATTTGTT CATAAAATGA TGTAATTAGA GTGAGACATT | 120 |
| | GTTTTATGTC TCAGGATCCA GTTATTCATT ATATCTACAA TATTTACGAT TATATAAATA | 180 |
| | ACCCGAGATT TTAGTATGAT TCATTLCACT AAAATCTCGG GTTTCTATTT GATAATTTTT | 240 |
| 15 | AATGGGATAT GGCATGTATA CGTTCTTGCC TTTTATCTCA TTTCCAATGA TTAATCTGGA | 300 |
| | TATTGTTCTA AAAATGCTTT CGCTTCTTTA TTAACTGTTT TAAAATCAAT ACCTTGTTGC | 360 |
| | ATCGCTGCAA AGACACATCC ACAATAACAC TGCCTAAAGA TATTATAGTC ATTACACATT | 420 |
| 20 | TCTATGGAAC GCTCATAACC TTTACTTTTC YTAAAATCAC TTGGCAAATA GTTCACATCG | 480 |
| | TATATTTTT GGACATCCAT ACCAAGTTCA TTGATTAATT GTGCGTTC | 528 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 714: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 731 base pairs (B) TYPE: nucleic acid | |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714: | 1 |
| 35 | TTTAATGGCA TGAAGTCACA GTATATAAAG AATCTGGTGT GACAATCAGT ATGACTAAGT | 60 |
| | ATATAAAAAA AGAGCAGGTG CGAAATAATG GCGAAAGAGT CGAAATCAGC TAATGAAATT | 120 |
| | TCACCTGAGC AAATTAACCA ATGGATTAAA GAACACCAAG AAAATAAGAA TACAGATGCA | 180 |
| 40 | CAGGATAAGT TAGTTAAACA TTACCAAAAA CTAATTGAGT CATTGGCATA TAAATATTCT | 240 |
| | AAAGGACAAT CACATCACGA AGATTTAGTT CAAGTTGGTA TGGTTGGTTT AATAGGTGCC | 300 |
| | ATAAATAGAT TCGATATGTC CTTTGAACGG AAGTTTGAAG CCTTTTTAGT ACCTACTGTA | 360 |
| 45 | ATCGGTGAAA TCAAAAGATA TCTACGAGAT AAAACTTGGA GTGTACATGT TCCGAGACGT | 420 |
| | ATTAAAGAAA TTGGGCCAAG AATCAAAAAA GTGAGCGATG AACTAACCGC TGAATTAGAG | 480 |
| 50 . | CGTTCACYTT CTATCAGTGA AATAGCTGAT CGATTAGAAG TCTCAGAAGA AGAAGTGTTA | 540 |
| | GAAGCAATGG AAATGGGACA AAGTTATAAT GCGTTAAGTG TTGATCATTC CATTGAAGCT | 600 |

GATAAAGATG GTTCAACTGT TACGCTATTA GATATTATGG GGCAACAAGA TGACCNTTAT

| | | | | 7.5.1 |
|-----|---|----------------------------|------------|-------|
| • | (2) INFORMATION FOR SEQ ID NO: 715: | | • 1 | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 830 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | * * * | | |
| 10 | (D) TOPOLOGY: linear | | | |
| | · · · · · · · · · · · · · · · · · · · | 1 - 10 - 2 - 2 1 - 2 1 - 2 | a a second | · |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO |): ×715: | | |
| 15 | TTTTAGrGGa AAGCGAATTA GtCaTATwCg CaGCAGAT | wg aatgattgaa | AAmGaAATTG | 60 |
| | attcgattcc aattgtaaga aaaaaagata atcaaaag | TA TGAAGTAATT | GGAAGAATTT | 120 |
| • 5 | CCAAAACAAC AATAGCTAAG TTATTAGTAG CATTATAT | AA AGAATAGGTG | AGAAGTAATG | 180 |
| 20 | GAAAAATTA AAATTATCGT AGCTTCAGAT TCTATAGG | TG AAACGGCAGA | GTTAGTTGCT | 240 |
| : | AGGGCAGGTA TTTCACAATT CAATCCTAAG CAATGTAA | AA ATGAATTATT | AAGATATCCA | 300 |
| | TATATIGAAT CTTTTGAAGA TGTTGATGAA GTGATTCA | AG TTGCAAAAGA | TACAAATGCT | 360 |
| 25 | ATCATTGTTT ATACACTTAT TAAACCTGAA ATGAAGCA | AT ATATGAGTGA | GAAAGTAGCA | 420 |
| | GAATTCCAAT TGAAGTCTGT CGATATCATG GGGCCATT | 'AA TGGATTTATT | ATCTGCTTCG | 480 |
| . 9 | GTTGAAGAAA AACCTTATAA TGAGCCAGGT ATCGTTCA | TA GATTAGATGA | TGCATATTTC | 540 |
| 30 | AAGAAAATTG ATGCGATAGA GTTTGCAGTT AAATATGA | TG ATGGTAAAGA | TCCTAAAGGA | 600 |
| | TTACCTAAAG CTGATATTGT TTTACTTGGT ATTTCGAG | AA CTTCAAAGAC | ACCATTATCT | 660 |
| 35 | CAGTATITAG CGCATAAGAG TTACAAAGTT ATGAATGT | AC CGATTGTACC | AGAAaGTGAC | 720 |
| | ACCGCCAGAT GGCTTATATG GATATTAATC CAAAGAAA | TG TATCGCACTT | AAAATAAGTG | 780 |
| | AAGANAAATT AAATCGCATT AGANAAGAGC GACTAAAA | CA ATTANGACTA | • | 830 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 716: | * | | * |
| | (i) SEQUENCE CHARACTERISTICS: | | | |
| | (A) LENGTH: 1159 base pairs(B) TYPE: nucleic acid | * | | 171 |
| 45 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | |
| | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO |): 716: | | |
| 50 | ngaagaacaa gtttancatc taaatgcccg tttaaaac | TA CAACTACTTG | ACGATGTTAA | 60 |
| | ATCAGTGTTT AANTCTCAAA TGACGCAAAA TAGTGATT | TT AATGAAGAAA | AGAAAGTGTC | 120 |
| | | | | |

| | AGAACGTATA | AAAAAATACT | TTAATAAGCA | ACTCACTGAG | CAAATTGCAC | CAATCGTTCA | 24 |
|------|-------------|--------------|--------------|------------|------------|------------|-----|
| | ACAATTAGCA | GATTTACATG | TCATTATTAA | TCCTCAGTTT | AACTTTGAAT | CAGCTAATAT | 30 |
| 5 | AGAGCAACCA | TTATTGCACA | TCGATTTCAA | CGATATGCTA | AATGCATTGC | CTAAACAATT | 36 |
| | AACAAAACGT | AAAATTTTGA | ATCCAAATGG | GCAAAGAGAT | ATACATGAAT | CAATTTGTCA | 42 |
| | AAGTACGTTA | GGATTATTAC | AACCACAAAT | GGGATTATTG | AGGCAACAGC | TTGAATTATA | 48 |
| 10 | TGTAAAGCAA | ATGGCTGTAG | AAGCTGAATC | GCAATTTGAA | AGTTTTGAAG | CTAATATTCA | 54 |
| - | AACGCAAATA | AACGATTTAT | TAGCATTTGA | TTTAGATACA | ACACTTATCA | ATCAATTGAA | 60 |
| 15 | AGATAAACAT | CAACAACTGA | AAACTATTTT | ATATTAAGAa | AGAAGGAACG | TTTTAAATGC | 66 |
| 75 | CTAATAAAAT | ATTACTTGTA | GATGGTATGG | CGCTATTATT | TAGACATTTC | TATGCTACAA | 72 |
| | GTCTTCATAA | ACAATTTATG | TACAATTCAC | AAGGTGAACC | TACAAATGGA | ATACAAGGAT | 78 |
| - 20 | TTGTGCGTCA | TATCTTTTCG | GCAATACATG | AAATACGCCC | TACACATGTA | GCTGTATGTT | 84 |
| | GGGATATGGG | ACAATCAACT | TTTAGAAATG | ATATGTTTGA | tGGTTATAAG | CAAAAkCGTT | 90 |
| | CTGCACCACC | AGAAGAATTG | ATACCACAAT | TTGATTATGT | TAAAGAAATT | TCAGAGCAAT | 96 |
| 25 | TTGGCTTTGT | AAATATTGGC | GTTAAAAACT | ATGAAGCGGA | TGATGTTATA | GGTACATTAG | 102 |
| š. | CACAACAATA | TTCAACTGAT | AACGATGTCT | ATATTATTAC | GGGCGACAAA | GATTTACTGC | 108 |
| 2 | AATGTATTAA | TGACAATGTT | GAAGTTGGCT | AATTAAAAAÀ | GGTTTAACAT | TTATAATAGA | 114 |
| 30 , | TATTCATTAC | ATCGTTTTn | | | | | 115 |
| | (2) THEODIN | ATTON FOR CI | -0 TD NO. 71 | | | | |

(2) INFORMATION FOR SEQ ID NO: 717:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 574 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717:

| GATTTAATCA | ATGCAGTTGC | AGAGCAAGCT | GATTTAACTA | AAAAAGAAGC | TGGTTCAGCA | 60 |
|------------|------------|------------|------------|------------|------------|-----|
| GTAGATGCTG | TATTCGAATC | AATCCAAAAĆ | TCACTTGCTA | AAGGTGAAAA | AGTACAATTA | 120 |
| ATTGGTTTCG | GTAACTTTGA | GGTACGTGAA | CGTGCTGCAC | GTAAAGGTCG | TAACCCTCAA | 180 |
| ACTGGTAAAG | AAATTGATAT | CCCAGCAAGT | AAAGTTCCAG | CATTCAAAGC | TGGTAAAGCA | 240 |
| TTAAAAGATG | CTGTAAAATA | ATTTTACTTA | AAAAGCCCTG | AATAAGGGCT | TTTTATTTTG | 300 |
| CTTTTAATAC | TTACAACCTG | TACATAAATT | GTAATGTTCT | TCTAAGTTTT | TAATCTTTGG | 360 |

| | AACTACAAAA TATACATATG AATATTGAGA TTAATTGTTA GCGTTGAATT TACTTAAAAG | 480 |
|--------|---|-----|
| | GTAACCATGT CTACTATAGT ATTTACGTT ATTTAAAAAG ATGAATAATG TAAATGAAGT | 540 |
| 5 | AAAGGTTATT ATGAGAATTA CAAAAGCTAC ATAA | 574 |
| • | (2) INFORMATION FOR SEQ ID NO: 718: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 493 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718: | |
| | AAGaTATTGA AAMTGMAATG GAGCACGCCC TTATTTGATA GAAGTAAAAG ACATTTAATT | 60 |
| 20 | CTTACCGATG CAGGTCAAAT TTTTTATGAG AAAAGTAAAG AAATTGTLGC ACTGTATGAT | 120 |
| | TATTTACCAT CTGAAATGGA ACGCTTGAAT GGACTGGAAA CAGGACATAT AAACATGGGC | 180 |
| | ATGTCGGCAG TCATGAATAT GAAGATTCTT ATCAATATTC TTGGTGCATT CCATCAACAA | 240 |
| 25 | TATCCAAATG TTACATATAA TTTGATAGAA AATGGCGGTA AAACAATTGA ACAGCAAATT | 300 |
| | ATCAATGATG AAGTAGATAT AGGCGTGACC ACTTTGCCAG TCGATCATCA TATTTTCGAT | 360 |
| | TATACTACCC TAGATAAGGA AGATTTGCGA CTTATCGTGA GCAGAGAGCA TCGACTCGCA | 420 |
| 30 | AAATATGAAA CTGTTAAACT CGAAGATTTA GCAGGTGAAG ACTTCATTTT ATTTAATAAA | 480 |
| | GACTTTACT TGA | 493 |
| | (2) INFORMATION FOR SEQ ID NO: 719: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1257 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719: | |
| 45 | GCATTGCCAA AACAATACGT TTATATTATT GAGGAACTAC TGTATAAAAG TAATGAATAT | 60 |
| | CAAAATAAAA AATCATATTA CGAAACACTT GTTAACCAAG TAATTGAACT TAAACAGGCA | 120 |
| | GATGATTTAA TTATTGGACT CGCTTATTCC GTACAACGCT TAGTCGTCGA TCATTTACAC | 180 |
| 50 | GTTGTCGGTG ATATTTATGA TCGTGGACCA CAACCAGATA AAATTATGGA TACACTGATT | 240 |
| | AATTATCATT CCCTAGATAT TCAATGGGGT AATCATGATG TGCTTTGGGT TGGAGCCTAT | 300 |

| | GATATTATCG | AAGACGCTTA | TGGCATTAAT | TTAAGACCAC | TGCTTACTTT | AGCTGAAAAA | 420 |
|-----|-------------|--------------|-------------|------------|------------|------------|------|
| | TACTATGACG | CAGATAATCC | TGCTTTTAAG | ССТАААААА | GACCTGACAA | ACACGAACGT | 480 |
| 5 | TTAACTCAAC | GTGAAGAAAG | TCAAATTACT | AAAATTCATC | AAGCTATTGC | GATGATTCAA | 540 |
| | TTCAAGTTAG | AAATACCAAT | TATTAAACGT | CGTCCAAATT | TCGAAATGGA | AGAACGTCTT | 600 |
| 10 | GTGCTTGAAA | AGGTTAATTA | TGATACAAAT | GAAATTACAG | TTTATGGTAA | TACATACCCA | 660 |
| ,,, | TTGAAAGACA | CATGTTTCCA | AACTGTCAAT | CGTGATAATC | CAGCAGAATT | ACTACCTGAA | 720 |
| | GAAGAAGAAG | TCATGAATAA | ACTATTATTG | TCATTCCAAC | AATCTGAAAA | ATTACGTCGT | 780 |
| 15 | CATATGTCTT | TCTTGATGCG | TAAAGGCTCT | CTTTACTTAC | CATATAATGG | CAATTTACTC | 840 |
| . 1 | ATTCATGGTT | GTATTCCAGT | TGATGAAAAT | GGTGAGATGG | AATCATTTGA | AATTGATGGT | 900 |
| | CATACTTACA | GCGGCCAAGA | ATTATTAGAT | GTGTTTGAGT | ATCATGTCCG | TAAATCATTT | 960 |
| 20 | GATGAAAAAG | AAAATACTGA | TGACTTATCG | ACGGATTTAG | TTTGGTATTT | ATGGACTGGG | 1020 |
| | AAATATTCGT | CACTATTTGG | TAAACGTGCC | ATGACTACGT | TTGAGCGATA | CTTTATTGCA | 1080 |
| | GATAAAGCTT | CTCATAAAGA | AGAAAAGAAT | CCGTACTATC | aTCTTCGTGA | AGATGTGAAT | 1140 |
| 25 | ATGGRTCGTA | AAATGCTCaG | TGATTTCGGA | TTAAATCCAG | ATGAAGGACG | CATTATTAAT | 1200 |
| | GGTCACACAC | CAGTGAAAGA | AATCAATGGC | GAGATCCTAT | CAAGGCTGAT | GGAAAGA | 1257 |
| • | (2) INFORMA | ATION FOR SE | Q ID NO: 72 | 20: | | | |

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720:

| TGAGCACATG | ACAGTGGCTG | AAAACATTAA | ATTTTTTAAA | TCACTTTGTA | AAAATCCAAT | 6 |
|------------|------------|------------|------------|------------|------------|-------|
| TAACGATACA | ACTATCAACG | AATATTTACA | GCAATTAAAC | TTTGATGATA | CGTCTGCCAA | 12 |
| AGTATCTACA | TTGTCCGGTG | GGAATAAACG | TAAAATTAAT | ATATTAGTAG | GTTTACTAGG | 180 |
| TCAACCTCGA | ATTCTCATTT | TAGATGAACC | GACAGTTGGT | ATTGATTTAA | AATCTAGACA | 240 |
| TGACATCCAC | CAACTACTTA | ACATCATGAA | ATCTAAATGT | TTAATTATAT | TAACTACCCA | 300 |
| TCATTTAGAT | GAAGTTGAGG | CACTTGCAGA | TGGTTATCAA | GTTAATTGGG | CCAGGTnCCC | 36 |
| TTTTnTTCAA | CAGTTTTTGG | GGGCCAACCA | TGGGCTTATA | | | , 400 |

(2) INFORMATION FOR SEQ ID NO: 721:

| 5 | (A) LENGTH: 570 base pairs (B) TYPE: nucl ic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|------|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721: | |
| 10 | CTTATTTATA TTATAATATA AATATTTTAT TTTTCAATAC TTAATTTTAA AAATCCCCTA | 60 |
| | TGAAAATGTT GATGAGCTAC ATCTTTAAAT CTTATTATAC ATTGTATAAA ATTATATTGC | 120 |
| | GAGGTAGTAA ATTGATATTA TACACTTTTG GTTGTGTATG CATCTCACCT ATCTTTTTTG | 180 |
| 15 | CTTTTTCAA ATAAGAAAGT ATTAAAAATY AATGCCTATA CAGGAACAGA CATGGCTAAA | 240 |
| | CTTGATTTAA ATAGTCTTGA CGACGAGCAC GTAAAATTAT TAATAAATGA ATTAAAATAT | 300 |
| | CCAGAAACTC ATATCGATGT AAATGAATTA AAAACAATAG TTGCTAGTCG AATAAATGAA | 360 |
| 20 | AGGCAAGAAA-TAATAAGTTT-TAAGTTAGGA-ATAAAGTACT-TATTAACAAT-AAAAAGAGGG | _420 |
| | AACATAGAAA AAGATAGGTT TTCAATTTCA ATCATTTTCA AAGATACCTA TCACACCCTA | 480 |
| 25 | GTTAGAATAG ATATTAACGG TGGTACTCAC GATAATCCAG ATGGAACAAT CGCTCCGAAA | 540 |
| 25 | AGTCATATTC ACATATATAA TGATAAGTAT | 570 |
| | (2) INFORMATION FOR SEQ ID NO: 722: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| , | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722: | |
| | ATTITAGTCT TAGGTGTTGA TTGCATGATG AATGCAGAAG TTATACCTGC AGCCATATTA | 60 |
| 40 | GCACCTTCAT TATTGTGTAT AATTTGAATA TTATTTGCTT TTAAAGTATG TCCAATTAAG | 120 |
| | TTTGAAGTCG TTGTTTTACC ATTTGTTCCA CTGATAAATA CAATATCATC AACTTGCTCT | 180 |
| 45 | GCTAATTTTC TTAATATATC TGTATCCACT TTTCTAGCGA TTTGTCCAGG TAAATCTGTT | 240 |
| | CCTCTTTTAC CTACTGCTCT ACTTGCTTTA CGCGCCAATT TCGCTAGATG GATTGCCGTC | 300 |
| * | CACTGTCTCA TGTGTTTCCT CCtCAAATTt CCACTCGCAT CATTATAACA TGACAAGGCA | 360 |
| 50 | ACTTCAAAAA AGTTTCTCAA TCACAAATnG ATACCAGTGT | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 723: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1113 base pairs | |

| (C) | STRANDEDNESS: | double |
|-----|---------------|--------|
| (D) | TOPOLOGY, lin | ear |

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| | (XI) | SEQUENCE DES | SCRIPTION: S | SEQ ID NO: | 723: | | * |
|----|------------|--------------|--------------|------------|------------|------------|------|
| | GATTATATGC | TGTTGGCAAA | ACAATATACC | CAGATGAATT | TTTATTTTTA | GTAATAGTAT | 60 |
| 10 | AACCATGCTT | TGTCTTACTA | ACTTTGACAG | CTTCTAATGA | ATTTGAAGCG | TCTTTAAGCG | 120 |
| | TGGTATAATC | TTCGCCGTAT | ATCCCTTTTA | AATTTACTCG | ATACTTACCT | TTAGGCAATG | 180 |
| | ATAATCTAAT | TCTATCTGGA | GCTTTAATGC | GTATCGTTAC | GGGTGTTACA | ACGCGTCGAT | 240 |
| 15 | ATTTATAAGT | GAGTTTATTT | CTTTCTTGTG | TATATTCATT | CACTTTAACA | TCATGAGCTT | 300 |
| | TATCCGGCGA | AAGTAATTCT | AAATCCATTT | CAAAATACAA | ATCTTTAAAT | TGATTAGAAA | 360 |
| | CTGATTTTGG | CAACTGTACA | GTTAGACCAC | CATTATTTTG | TTTAACTTGT | AATAAATGTT | 420 |
| 20 | TTGTAGGAGA | TTGCCAGGCT | GCACTATTTA | ATTTAATTGT | TGAATCTGAT | AGTAAATTTT | 480 |
| | TATTGGCTTT | AAAATGTGTA | TTAACATCTT | TAATATTGTT | AGAAACAATC | CCTTGCAACA | 540 |
| 25 | TTGCTTGTTC | TTTATCTAAT | GGAGATTTTA | ATTCTTTATT | GGAAAAGACC | TTATTTGTAA | 600 |
| | TATGTGCACT | TGGATAATGG | ATGGTATTTT | TAGAATGAAT | CCAACGAACT | TTATTGTCTT | 660 |
| | TGTGTTCAGA | CTTAATTTTA | AATCCATATG | GtAAGTTGTC | ATCATGATtC | ACTCTAATTC | 720 |
| 30 | GATCATTAAC | ATTCCAAAGT | GATAGTAAAT | TTgACGATgC | CAAGTAATCT | ATAAGTGCTG | 780 |
| | TTTTTATCGA | TTGGCATATT | AATTTGGAGT | GTCTTGTCAT | AATATTTTAA | AATGTCTCCA | 840 |
| | TTAAAAATAC | TAGAATATAA | TGAAATGCCA | TTATAATGAT | ATATAAATGG | TGAATTTAAT | 900 |
| 15 | GCATAGTCTG | ACATATAATC | AATGCGATTA | AATGAGCCTG | TTGCATTTTG | ATTTATCTTT | 960 |
| | TTTATAAGCT | GGTTTACATA | GTTACTATGG | TAATCATGTT | GTTTCAACGT | TGATAATGAT | 1020 |
| | TGTTGATAAG | GTTTGATTGC | CATGTTTTTG | TTGTTATCTA | AAATGACGAT | TTGTTGAATC | 1080 |
| 10 | ATaACGATTA | ATACTAATAT | TGCAACGGTT | AAT | | | 1113 |
| | (2) INFORM | ATION FOR SE | Q ID NO: 72 | 24: | | | |

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- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 464 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724:

| IGCCGTTTAG | CAAAATCTAG | TATCGCTTGA | TGATCAGATT | CTGAAATTTC | AGTGTGTACT | |
|-------------------|------------|------------|------------|------------|------------|--|
|-------------------|------------|------------|------------|------------|------------|--|

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| 10 | AATTTTAGCA | GCACCGACAC | GATTCATTGG | CCAGCANCTA | TACC | | 464 |
|----|------------|------------|------------|------------|------------|------------|-----|
| | AAAAATCCAT | CAGATACTAA | CGGCTACATG | ATCATTGATT | TCAATAGCTC | TCTCTAACGC | 420 |
| | GGTTGGATAA | TTGCCTTTAT | ACCATGTTGT | GCTGCAAGTT | CAACTGTATC | TCCCATAGGG | 360 |
| 5 | ATTGCAATAC | CATGTTTATT | AGCCATATCA | ATTGAATCTT | GATCTTTAAT | CGAACCACCC | 300 |
| | TTCATTTATG | TTACGCCCCT | TTAAAATTAG | TGTTTAAAAT | GTCGAGTGCC | TGTGACTACC | 240 |
| | GATTGATTAA | GTTTATATGC | AAGTGCATGT | TCTCGTCCAC | CAGCACCAAT | TACTAATACA | 180 |

(2) INFORMATION FOR SEQ ID NO: 725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear

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| | (xi) S | EQUENCE DES | CRIPTION: S | EQ ID NO: 7 | 25: | | |
|----|------------|-------------|-------------|-------------|--------------|------------|------|
| | GTTAAATnCA | nTATTTnAAA | TATATTACCT | TATTAGAAAA | AGTCGTAATA | TGAGGTGTAC | 60 |
| 25 | AAATGACGCA | AATTTTAATA | GTAGAAGATG | AACAAAACTT | AGCAAGATTT | CTTGAATTGG | 120 |
| · | AACTCACACA | TGAAAATTAC | AATGTGGACA | CAGAGTATGA | TGGACAAGAC : | GGTTTAGATA | 1.20 |
| | AAGCGCTTAG | CCATTACTAT | GATTTAATCA | TATTAGATTT | AATGTTGCCG | TCAATTAATG | 240 |
| 30 | GCTTAGAAAT | TTGTCGCAAA | ATTAGACAAC | AACAATCTAC | ACCTATCATT | ATAATTACAG | 300 |
| | CGAAAAGTGA | TACGTATGAC | AAAGTTGCTG | GGCTTGATTA | CGGTGCAGAC | GATTATATAG | 360 |
| | TTAAGCCGTT | TGATATTGAA | GAACTTTTAG | CAAGAATTCG | TGCAATTTTA | CGTCGTCAGC | 420 |
| 35 | CACAAAAGGA | TATTATCGAT | GTCAACGGTA | TTACAATTGA | TAAGAACGCT | TTTAAAGTGA | 480 |
| | CGGTAAATGG | CGCAGAAATT | GAATTAACAA | AAACAGAGTA | TGATTTACTA | TATCTTCTAG | 540 |
| 40 | CTGAAAATAA | AAACCATGTT | ATGCAACGGG | AACAAATTTT | AAATCATGTA | TGGGGTTATA | 600 |
| | ATAGTGAAGT | AGAAACAAAT | GTCGTAGATG | TTTATATAAG | TATTTACGA | AACAAGTTAA | 660 |
| | AACCATACGA | TCGTGACAAA | ATGATTGAAA | CAGTTCGTGG | CGTTGGGTAT | GTGATACGAT | 720 |
| 45 | GACAAAACGT | AAATTGCGCA | ATAACTGGAT | TATTGTTACC | ACGATGATTA | CGTTTGTCAC | 780 |
| | GATATTTTTG | TTTTGTTTAA | TTATTATTTT | TTTCTTGAAA | GATACACTGC | ATAATAGTGA | 840 |
| | GCTTGATGAT | GCaGAACGAA | GCTCaAGCGA | TATTAATAAt | TTATTTCaTT | CTAAGCCTGT | 900 |
| 50 | TAAAgATATA | TCTGCaTTAG | ACTTGAATGC | aTCTTTAgGT | AALTTTCaAG | AGATAATTAT | 960 |
| | TTATGATGAG | CATAATAATA | AATTATTTGA | GACATCGAAT | GATAACACAG | TGAGAGTTGA | 1020 |
| | | | | | | | |

| | ATATTTAATT ATTAAAGAAC CAATTACAAC GCAAGATTTC AAAGGGTATA | GCTTGTTAAT | 1140 |
|----|---|------------|------|
| | TCATTCACTA GAAAATTATG ATAACATCGT AAAATCATTG TATATCATTG | CGCTGGCATT | 1200 |
| 5 | TGGAGTGATT GCAACAATTA TAACTGCCAC AATCAGTTAT GTATTTTCAA | CACAAATTAC | 1260 |
| | TAAACCGCTT GTCAGTTTAT CAAATAAAAT GATTGAGATT CGACGAGATG | GTTTTCAAAA | 1320 |
| | TAAATTGCAA TTAAATACAA ATTATGAAGA AATAGATAAT TTAGCAAATA | CGTTTAATGA | 1380 |
| 10 | GATGATGAGC CAAATTGAAG AATCATTTAA TCAACAAAGA CAATTTGTTG | AAGATGCGTC | 1440 |
| | (2) INFORMATION FOR SEQ ID NO: 726: | | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| 20 | χ. | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726: | | |
| | TGATATTCCG ACTTGCGAGG ATTATTGCGC ATTAAGGATT AACGCAGTAT | GAGTCCAAAG | 60 |
| 25 | ACGCGCGACA CCTGGAAAAA GGATTACCTA ATGCCTTATT TACAGTAACC | TTGTATGATA | 120 |
| | AAGATCGGTT AATTGGTATG GGTAGAGTGA TTGGCGATGG CGGAACTGTT | TTTCAAATTG | 180 |
| | TTGATATTGC AGTTTTGAAA AGTTACCAAG GTCAAGGTTA CGGCATCTAA | TTATGGAGCA | 240 |
| 30 | TATTATGCAA TATATTAAAG GTGTGGCTGT TGAGAGTACA TACGTTATCT | GATTGGCAGA | 300 |
| | CTACCCAGCG GGnTAAATTA TATACCAAAT TTGGGTTTnA TACCTACCGA | ACCAGAnTCC | 360 |
| | AGGCGGTGAT GTATG | | 375 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 727: | - | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 471 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | | | • |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727: | -90- | |
| | TAAAAAACTT AGAGATGAAA ATCATATTAT TTATCTGTTT TTGGGACAAT | TTTTTACTAA | 60 |
| | AAATGAAGAT CCATGGCATC AAATACTTAA TGATTTAGAA GTTACAAATT | CTGTTGATAA | 120 |
| 50 | TTTTTTAAGG TCAATAAGTA ATAAGGCCAA AGAAACAAAA AAAAGAGCTT | TTATTATTAT | 180 |
| | TGATGCGCTT AATGAAGGTG AAGGTAAAAG GTTATGGGGA AATTATTTTC | AAAGCTTTAT | 240 |

| | AGGTTTTAGT AAGGAAGAAA ACTATAATCC AATTGTATCT TTTTTGTGATT TTTATGGATT | 420 |
|-----------|--|------|
| 5 | AGAGCTACCT AAGTTACCTA TATTAAATCC AGAATTCAAC AATCCATTAT T | 471 |
| | (2) INFORMATION FOR SEQ ID NO: 728: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1750 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728: | ٠. |
| , | TAGGATGTTC CACCCTGGCA ATTGCTCTAA GACATCLACa GCAGTAGAAT ayCCTGTTTT | 60 |
| 20 | CGTCLTTTTA ATAACAGGTA ATTGTAATGT CTCAAACAAT ACAACACCTA ATTGCTTAGG | 120 |
| - | AGAATTTATA TTAAAATCTT CACCAGCTGC ATCATGGATA TTTCGAATCA AGACGTCTAA | 180 |
| | TTTTTCTTGA ATTTCTTTTT CCATTTCTTC TAAATCATGA ACATCTGTAA ATATACCAAT | 240 |
| 25 | TTCTTCCATT TCACTTAAAA TCTTAGCTAG CGGTAGCTCT AAATCAGCCA AGAGTTCTAC | 300 |
| | CTGATTGTAT TCTTCTAATT GTTTATCCAT ATTTGGTTTC GCAAAGTAAA TTGCATCAGT | 360 |
| , | AATAGAAGCA ACATATGGAT TTAAAACATC ATCTTCAGGT ACCTTAAATT TCTTACCTTT | 420 |
| 30 | TCCATATATA CTCACATCGT CTTTCACAAA ACTTTGACCG TACAATGAAA CAACTGATTG | 480 |
| , | AACATCACTA ATCGTACGAG ATGGATCAAT TATATAACTG GCCAACATAA TATCGAAAGA | 540 |
| <i>35</i> | AATATTTTGA ATATCAATCC CCAATCTATG TGATGCTACA TATGTTTTTT TAGCATCATA | 600 |
| | TACGACTTTT TTCGAATTCG GATTTTCTAA CCATGAAACT AGTTCGACAT AATTATTTAT | 660 |
| | GTCATCCGCA TTAATTACAA TATGTTTCTC ACCTGLAAAT AAAGAGAATT TTAAAALATT | 720 |
| 40 | ATTECGCAAA TAGETACCAC CGECTAATTC GAAATGGATG GCCGCTTCTT TCAATGAAGT | 780 |
| | AAAATCCAAT ATTATCAAAA GACGTTTCCA ATTTCAAATG TCTTLTCTAT TGCATCTTCA | 840 |
| | ACGCTEGCTG ATTGATCAAT GTCAGCCAAC AATTGTTTGA ATTCTAACTT CTTAAACAAT | 900 |
| 45 | TCGATTTTTT CTTGTTGTTC ATCTLGAKGA GTCATTAACG TATCTTCaAG TTTTACTTCa | 960 |
| | ATCGGACTAT CTACATTAAL CGTTGCTAAT TCTTTACTCA TTAATGCATC TTCTTTGCTA | 1020 |
| * 00 | TTTTGAAGTT TTTCTTTTAA CTTTTTACCT GAAATTTCAT CTAAATGTTC ATAGACACCT | 1080 |
| 50 | TCTACTGTGT CAAATTGGTT TAGCAATTTT ATTGCTGTTT TCTCTCCAAC ACCTGCAACA | 1140 |
| ٠ | CCTGGTATAT TATCAGAAGT ATCTCCCATT AATCCTTTCA TATCAATAAT TTGATTAGGT | 1200 |
| | | |

| | CCTTTTTTAG TGTAATAAAT GGTTACATTA TCCGTTGCAA GTTGTGTTAA ATCTCGGTCT | 1320 |
|----|---|-------|
| | CCCGTAATAA TAATTGTCTG AAAGCCCGCT TTATCTGCTT CTTTACTTAA AGTTCCGATA | 1380 |
| 5 | ATATCATCTG CCTCATAGTT ATCTAATTCA TAACGTTTAA TATGATAAGC ATCTAATAAT | 1440 |
| | TGGCGAATAT AAGGAAATTG CTCACTTAGT TCAGGCGGCG TTTTCTGGCG TCCACCTTTA | 1500 |
| | TATTCACTAT ATTTTCATG TCTGAAAGTC GTTTTACCTG CATCAAACGC TACTAAAAAA | 1560 |
| 10 | TGATTTGGCT TTTCTTCTTT TAAAATCTTC TCTAGTAACA TTGCAAAACC ATATACTGCA | 1620 |
| | TTGGTATGAA TGCCTGCTTT GTTTGATAAC AAAGGTAATG CATAAAAGC TCTAAAACTT | 1680 |
| 15 | AAGCTATTAC CATCGATTAA TACTAATTTA TTCACAATTT TAACCTCCAG AACTAATTTA | 1740 |
| ,, | TATATnTGTG | 1750 |
| | (2) INFORMATION FOR SEQ ID NO: 729: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 439 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | *(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729: | |
| | AAATTAÄTTT TAACATCCTT TCAAAATAGT TTTAACGGAT CCTCCCAAAA CGTAAACTCA | 60 |
| 30 | CATCAGTTAC TTGTAACATG CATTTTCTCC TTTTTTTCAT TCGATATTCT AACGGAAGAA | 120 |
| | TTATATCATA TTATCGTCAC AGTTTCGACC TCATATAAGT TGTAATGATA GAATGACTCA | 180 |
| ~- | CACATGTTAT AATAATAAAG AATACAAGAA TCGAAGGAGA ATAAACATGG CATTAGACAA | 240 |
| 35 | AGATATAGTA GGGTCTATAG AATTCCTTGA AGTAGTAGGG TTACCAAGGT CAACTTACCT | - 300 |
| | TTTAAAGGAC CAACGGTGAA ACGTAAAGTT AAACCAATCA GAATGAACGT GATGATTGAA | 360 |
| 10 | TTAGAAGTAG GGGAGNATAT AGTTCCTCAT TTATCCAACC GGTCAGGTGG ATTATTGCAC | 420 |
| | TCAAATATGC ngnTATACG | 439 |
| | (2) INFORMATION FOR SEQ ID NO: 730: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 481 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | , · · |
| 50 | | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730:

| | AGTTTAGGAT | TGATGACAAA | GCCATTACGA | CCAACAAATC | CTAAACCTGC | ACGTTCTGCT | 120 |
|-----|------------|------------|------------|------------|------------|------------|-----|
| | ACTGCCCTAT | CTGATAATAC | ACCCGTATCT | ACCATAGATT | TGATTTCAAC | ATCTGGAACT | 180 |
| | TTAGATTCAA | TAAATGCAGC | TAACATGTCT | AATCGTTTAC | GCATAATTGT | ATGATAATCT | 240 |
| | TGACCCCACG | ATGCTCTAGC | AAATAAGCCT | CTGCGATCAC | CTCTAACACT | CTTAGGTGCA | 300 |
| | CCTTTCAGTT | TGTTAGGATA | ACCAACTGCA | ATTGCTATGA | TTGACCTTGC | TGTTGGTAAG | 360 |
| | GATAATTTAG | GCTCCGTTCG | TAAAGCAATA | TCAGATTCTT | CAAaTCCTGA | GGCATAACCA | 420 |
| -,. | TTTGCATGAT | ATGCTTCTAG | CTTTTGCTTC | AATTCATCAA | AGGGnTCGGC | AGTAGTAAAT | 480 |
| | С | | | *. | * | * | 481 |
| | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731:

| GTGATGAAAA | ATCTTTTTCT | ATTGATTGAG | AAAATAGTTA | TTTATATAGT | TTTTAAAGAA | 60 |
|-------------|------------|------------|------------|------------|------------|------|
| AAAAGTGAT | AATATTTAGC | TAATCTAATG | AAAATTGATT | TATTGGACAA | AAAATACATT | 120 |
| TTAAATGAGT | AGAGGAGGCT | GCAAWTGGGT | TACAGAACTT | TAAAAAGTAT | TTTTCATGAA | 180 |
| CACAATGAAA | GTAAAATGAA | GGAAGAGTAT | ATTAAAAGAT | TTAATTCTTT | mGCTTCTTTC | 240 |
| AATACTAATA | TTAATATCAT | ACCTATGGAA | AATGGAAAAA | AAGTTAATGA | TTTGGAATAT | 300 |
| CCTCTATTCT. | TTATGGTGAC | тааааатста | TCAAAAAAAC | AAGAATTAAT | ATCAATTAAT | 360 |
| AGTAGAAAAA | TTGATAGAGC | ACTTAATTCT | TTACCATATG | CAGCTAGAGA | ACAATATTTT | -420 |
| AATGATTTAT | TAATCGATGA | ATTACAAAGT | ACTAATGAAA | TTGAAAATGT | ATTTAGTACT | 480 |
| AAACAAGAGA | TTGCACATGC | GTTAAATAAC | CAAGCATCAG | AATTTCTTAA | GTTCAGAGGC | 540 |
| CTCGTGGATC | AATATAAAGA | GATAGAACTT | AAAAAAAA | TTAAAGTTGA | TAATGTAAGA | 600 |
| GACATTAGAG | CGATTTATGA | TAAATTAGTT | TCAAATGAAA | TTAACGAACA | AGATAAGTTA | 660 |
| GATGGAGAGC | TATTTCGTAA | AAATTTTGTC | GGTGTGCATG | ATGGGTCAAC | GAATAAATAT | 720 |
| ATACATGTTG | GGTTACAACC | TGAAACCAAA | ATTGTTGAAT | TTATAGGTGA | AATGCTAACA | 780 |
| TTTTTAAAAT | ATTTTGATGC | GCCTCAGCCG | TTCAAAATCA | TGGCTAGT | | 828 |
| | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 732:

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- (A) LENGTH: 1622 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732:

| 10 | CGTATGTTTC | GAATTTTATG | nATTGCATTG | GATAATAGTA | CCAGTTAAAA | GAACTAAGAT | 60 |
|----|------------|------------|------------|------------|------------|------------|------|
| • | TGTAATTATC | CCCCCTTAAA | ATTCAAGAAT | ATATTTTCTT | AATCTATCAG | CAAGAGGTTA | 120 |
| | TATTTCAAAG | TGTTTATTTT | TAAAACAACA | TCTAAAAGCC | ATTTCATAAt | AAWGTTAAAT | 180 |
| 15 | Cattagaatg | TATAAAGATT | CCAATTAATA | AAAATAGATA | AAATGCAATA | AAGTTCCAAA | 240 |
| | TACTTATTAT | TATTCATCAC | AAATTACGTG | ATGCCCTCTA | CAACACTAAA | TCAAGGATGA | 300 |
| | TATTTATTTT | ATATACATTA | GCATTCATTG | TTTGCTTACC | CACATTATCC | TGTTTAGTCT | 360 |
| 20 | TTTTTATAAC | TCTAGTCTTG | AATGTCATAT | TTACAAAGAA | AAAAACACTA | AAATATTTAA | 420 |
| | AACTAACACT | ATTTATTCAC | TTTGTTCTTT | TATAGCACCT | TTTATGTTTA | TTTTCTTGTA | 480 |
| 05 | TTCAATAAAT | AGTATGGAGA | TGATAATTTA | AAGTAGATAT | ATTTGAAGTA | TACTATAGAG | 540 |
| 25 | TAAATTATAT | TGGGGAAATA | TGTAAACGAA | CCGGTTGATT | TTATAGTGGA | TTAACACTTC | 600 |
| | ATAGAGAATA | TAATCAAGAA | CAAAAACAGT | CAATAGGTGT | GAATTTTTT | AAAGACGGAT | 660 |
| 30 | CTGTTGCTAC | TAAAAAAAGA | AGTATACAAT | TCAATAGTTA | AACCTTAAAA | CAAGAAATAT | 720 |
| | TATTCAAAAT | CAATGAATTT | CCTATCTTAT | TAGTTTTAAC | AATATTTATT | CTCATAGAGT | 780 |
| | TTGTCCAATT | AAATATAGAT | GATTCAAATA | TTTATAAGCA | TACAAAAGAG | CAGTAAGACA | 840 |
| 35 | TTTTCTAATA | GAAAATAACT | TTACTGCTCT | TTGTACATTA | CTCATCAACT | ATTGTAAATT | 900 |
| | AAATAATAAA | TAACTACCTA | TTTTATTATT | CAGCTAAAAA | ATGCTCTGCT | AAATATTTTG | 960 |
| | CTGCGCCATC | CTCTTCATTC | GTGTATGCCG | TTACATCTGA | AGTTAATGCT | TGGATTTCAG | 1020 |
| 40 | GGCGTGCATT | TTTCATAGCA | ACTGTATAAT | GACCAAATTC | AAACATTGCT | CTATCATTGT | 1080 |
| | CGCTATCTCC | AATAACTAAC | GTTTCTTCTT | GATGAATACC | AAAATGTGCA | ATCATTTCTT | 1140 |
| 45 | TAATGCCTGT | ACCTTTATCA | GTTTGATAAG | CCATTGTTTC | CGCATTAAAT | CTTGATGAAT | 1200 |
| 45 | TTGATACACT | AATCTGTAGT | TGCACATGAT | TTTGCTTTAA | TTCATCTCTA | AATGCTGTTA | 1260 |
| | TTTTTTCTAA | ATTAGAACTG | AATAGATAAA | TTTTTGÄATA | TTCACCTTCA | GGAAACTTAG | 1320 |
| 50 | TTACCCAATC | TATCTTACCA | GCAAGCGCAT | CTTGTCTTGA | AGACCATTCA | CTATGACTTA | 1380 |
| | CGCCATTAAT | AGGATCTTGA | CTACGAATCA | TATCTCGCAT | CCATGTTTCA | TCTTCTTTTA | 1440 |
| | AAGAAACTCT | ATTACCTTCA | AAAGGAAATA | CCTCATAATA | AATTTGTTGG | CGCTTAGCTA | 1500 |

| | CTACTTCTCC AATTGTTCCA TTTGAACTAA TGATGCCATT AACCGCAAAA TCTTGAGGTA | 1620 |
|----------|--|------|
| | CA | 1622 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 733: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 472 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| - 4 | the first of the control of the cont | |
| | | |
| 1,1 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733: | |
| 15 | AATGCCANAT AAATCCAAAT TCTTTTAACG AACAAGAGTG CCCAAGTTAT TGCTGATCGT | 60 |
| | TATGCCAGAT ANGCATATCA ATGATAATTA TGGTTTAGAA AGAATTTCTA AGACAAATCA | 120 |
| 20 | TGGATATAAT TATGTGTATT CCAATGATAA TTCAACTAGT AAGCAACATG TAAGTATTTC | 180 |
| | AAATCAAGGC ATAATAACGA AATAATAGAT GGAACAGTGT ATTCTAATTG GATATACTGT | |
| | TITTATTTTG CAATAATTTA ATTTAAAAAG GTGAATTCAA CTTATAAAAT GATGTAAATG | 300 |
| 25 | TTATGTCAAA ATCAACCAAT CCGTAATGTA TTTTAAAATG TTAATATAGT TCTGAAGAAG | 360 |
| | TATAAATGAG GTGTTGAAAT GGCTAAAAAT AAGAAAACGA ACGCGATGCG TATGCTTGAT | 420 |
| • | CGTGCAAAAA TTAAATACGA AGTTCATAGC TTTGAGGTAC nTTAAGAACA TT | 472 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 734: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 519 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * * |
| 2 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734: | |
| 40 | CATAGCCCCA AATTTTTCT ATTATTGTT CACGAGTAAA GATTTGCTTA GGACGTGCTG | 60 |
| | CAAGCATAAA TAATAATTGA AATTCCTTGT TCGGTAACGT CATCGTTTTA TTAGATACTT | 120 |
| 45 | GGAGTTCCAA ATAGGATTGG TTTAGCGTTA AGTTGCCAAT AGTCATTTCT GAATTTGAAT | 180 |
| | TGATATTATA TCGACGTAAT ACAGCACGAA TTCTAAAAAT AAGTTCCTTA ACCTCAAAGG | 240 |
| | GTTTGGTTAC ATAATCGTCA GTACCGCTTA TAAACGCACG CTCTTTGTCA CTAAGTGCAT | 300 |
| 50 | CCCGCGCTGT TAACATAATA ACTGGTATAT CATAATCATT TTTTAATGTA TTACATAATT | 360 |
| | GAAAGCCGTC CATACCATCC ATCATAATAT CTACCACTGC AATATCGACA CGCTGTTTTT | 420 |

| | GTTTTGTHAA ATGGGCTAGC TATAATAATT TAGGGGATT | 519 |
|-----------|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 735: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735: | |
| 15 | ACTTGAAAAC GATAAACAGT ACTTTCCAGC TACACATTGG AAAGCTATAA ATGGGATACC | 60 |
| ,, | TTATGCAGGC AGTAGTGATA TTGATGGATT GCCTCAAGAC GGTATCATTT CGGTAAATGA | 120 |
| | TAAAAATAAA TTAGATAATT TAAAAATAGG CGAACAGGAA TTATTCAAAA TAGCATTGTA | 180 |
| 20 | CAGAAATCCC CAAACGGTAA ATTGTGGAAA ATAACAGTTG ACGATAGTGG GAAACTTGGT | 240 |
| | ACAGTGCTAT TTTATTAGAA AGGAAGGTGC ATTATGGAAA ATTTGTATTT AATAAAGGAT | 300 |
| | TTGGGAGCTT TAGCAGGTCG AGATTATAGA GCTAAGGAAA TACAAAACTT ACAAGGAATA | 360 |
| 25 | GGCATTGCGC TGGGCTGACC ACCAGGGTTT AnGTGnCCnC | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 736: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 780 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | ** *** *** *** *** *** *** *** *** *** | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736: | |
| | CTTTTTATT GAAAAGTGG TATTTGATTA TCTATTTACT ATTTATATTA GCGGCACTCC | 60 |
| 40 | TTATTACATT AACGACAATC CAACATGTAA CAGAAGATGA CAATCATnTT AATATAGGTG | 120 |
| 40 | TCGTAGATAA AGATCAATCA AGTGAAACGA AATTAATCTT AAACTCTATT GGTAAAGGGA | 180 |
| | GTAACCTAGG AAAAAACGTG AGCATTAAAG CATATGATGA TAAGCAAGCA CATACTTTGT | 240 |
| 45 | TAAAAAAACA TAAACTTCAA GGCTATTTTG TTTTTGATAA AGGTATGACC AAGGCATTTT | 300 |
| | ATAAACAAGG CGAACTACCA ATTTCAGTAT ATACATATGA TCAACAATCC ATGAAAAGTG | 360 |
| | TCGTGCTATC TCAGCTAACA GATTCTGTTT ACCAACGTCT TATGCGATCA ATGGGTGGCA | 420 |
| 50 | TCTTAGCTTT TCAAGACTTA GCACCGAAAG CATCACATTC TGACAGTATC AATGTTATGA | 480 |
| | CTGATTTGCT GATLACAGGA TTAAACCGTT CAGGTGCALT TAACTTAGAA CCGATTCATT | 540 |
| | | |

| | CACTATETT ATTTACAGTT TIGAARATGA ATCAAGATAC TGTATTGAAA GCGCGATTGA | 000 |
|----|---|------------|
| | AAATGTTTCA TTTTTCTAAA GAGCGTTTAT TAATCATTCG TACGTTGATT ACATGGTTTT | 720 |
| 5 | ATACTATGTT ATGGGNGTAT CGNTGGTGTA GTTTGGAATG TGGTTCAGTA TTCCGAATNA | 780 |
| | (2) INFORMATION FOR SEQ ID NO: 737: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 946 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737: | |
| | TATTTAATTT CTTnATTnTG GTTTTTAATT nTAAGATGAC CATAAATGAA TTTCTTCTGC | 60 |
| 20 | TGTCATAGAA TTAGAGCAAA ATACGAGCAT AAATTTAACT AATTTCTTGC TTGTCTTATA | 120 |
| * | GTCTTGATTG CCTTGTAAAA ATGTTAGTAT TAATTGCTTC ATCGTTTCGA ATTGTTGTGT | 180 |
| | TGATTTAATA GCGATTGCTA AACCTATATT TTTTTCGAAA AGCTTTTCAA AACATCTATT | 240 |
| 25 | TAACAGGTTG TAATTCGTTT GGCTAATCTC AATATCGTGA ATATCGTCAA TGAAAACGAC | 300 |
| | AGGTTTTGGT AAGTGCTCAA AGTTAATATC GTAATATTCA TTGAAAALAA ATTGAAATAG | 360 |
| | TTCATTGAAA TTACTAAATC GAACAAATAC TTTGGCACGC TGACTTCGAT CTTTCGGATT | 420 |
| 30 | AAAATCATCT ATATGAATAT CTGTTGTATT TGTAGCCAGT TGAGCTGTTA AATCAATTGT | 480 |
| | TGAAATTAAC TCAGTGAATT GTGATACGTT ATCTTGTTGG AAGTGTATTT GTGGTGGTTC | 540 |
| | AGTAATCTTG GAAACGAGTG AACGGAACTG TTTAGGACTA AAATGCAAGT AATTCTTAAA | 600 |
| 35 | TTGATTTGCA AAATTTGTAT GACTGTTAAA ACCGGCCAAT TCAGAAACAG TTGTAATAGA | 660 |
| | ATGTTTTGTA GAAAGTAATA AATTGATGGC GTTAACAAGT TTAATACTTG TAAAATAATC | 720 |
| | TTTAAAATTC ATACTCAAAT ATCGAACAAA AAGATTAGAA CAATATGATT CAGAGATGTT | 780 |
| 40 | GCAATGCATC GCTATATCTT TTAAAGACAA GTGCGCATCA ATATKGTCAT GAATATAGTT | 840 |
| | TACACAGTCT ATGAACACCG GATTGCTTAA AGCAATATTT GGTAAATATT CATGATCTAT | 900 |
| 45 | TCTTATAAAA GCTTCTTTAA GTAAAGTGTC TATHATACTT TGACCT | 946 |
| | (2) INFORMATION FOR SEQ ID NO: 738: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 397 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . . |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738: | |
|----|---|-----|
| _ | TTTATTTGAT GATGTACTAA AGCAAGATGA AAGATTTGTT ATTGTAGTTC AAGCATTAGA | 60 |
| 5 | AGAAAAGAAC GGACAATTAT TAAAGAGAAC TTTAAGGGAA TATCCCGGTT TAAACCATAA | 120 |
| | ACAAATGAAT GATTTATTTA TGCACTTAAA GGAATTATTT TCCGAAGAAT CATTTGCTGA | 180 |
| 10 | AAACCAATCA GCGTTCAGTA TTACAGTTTA TACAAATTTA GATTATACTG CTGACCAAAT | 240 |
| | ATATGCTCAT GTAAAACGTT TCAGAGGTAA GCATGACTGG ACACAAACAG CTAAATAAAA | 300 |
| | TCAAGATGCT TGCAGTGGAT TKTAACmATT AATGETAGAT GTCmCyGcAT TTTTAATGCC | 360 |
| 15 | ATTCGGTAAT TAATCCGGAT GGTCCAATTT AATTAAC | 397 |
| | (2) INFORMATION FOR SEQ ID NO: 739: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 915 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739: | |
| | CAAGGTATTT CATTTGACCC ATTCACACCA TTAATAGTGG CAGCAGCATT ATACTTTGTC | 60 |
| 30 | TTAACATTTG TACTTACACG CATTATGAAC ATGATTGAAG GGAGATTGAA TGCCAGTGAT | 120 |
| | TAAAATAAAC AATCTTAATA AAGTTTTTGG AGATAATGAA GTTTTAAAAS ATATCAATCT | 180 |
| | TGAAATCAAT CAAGGGGAAG TAGTAGCAAT AATAGGTCCA TCTGGTAGTG GTAAAAGTAC | 240 |
| 35 | ATTGTTAAGA TGTATGAATT TATTAGAAGT ACCTACTAAA GGTCAAGTGA TTTTTGAAGG | 300 |
| | CAATGACTTA ACGGAAAAAG GGACACAAGT AGATAAACTA CGTCAAAAAA TGGGTATGGT | 360 |
| 40 | ATTTCAAAAC TTCAACCTAT TTCCACATAA AAAAGTTGTC GATAATATTA TTTTAGCTCC | 420 |
| | TAAATTATTA AAGAAAGATA ATAACGATGA ATTACATAAG GAAGCATTGT CGTTATTAGA | 480 |
| | TAAAGTGGGA TTAAAAGAAA AAGCAGATGT ATATCCGAAT CAATTATCAG GTGGTCAAAA | 540 |
| 15 | ACAAAGGGTA GCAATTGCAA GAGCTTTAGC AATGCATCCA GATGTTATTT TATTCGATGA | 600 |
| | ACCAACTTCA GCATTAGATC CTGAGGTAGT TGGTGATGTA TTAAAAGTAA TGAAAGACCT | 660 |
| | AGCCAAAGAA GGTATGACCA TGGTGGTTGT GACACATGAA ATGGGATTTG CCAAAGATGT | 720 |
| 50 | AAGTGACAAA GTCATATTTA TGGCAGATGG CGTTGTCGTA GAGTCAGGCA CnCCAGTCGA | 780 |
| | AATATTTGAA CAACCGCAAC ATGAAAGAAC ACAAAATTTC TTAGCAAGAG TATTATAACA | 840 |
| | ACCTAACGAG GCTTGAATAT ATGATACGCA CCACAAAGTT ATATCATATA TTCAAGCTTT | 900 |

(2) INFORMATION FOR SEQ ID NO: 740:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 435 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740: | |
| | AGTAAATGCG ATGTTGCATG GAGGCTATAG CAATGAGCAA TAAAGCTTGG GGCGGTAGAT | 60 |
| 15 | TTGAAGTACA ACCTGAAGAG TGGGTTGACG ACTTTAACGC ATCCATTACT TTTGATCAAA | 120 |
| | CGCTCATAGA TCAAGATATC GAAGGCAGCA TTGCACATGC AACTATGCTT GCGAATCAAG | 180 |
| | GCATTATTAG TCAACAAGAC AGCGAACAAA TTATACAAGG ACTAAAATCT ATTCAACATG | 240 |
| 20 | ATTATCATCA AGATCAAATT CAATTTAGTG CATCATTAGA AGATATTCAT TTAAATATTG | 300 |
| | AACATGGAAT TAATTAAACG TATCGGTGGA TGCTGGTGGT AAGTTGCATA CTGGACGCGT | 360 |
| | AGTAAACGAT CAAGTTGCAA CAGACATGCA CTTGTACACT GAAGAAACAA GTGCAAGnnn | 420 |
| 25 | TCATCGCATT GGATG | 435 |
| | (2) INFORMATION FOR SEQ ID NO: 741: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1198 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741: | |
| | AATATCATAA CCAAAGCTTG TCATTACTTA TATGTAAAGA TTAGAGGCTA ATTACATAAT | 60 |
| 40 | CCTAACTTAT TTAACAGGAA GTCATGAAAA CTATATTACA ACTAAAAGTA TAACTTTCCA | 120 |
| | TCACCAAAGT CAGAATTTAT TGAAACACTC AACTGATAAT ATAGAAGGCT AATTATAAAA | 180 |
| 45 | ATACCTGGCG ATTAATAAAC TGTTTCCGTT TTTTAGCACT TAATATATTT AAAAAGACAA | 240 |
| 43 | ATAGAGCCCT TTCAGGCTCT ATTTNCTGTA TCCTTAACAA CAGAAGCTGT TAAAACTACC | 300 |
| | CGTCTTTTCa CAaCCAAaGc TaCAAAAaaG aTgGCTAGTT ATTCTTTCGT CACCCGCTGA | 360 |
| 50 | ATCATTAGTG TTGTTATTTC CTTTAACTTG CACGTCTAAA TCAAGAaCTT TTTCCAAaGA | 420 |
| | TAAAACCCCC TATTTAAAAG TTGAAGTTAA GACCCCTTCA ATTGTCATAT TAATCATTAC | 480 |
| | CACACAATAA ATCAATGAAT TTAATAATAA TTATTTGTTA TTAATTTGTA AATCGTCATT | 540 |

| | TGAATATTTT | TTGTTTAACT | CTTAAATTTC | GGGTTTAACT | TCCTCTATTT | CTAACAGTTA | 660 |
|----|-------------|-------------|-------------|------------|------------|------------|------|
| 5 | TACTCCAGGA | TTAGTTTCTT | TAGAATCCGT | ACCGATTAAT | TTAACAGTAT | GGTTTTGCCA | 720 |
| 5 | GTCAACTTCA | TAAGTAGATG | TAAACGTTAC | TGTATTTTGA | TnTTTGTAGT | TATTTCCAAC | 780 |
| | CCAGTGTAGT | CGATTCCATT | GATTAGTATA | TCTATCCATT | TCTCTTTGGT | AAGTTACTTT | 840 |
| 10 | GATTTTAGAT | TETTTTGTAT | CATTTTGTTT | ATGAGAAAGT | ACGCTTATAA | ATTCTGGGTT | 900 |
| | AAAGTTACCA | CGCGCCAATA | AAGGCATTTG | ATGTGTTGGC | AAGAAATTTT | GACCAGCATT | 960 |
| | TGAACTACTT | TGTCTACCAC | CTAAAAACAG | TTCATTACCA | TATGTTGGGT | CATAACTATC | 1020 |
| 15 | TCTACCATAT | GGTCCCCAAC | CATTATTCAT | AATTTTGTGC | GCCTCAACAC | CCCAGCCAAT | 1080 |
| | TGATTTATGA | TTTGTTTTTC | TATCAATCGT | AGTTCTGTAA | CTITCTTGTT | TATAATTTAT | 1140 |
| | CGTTTCTGAA | AATGATTTTG | ATCCATTTAA | TCCACCTGAT | AAGCCATTAG | ATATATTA | 1198 |
| 20 | (2) INFORMA | TTON FOR SE | O TO NO. 74 | | | | |

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 818 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

| 30 | (X1) | SEQUENCE DES | SCRIPTION: | SEQ ID NO: | 742: | | |
|----|------------|--------------|------------|------------|------------|------------|-----|
| | GTGGCATATn | CAAACTACTA | CTGAAAGATC | AATTACATAC | GTACAGATTT | TGCAAAATGA | 60 |
| | TCAAGATTAT | CCAACAATTT | TTAGATGAGa | CAAAACGTAA | ATCTGTAATT | AATTCAGATG | 120 |
| 35 | TTAATGTAAC | GGTAAAAGAT | AGAATAATGA | CTTTATCAAC | GTGCGAAGAT | GCATATAGTG | 180 |
| | AAACGACGAA | AAGAATTGTT | GTTGTCGCAA | AAATAATTAA | GGTAAGTTAA | ACAGAAAmGA | 240 |
| 40 | GGATAATTAT | GAAATTTATG | GCAGAAAATA | GGCTGACGTT | AACaAAAGGA | ACAGCAAAAG | 300 |
| 10 | ATATTATAGA | ACGATTTTAC | ACGAGACATG | GGATTGAAAC | ATTAGAAGGC | TTTGATGGCA | 360 |
| | TGTTTGTTAC | ACAAACTTTA | GAACAAGAAG | ATTTTGATGA | AGTGAAAATT | TTAACAGTTT | 420 |
| 15 | GGAAATCAAA | GCAAGCTTTT | ACGGATTGGT | TAAAATCTGA | TGTCTTTAAA | GCAGCGCATA | 480 |
| | AACATGTTAG | AAGTAAAAAT | GAAGATGAAA | GTAGCCCGAT | TATAAATAAC | AAAGTAATTA | 540 |
| | CATATGATAT | AGGCTATAGT | TACATGAAAT | AATTGAATTT | AAAGAGGTTG | CAGTACTTGT | 600 |
| 50 | TATGACAATT | GGTATTGTTA | GCTTTTGTAA | CGACCATACA | TGATACCGAT | GATGGTCGTT | 660 |
| | TTTTTAATGa | ACACAAACAT | GCTAACAACA | AATTGCTAAA | ACATAGTTTG | aTTTGAATGT | 720 |
| | GgCTTTGGAA | AATAATCATC | CAtTATATCa | TTtTGGATTn | TATTTTGGAA | GAAGAAAAGA | 780 |
| | | | | | | | |

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(2) INFORMATION FOR SEQ ID NO: 743:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1209 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743:

| | | | | • | | | |
|----|------------|------------|------------|------------|------------|-------------|------|
| | TGCTGGTAAA | TCTTCCCTTA | TCAAGTCTTT | AATTGGTGAA | TTTAATGCTA | CCGGTACTAA | 60 |
| 15 | ATTGTTATAT | AACAAACCTA | TACAACAACA | ACTGCAACAT | ATTACATATA | TTCCACAAAA | 120 |
| | AGCACATATT | GATTTAGATT | TTCCTATAAG | TGTGGAACAA | GTGATTTTAT | CAGGTTGCTA | 180 |
| • | CAAAGAAATT | GGATGGTTTA | GACGACCTAA | TAAATCAGCA | AGGGATAAAC | TCAAACAGTT | 240 |
| 20 | ATTAAGCGAT | TTAGAATTAG | AATCTTTACG | TCATCGACAA | ATTTCAGAAT | TAAGTGGTGG_ | 3.00 |
| | ACAATTACAA | CGTGTGCTAG | TAGCAAGAGC | ATTGATGTCC | GnAAGTGAAG | TTTATTTTCT | 360 |
| | AGATGAGCCG | TTTGTCGGAA | TTGATTTTAG | TAGCGAAAAA | tTAATCATGA | CAAAAATcGA | 420 |
| 25 | GAACTTAAaA | CAACAAGGAA | AACTTATTCT | TATCATCCAC | CATGATCTAT | CAAAAGCAAA | 480 |
| | GCAATACTTT | GATCGCATTA | TTCTATTAAA | TCAAACATTA | CGATACTTTG | GTGATAGTGA | 540 |
| 30 | AGAGGCTATG | AGTGTCACTC | GCTTAAACGA | AACATTTATG | AGTAGCACTG | ACTGTAGTGA | 600 |
| | CCCTAGTCAA | AGGAGCAATA | TAACATGTTA | GAGTTTGTCG | AACATTTATT | TACATATCAA | 660 |
| | TTCTTGAATC | GAGCATTGAT | AACTTCAATT | ATTGTAGGGA | TAGTTTGTGG | TACAGTTGGT | 720 |
| 35 | AGTTTAATTG | TATTACGTGG | TCTTTCATTA | ATGGGAGATG | CAATGAGTCA | CGCAGTATTA | 780 |
| | CCTGGTGTTG | CCCTATCATT | CTTATTTGGT | ATTCCAATGT | TTGTAGGCGC | ACTTATAACT | 840 |
| | GGTATGATCG | CAAGTATTTT | TATCGGTTAT | ATCACATCTA | GTAGTAAAAC | GAAACCTGAC | 900 |
| 40 | GCCGCTATTG | GAATTAGTTT | TACCGCTTTC | TTAGCTTCGG | GGATTATTAT | TATTAGCTTA | 960 |
| | ATAAACACTA | CGACAGATTT | GTACCATATT | CTGTTTGGTA | ATTTACTGGC | AATCACAAAT | 1020 |
| 45 | AGTGCATTTT | TAACAACTAT | TGTGATTGGT | TCAATCGTCC | TTATTCTAAT | CATTATTTTC | 1080 |
| 45 | TATCGTCCAT | TAATGATTTC | TACATTCGAT | CCAACGTTTA | GTAGAATGAG | TGGTCTAAAT | 1140 |
| | ACGACGTTAT | TACATTACTT | TGTGATGTTG | tTACTCTCAT | TAGNAACAGT | AGCAAGTALT | 1200 |
| 50 | CmAACGGTA | | | | | | 1209 |

(2) INFORMATION FOR SEQ ID NO: 744:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 675 base pairs

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744: | |
|----|---|-----|
| | CCGCCTTTCG TAAACCTAAT ATAATACGAA ATTTTCGTAT TGTCAACATT AAATACGTTT | 60 |
| 10 | TTTTCGTAAA AAACTTTACT ATGATATGAA AATTTCGTAT AATAAGAAAA AAGGAGGTAA | 120 |
| , | GTAATATGAA CAAAGAMAGM AATATTATTA TAGCCAAAAM CATTAGAAAA TTTCTCAACG | 180 |
| , | ATTCAAATAT GTCTCAAAAG AAACTTGCTG AACTCATTAA CATAAAACCA TCTACTTTAA | 240 |
| 15 | GCGATTATTT AAATTTACGT TCCAACCCCT CTCACGGCGT TATACAAAGG ATAGCTGATG | 300 |
| | TTTTCGAGGT TGGTAAAAGC GACATAGATA CTACATACAA AGACGATAAC GACATCACTT | 360 |
| | CCATATACAA CAAACTCACA CCTCCCCGCC AAGAAAACGT ACTTAACTAT GCAAATGAAC | 420 |
| 20 | AATTGGAAGA ACAGAATTCT AAAGGAGATA ACGTTGTAGA TATTAATTCA TATAAACAGG | 480 |
| | AGAAAACTCC AGTTAACGTC AATGGTTGCG TCTCTGCTGG TGTAGGAGAA CGTTTACACG | 540 |
| | ATGAAACGCT ATTTACTGAA ATGGTTAAAG GACCTATCCC CACACACGAT TTAGCGTTAA | |
| 25 | AAGTAAATGG TGATTCTATG GFACCTATGT TTAAAGATGG CGAAATCATA TTTGTGGAGA | 600 |
| | AAACTCACAA THTGA | 660 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 745: | 675 |
| 30 | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 924 base pairs | |
| 35 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | · |
| | (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745: | * |
| | CAGGTGTCAT AGTTGAACTT GGLGGTTTTG GACTAATCGT TAAATCATCA ATTTGTGTCA | 60 |
| | TCCAAGGTTG GAATTTACTG CCTTGTGTCT CCAGTGCGCT GAAAATACCT TTATCTTGAA | 120 |
| 45 | ATAAGTCAAC TAACTCTTGG ATACCTTTAA TTAATGCTGG GTTACCACCA GAAATTGTAA | 180 |
| | CGTGGTTAAA TAAATCGCCA CCAATTCGTT TTAATTCATC ATAAATTTCT TCAGCGGTCA | 240 |
| | TGAGTTTTAT ATCGCCTTTA GCACTACCAT CCCAAGTAAA TGCAGAATCA CACCAGCTAC | 300 |
| 50 | AGGATAATCA CATCCAGCTG TTCTCACAAA CATCGTTTTT CTACCGATTA CTCGACCTTC | 360 |
| | ACCCTGAATG GTTGGACCGA ATATTTCGAG TACAGGAATT TTAGCCATTA GTTACACCTG | 420 |
| | TTCCTTTGGT CTAAATACGA CATAACTTGT TGGTGTTTCT CTTACAAATA CTTGAATACA | 480 |

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| (2) INFORM | ATION FOR SI | EQ ID NO: 74 | 46: | | | *. |
|------------|--------------|--------------|------------|------------|------------|-----|
| CCACAGCCAT | CCCCAATGAT | ACCG | * | * | | 924 |
| CCTTTACTTT | CAAGATATTG | ATTTAGTCCA | CGTTGACGTA | AATGACAAGC | TGGACATTCA | 900 |
| ATTCGAATTG | ATATGGATGC | GTTGTACTAG | GATAGATTTG | TTGTAACATT | TTAAAGCGCT | 840 |
| AAATACCTGC | TTCTTCACAT | GGAATGTGAT | GTGCAGCCGA | AAAATTAAAA | TCTTTATTTA | 780 |
| ATCTAGTTTA | TCACCGACAA | TTGTTAAaya | CAAAGTAAGT | ATGACCATGG | ACATTTTGAC | 720 |
| GTCAAATTTA | CCGTGTATCA | TCTTTTTCAA | ATGGCTAAAG | TTCACTAAGA | AGCCAGTGTC | 660 |
| TACGATTTCA | GTTGAAGGGA | TTTTGTTTTT | AAAAGCAGGT | AAGTTATTTA | ACAGTTGATG | 600 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 971 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746: 25 ATCTTTTGGG TATTTCTAT ATTAGCTGTT GTTTTCTTAG TATTATTTAG TTTTGCTGTT 60 GGTGCATCAA ATGTACCAAT GATGATTTTA ACATTTATAT TACTCGTTGC AACCTTTGGA 120 ATTGGATTTA CTACAAAGAA AAAATATCGA GAAAACGATT GGCTATAAGT TATATCGACA 180 30 ATAACACGCG TTGATTTAAG ACCACACATG TTCATGATGA ACATTTAACT GGTTTTATAT 240 TGGCGCGTGT TTTTATTATT TAAGGTATAA AAGCGTAATA TGTTACCTAA TTGTTAGGAC 300 TACATATTAC GCTTTTGGTA ATTATTTTGA TTTTCTTTTA AATCGTTGTT CATGTAATTG 35 360 TATTAACGCA TCATGGTGGG GCTCTAAaTA ATCATLGCTA ATTCTTGATG GAGACCmCGA 420 TTtCCAACTA rGATkGAATT kGGACCmCTA ATkGTTAATG GTCctCCTAG TAAATTGGAA 480 40 GCTTGTCCAT TACTTCCATA TAAALAACCA ATCCGCCAGC AAALCCCCAT GGTKGAAGTC 540 TTGGCGTCAT ATATGCTTCT AAATTACCTG TAGCAACTGA AACGATTTCA AGCGCTGCAC 600 TACCATATGC CCTTGCACTT CTAGAATCAT TAACAATTTC TTTAAAGATT TCTCCTAAAA 660 45 TTGGTTTAGT TAACCAGTTC GGATTGATCC CAATAATGCT TTGTCTTAGA TTAGAATCAT 720 TCAATGGTTT CAAGGGTTGG CTACCACGAT ATGCACCTTC CCCTACTTTA GCATGATATA 780 AGACATCAGC CATAACATCA TATACAAAAC CTGCATAAGG TTTACCATCG ATATAAATAC 840 50 CAATTGAAAT TGCGAAATTT TCTTGTTGAT GAACAAAATT CAATGTACCG TCTATTGGGT 900 CAACAATCCA TACCGTACCT TTGGAAGTAT CGATGTCATG ACCATGCCCT TCTTCACCTA 960

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(2) INFORMATION FOR SEQ ID NO: 747:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 865 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747: | |
| | TTCTCGTCAC TGTACGTTGT ATTGCGGCAT CATCCATTAT GATACGTTCA GACATATTCT | 60 |
| 15 | CACCCTTTCA AAATTTAGAA ACAAAAAACC TCATGTCTTT AATATCGACA TGAGGTTTAG | 120 |
| | TATATACAAT CAGCCTATTT ACATAGAAGA ATCGTAGTAT TACTACTTAT TCTTGCATAT | 180 |
| | GTGAAAGTGT TATGATCATT TTAGTATATA TCTATATTTT CATGTCTTTG ACGTCTCTCT | 240 |
| 20 | GGACGCTCAA TTAAAGACTC TTTATGTTGT ACTTAAACTG TTATAAGGAT AATACTAATC | 300 |
| | AGGCGCTTTG TCAATCTATA TTGAAAAATT AACCATACTC AGTAAAAATG TTAACCTTAA | 360 |
| | TCTATTTTAT AATGTGTTTT CATTTAAAAA AAACGAAAAC GATAAACACT TATAGTTTAC | 420 |
| 25 | ATAATAATGT TATCGTAATT ATAGCACGAC ACAATTATGC ATCTCTTTTT CGAATTGTAT | 480 |
| | CTAATAAATC TTCAAAGTCT TGTGGTAATT CAGCATGTCT TTCAATATAT TCACCTGTTA | 540 |
| | CTGGATGTTC GAATCCAATA AGTCCAGCAT GTAGAGCTTG ACCACCAATA TCCAATGTCT | 600 |
| 30 | TTTTCGGTCC ATACTTTGGA TCACCAACTA ATGGGAAGCC AATATATTTC ATGTGAACAC | 660 |
| | GGATTTGATG CGTACGTCCT GTTTCAAGTT GACATTCAAC AAGCGTATAA TCTTTAAAAT | 720 |
| 05 | GTTCTAGTAC GTTAAAATGT GTCACTGCTT CCTTACCATC ATCAnCAACA GCCATAGATT | 780 |
| 35 | GACGATCATT TTTGTTTCTA CCAATTGGCG CATCGATTGT ACCGTAATCA TGAGGAATAT | 840 |
| | TCCCGTGGAA CTAAAnCGAT ATAGT | 865 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 748: | • |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 818 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748: | |
| 50 | ATAACATTGT GGAGCCTATG ACATTGATTT ATGTCTCGGT CTCAAATGTT CTTGTAAAAA | 60 |

1643

AACTAAGTAT AGTTGAATTT TAAGTTAAAA AAATTGTTTT TGCAAAAATA AAATAATCCA

*5*5

| | TTTTAGGTTC | TTCGCCTCTA | AAAATCCTTG | CGaTATTAGA | GCGATGTCTA | ATTATCAATA | | 240 |
|----|------------|------------|------------|------------|------------|------------|----------|-----|
| | TGATTGAAAC | TAAGAAACTA | ACGACTAATA | AAATATAGTC | TTGAATGATA | AGCGAGCCAA | | 300 |
| 5 | TCACACAGCA | AATTGCTGCA | ACGATACTTG | CTAAAGAAAC | ATATTTAAAA | ATCTTCAATA | * | 360 |
| • | CAATAAAGAA | GATAATTGCA | AGTATTAGTA | AAAGTATCGG | ATTGACTCCC | AAGACGACAC | | 420 |
| 10 | CTGCACTAGT | TGCAACAGCT | TTGCCACCTT | GGAATTTTAA | ATAAACAGGA | TAAACGTGTC | | 480 |
| | CAAGTATAGC | GAATAAGCCA | ACAATTAAAC | CATTTGTAAA | AAAAGTACTA | ATAGGGCCAT | un des . | 540 |
| | CTGCGTGAAC | TTGTAACCAT | AAAGGGAAGA | AAACAGTTAT | GAACCCTTTG | ААААТАТСТА | | 600 |
| 15 | GAAATGTTAC | CAAGAATCCT | GCAGGACGAC | CTAATACTCT | AAAGCTATTA | GTAGCGCCAG | | 660 |
| · | TATTACCACT | ACCAAATTGT | CTAATATCTT | TTTTGAAAAA | TAATTTTCCA | ATTACGAATC | | 720 |
| | CACTTGGGAA | AGCGCCGATA | AGATAACTTA | GTAGTAACAT | GACGATTATC | ATCATAAATA | | 780 |
| 20 | TTACACATCC | TTTAATATCT | TAGGACTATT | TTATCATA | *** | | ٠ | 818 |

(2) INFORMATION FOR SEQ ID NO: 749:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 971 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749:

| AIAICCAAIA | ACIGITCATI | GTCTTGATAT | TCCTTAAATG | TTTCATAATG | CTCATTAGAA | -60 |
|------------|------------|------------|------------|------------|------------|-----|
| ATGACAATTT | CAAGCAACCA | ACCCGTGCCA | CTTTCCTCTT | TATTAATTAT | TACGCCATCT | 120 |
| TCTAATTCAT | ATTCTATAAT | TCTGCCGTGT | TCATTCACAA | TTTGAAACCT | TACTGCTTTA | 180 |
| AAAGTTTTCA | TATTCCCACA | TCCCATTAGT | TTAATATTTA | TGATTTTTGA | ATTATTTAGA | 240 |
| AGATTTAAGG | TCATTTCATG | ACTAATTTCT | TTAAATATAA | CAAATAACGA | GATGCTATAG | 300 |
| CTATTAATTA | TATAAAATTT | GcCATTTTGa | CCATTTTTAA | GCTAGTAATT | AAGATATAGG | 360 |
| CATAGGAGGT | GAATCACACA | CTACATGCTA | AATAAAATCG | TAATTGTCGG | GAGCTGACGA | 420 |
| AAGACGCACA | AATATTTGAA | AAGGAGGATA | GAAAAATTGC | AACGTTTTGT | GTTGCAACGC | 480 |
| ACCGAAATTA | TAAAGATGAA | AATGGAGAAA | TCGTCTGTGA | TTACTTATTC | TGTAAAGCAT | 540 |
| TTGGCAAGTT | AGCTTCTAAT | ATAGAAAAAT | ATACTAATCA | AGGTACATTG | GTTGGTATAA | 600 |
| CTGGTCAAAT | GAGATCAAGA | AAGTATGATA | AAGACGGACA | AACACACTTT | GTCACTGAAT | 660 |
| TATATGTTGA | AACAATAAAA | TTTATGTCCC | CTAAATCCCA | AAATAATGAA | ATTCTCTCAG | 720 |

| | TCCAATTATC CTAAACATCC TTAATATACA TTTAATCCAT CCTAAATTTT TTATAGATCT | 840 |
|----|---|-----|
| _ | AATTAACTTG AAATATACTC ACTTAAAAAC GACTTACATG ACCTAGTACT GTTGGTAAGG | 900 |
| 5 | TCGnCTTTTG GTGTAGTTTT CCTAATAGAN AATAGACnTA GGTTGCCAAA CCGATTACAT | 960 |
| | AAAAAATTGC C | 971 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 750: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 832 base pairs (B) TYPE: nucleic acid | |
| 15 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750: | - |
| 20 | ATAGATTACT CTTTTGATCT GTAGATCCTA CTGTAACGAC ATTGTCCATA GATGCAGGAA | 60 |
| | CATCTITCAC TTCGCCATTA CCTTGATATT CACGCTGTAA TTTTAGTTTC TGTTTGTCAT | 120 |
| | TGACATCAAT ACCATCATTA CCAGCTGCAG CAACAACGAT AGATTTTTTC TTCTTGGCGT | 180 |
| 25 | AATTGATTGC TTTCTGTAAC GCATCGTATT CTACTTTTTC ATCTTTTCTA AATGTTTGAT | 240 |
| | GGTCATTTTT GTCCAAAATA ATATAACTAC CAACACTAAT ATTAATGACT TGaTTTCCAT | 300 |
| 30 | CATTTGCAGC TTGAACAATC GCTTTTGATA CCCAAAGCAG TTCTGTTTTT TTACTACCAA | 360 |
| | ACACGCGATA CATTGTAAAT TTGTTATTCG GTGCAACACC TATTAACTTA CCATTAGCAC | 420 |
| | TCGTTTGACC CGACACCATC GTGCCATGTC CTTTCCTATC ATTGACATCG TGAACATCAC | 480 |
| 35 | CTGTTTCCTC CGGTTCAGTA CCTCTAAAAC CGTTTAAAGG TACTAAATTT TTAGAATCAG | 540 |
| | TCGAGAAATT ATTTTCAAA TCGTCATGGT TTTTCATCAC ACCTGTATCT ATGATTGCTA | 600 |
| | TTTTGGTGTT AGCATGTTTT GGCAAATCAT CATACGATGC ACCATTATTG GTTATTTTAT | 660 |
| 40 | TCATATCCCA TIGTCTTGAA AATAATGACT CATTTGATGT TCTGTCTATT GTTTTCTCGC | 720 |
| | TAGTAATACA AGTTGAACAT GTGGCATTGA TATATTTAAL ATCATTTTTA TAGTTTGCTA | 780 |
| | AAGCATTAGC ATGCATTTTC GTCATTTTAA TCTGTGCCAC ATGGAATTCC GG | 832 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 751: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 475 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| GTAATATCAA | TCTCTTCATA | AGCTGAATTA | TTTTCATGCA | CTTCTTGATG | TGATGATTTG | 60 |
|-------------|--------------|--------------|------------|------------|------------|-----|
| TCACGAACCG | CTACAACTAA | CATTTTATCG | TCTAAAATAA | GTTGTTTATA | TTTTTCTAAT | 120 |
| TCATCAGGCG | CTAAGTTGTA | GCGTGATAAA | ACTGCATGTT | CACCATCTTC | TCCTGTTAAC | 180 |
| AGTITAGTCA | TTCTATCACT | AAATGTTCCA | CTTGTTGAGA | TAAGGGAGAT | TTCAGAGTCG | 240 |
| TGTAAGTCAT | TTAGGTGTAA | TTTACTTTTA | CTAATAATTG | TTAGCTCTGA | TTCTAAATAA | 300 |
| CCTTCAGATT | TCTTTTGATT | GATTACGTTG | TATAATTCGC | CAGTGTCATT | TACTACAGTA | 360 |
| ATATCTGCCA | TAGTTGTCGC | CCCTTTAAAA | ATTTGTTTAT | tTAATCTTTT | ACCCTTCTTA | 420 |
| TnATAAAGTA | AAACCCTTAC | ATTATTAAGT | nATAAGTCTT | CATTCGCATT | AAACG | 475 |
| (2) INFORMA | ATION FOR SE | EO ID NO: 75 | 52: | | | |

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 1019 base pairs(B) TYPE: nucleic acid

(C)_STRANDEDNESS:_double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752:

| GCGACACTTG | TGAGTTCTCC | AGCAGCAAAC | GCGTTATCTT | CAAAGGCTAT | GGACAATCAT | 60 |
|------------|------------|------------|------------|------------|------------|------|
| CCACAACAAA | CGCAGTCAAG | CAAACAGCAA | ACACCTAAGA | TTCAAAAAGG | CGGTAACCTT | 120 |
| AAACCATTAG | AACAACGTGA | ACACGCAAAT | GTTATATTAC | CAAATAACGA | TCGTCACCAA | 180 |
| ATCACAGATA | CAACGAATGG | TYATTATGCA | CCCGTAACTT | ATATTCAAGT | TGAAGCACCT | 240 |
| ACTGGTACAT | TTATTGCTTC | CGGTGTAGTT | GTAGGTAAAG | ATACTCTTTT | AACAAATAAA | 300 |
| CACGTCGTAG | ATGCTACGCA | CGGTGATCCT | CATGCTTTAA | AAGCATTCCC | TTCTGCAATT | 360 |
| AACCAAGACA | ATTATCCAAA | TGGTGGTTTC | ACTGCTGAAC | AAATCACTAA | ATATTCAGGC | 420 |
| GAAGGTGATT | TAGCAATAGT | TAAATTCTCC | CCTAATGAGC | AAAACAAACA | TATTGGTGAA | 480 |
| GTAGTTAAAC | CAGCAACAAT | GAGTAATAAT | GCTGAAACAC | AAGTTAACCA | AAATATTACT | 540 |
| GTAACAGGAT | ATCCTGGTGA | TAAACCTGTA | GCAACAATGT | GGGAAAGTAA | AGGAAAAATC | 6,00 |
| ACTTACCTCA | AAGGCGAACT | ATGCAATATG | ATTTAAGTAC | AACTGGTGGT | AATTCAGGTT | 660 |
| CACCTGTATT | TAATGAAAAA | AATGAAGTGA | TCGGaATTCA | TTGGGGCGGT | GTACCAAATG | 720 |
| AATTTaATGG | TGCGGTATTT | ATTAATGAAA | ATGTACGCAA | CTTCTTAAAA | CAAAATATTG | 780 |
| AAGATATCCA | TTTTGCCAAC | GATGACCAAC | CTAATAACCC | AGATAATCCT | GATAACCCTA | 840 |
| ACAATCCTGA | TAACCCTAAC | AACCCAGATG | AACCAAATAA | CCCnGACAAC | CCTAACAACC | 900 |

| | CAATTAAGTT CGTCTAGATA AAATAGGAAG CAAAGTCTTA GCAACGTAAA ATATTTTGA | 1019 |
|----|--|------|
| - | (2) INFORMATION FOR SEQ ID NO: 753: | |
| 5 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 533 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| 10 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEO ID NO: 753: | |
| | ATTCTTATCC CAGGTAGGTG NTTTACTTCT TATATTAGGT GCAATAACTC ATGCCACTCA | 60 |
| 15 | | |
| | TCTTGTGGCA CAACATGAAT CGCATTTTCA AAAATTGCAT GTCCTGCTTG ATCAGTCAAA | 120 |
| | CCGGCAGCAT GATCAAAATG CATATGTGTC ATTAGCACAT AATCAATATC CTTTGGCGTT | 180 |
| 20 | AAATTATAAT TTGCCAAATC AGCAATTATA TGACTTTCTT CATCTACTCC AAAATTACGT | 240 |
| | AATTGCTTTT CAGATAATTT ACCATTACCA ATACCTGCAT CTATAATCAA ATTATATTGA | 300 |
| | GCCGTTTGAA TCAAAATTGG ATGTGTCGGT AAATTGATTT GATTTCGTTC ATTTGCATTG | 360 |
| 25 | TATTGCTTTG ACCACAACGG CTTCGGAACA ACACCAAACA TTGCACCGCC ATCCATTTTT | 420 |
| | GTATTGCCAC CATTTAGATA ATGAATAGAT ATATCCCCGA TTTTCATAAC ATCACCTATT | 480 |
| | CTTTCTGTAT TCGTTATTAC AATTAGCATG TGTTTATTAC ATCATATCAC TAT | 533 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 754: | ÷ |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1225 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754: | |
| | ATCCCCTGCA AGTGATAAAA TTATTGAAAA AGGCGACATG ATTACATTAG ATTTTGGCGC | 60 |
| | GTATTATAAC GGCTATTGTT CAGATATTAC TAGAACATTT GCTATTGGAG AACCAGATCC | 120 |
| 45 | TAAACTGAAA GANATATATC ANATAGTACT TGAATCTCAA ATGAAAGCAA TTAATGAGAL | 180 |
| | TAGACCTGGC ATGACTGGTG CAGAAGCTGA TGCCATTTCA AGAAACTATL TAGAGTCAAA | 240 |
| | AGGGTATGGA ÀAAGAATTTG GACATTCACT AGGACATGGT ATTGGTTTAG AAATCCATGA | 300 |
| 50 | | |
| | AGGGCCAATG CTGGCTCGTA CGATACAAGA TAAACTTCAA GTTAACAACT GTGTTACAGT | 360 |
| | AGAACCTGGT GTTTATATAG AAGGTTTGGG CGGTATAAGA ATAGAAGATG ATATTTTAAT | 420 |

| | AGCGTGTAAA ATGAGGAGGA AACTGAATGA TTTCGGTTAA TGATTTTAAA ACAGGTTTAA | 540 |
|----|--|------|
| | CAATTTCTGT TGATAACGCT ATTTGGAAAG TTATAGACTT CCAACATGTA AAGCCTGGTA | 600 |
| 5 | AAGGTTCAGC ATTCGTTCGT TCAAAATTAC GTAATTTAAG AACTGGTGCA ATTCAAGAGA | 660 |
| | AAACGTTTAG AGCTGGTGAA AAAGTTGAAC CAGCAATGAT TGAAAATCGT CGCATGCAAT | 720 |
| | ATTTATATGC TGACGGAGAT AATCATGTAT TTATGGATAA TGAAAGCTTT GAACAAACAG | 780 |
| 10 | AACTITCAAG TGATTACTTA AAAGAAGAAT TGAATTACTT AAAAGAAGGT ATGGAAGTAC | 840 |
| | AAATTCAAAC ATACGAAGGT GAAACTATCG GTGTTGAATT ACCTAAAACT GTTGAATTAA | 900 |
| 15 | CAGTAACTGA AACAGAACCT GGTATTAAAG GTGATACTGC AACTGGTGCC ACTAAATCGG | 960 |
| .5 | CAACTGTTGA AACTGGTTAT ACATTAAATG TACCTTTATT TGTAAACGAA GGTGACGTTT | 1020 |
| | TAATTATCAA CACTGGTGAT GGAAGCTACA TTTCAAGAGG ATAATCTCTA ATTTGTTAAC | 1080 |
| 20 | AAATAGCTTG TATTCACTAT ACTGATTTAA CGTAAGANAT TCTAAATAAG TCTCATAAAG | 1140 |
| | CTATTGCCTA AAATGATTAT AGGTTATATG CTGATATGAG GCTTTTTATT TTTAAAATAA | 1200 |
| | TTTTTAAAAT ATAAAACGAA TCGTC | 1225 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 755: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1265 base pairs (B) TYPE: nucleic acid | |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| • | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755: | |
| 35 | ACAAACAAAT CACTTAGTTA AAATTGACAG TGCATTATAT TCCGATAAAT TATTCAACAT | . 60 |
| | TGTAGAAAnn AGAATTGATA CACCAGATAT TGGCTATAAT ACAGTGGTTT TATCAGAAAA | 120 |

ATGAGTGTAG AAATTAAAGG GATACCTGAN GTGTTGAATA AATTAGAATC GGTATACGGT 180 AAACAAGCAA TGCAGGCTAA GAGTGATAAA GCTTTAAATG AAGCATCTGA ATTTTTTATA 240 AAGGCTTTAA AGAAAGAGTT CGAGAGCTTT AAAGATACGG GTGCCAGTAT AGAAGAAATG 300 ACTAAATCTA AGCCTTATAC AAAAGTTGGT AGTCAAGAAA GGGCTGTTTT AATTGAATGG 360 GTAGGTCCTA TGAATCGCAA AAACATTATT CACTTGAATG AACATGGTTA TACAAGAGAT 420 GGAAAAAAT ATACACCAAG AGGTTTTGGA GTTATTGCAA AAACATTAGC TGCTAGCGAA 480 CGTAAGTATA GAGAAATTAT AAAAAAGGAG TTGGCCAGAT AAATGAATAT ATTAAACACC 540 ATAAAAGGAA TTTTATTATC TGATGCAGAG CTCAAAACAC ATATAAATTC TAGAATATAC 600

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| | TATGATTTGC CTTCAGACTT TATGTCTGAT AAATATCTCA GTGAAGAATA CTTAATTCAA | 720 | | | | | | |
|---|---|-------|--|--|--|--|--|--|
| | ATAGATGTAG AATCTTCAAA TAATCAGAAA ACAATTGATA TAACAAAACG AATAAGATAC | 780 | | | | | | |
| 5 | CTGTTATATC AACAAAATTT AATTCAAGCA TCTAGTCAGT TAGATGCTTA TTTTGAAGAA | 840 | | | | | | |
| | ACTAAACGTT ATGTGATGTC GAGACGATAT CAAGGCATAC CCAAAAATAT ATATTATAAA | 900 | | | | | | |
| ò | AATCAGCGCA TCGAATAGGT GTGCTTTTTA ATTTTTAAGG AGGAAATAAG CAATGGCAGA | 960 | | | | | | |
| Ü | AGGACAAGGT TCTTATAAAG TAGGTTTTAA AAGATTATAC GTTGGAGTTT TTAACCCAGA | 1020 | | | | | | |
| | AGCAACAAAA GTAGTTAAAC GCATGACATG GGAAGATGAA AAAGGTGGTA CAGTTGACCT | 1080 | | | | | | |
| 5 | AAATATCACA GGTTTAGCAC CAGATTTAGT AGATATGTTT GCATCTAACA AACGTGTATG | 1140 | | | | | | |
| | GATGAAAAA CAAGGTACTA ATGAAAGTTA AGTCCTGACA TGAGTATTTT CAATATTCCa | 1200 | | | | | | |
| | AGTGATGATT TAAACACAGT TATTGGACGT ACTAAAGATA AAAATGGGTA CATCTTGGGT | 1260 | | | | | | |
| 0 | AGGAG | 1265 | | | | | | |
| | (2) INFORMATION FOR SEQ ID NO: 756: | * * . | | | | | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1111 base pairs | | | | | | | |
| 5 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | | | | | | |
| | (D) TOPOLOGY: linear | | | | | | | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756:

| CATATACCCG | GGTTCCAAGA | ATCCTCTATC | CATATGGTCC | CCCAATTTTG | ATTCCACCAT | 61 |
|------------|------------|------------|------------|------------|------------|-----|
| ATTGTTAAAT | ATCACTTTCC | CAGCCTACTT | TTTTATnCAG | TTGGGCTCTC | TAAAATTGTT | 120 |
| TTGAAATCCA | GGTTGAACAT | ATTTCCAGTG | TATGACCAAT | CGAAACATTT | GCACCAATAA | 180 |
| GGCCGCCAAT | TTTTCCTGTA | TCATCACCAG | TAACATTACC | GTTGAATCCA | TAAGTTAAAG | 240 |
| TACTCATATA | CTCTTTTGTA | TCAATCGAAT | TTCTTGGATA | GTAATCAGAT | ATTTGAGCTA | 300 |
| CTTCATTATC | AGGTAGTTGC | AACTGTACCT | TAAAGGCTGA | AGGCCÁGGCT | AAACCACTTT | 360 |
| TGTTAGCACC | TTCTTCGCTA | TAAACTCTAT | ATTGACCAGC | AATGGTACCT | TTCGTTCTAA | 420 |
| TAACTAGCAG | TTTTTTTTA | TGATTTTTAT | CATCGATAAA | ACTATAAAAT | ACTITITIGT | 480 |
| GCATGCCATT | TTCTTTATCA | TAAGTGACTA | AATCACCTGT | TTTTACTGTA | GTATTGCTTC | 540 |
| CAATATCTGT | AGTACCGGTT | TTAATATTAA | TATCAGAATC | TGCGGCATTA | GCGACAGGAT | 600 |
| TCATTÄATAT | GGAACCTAGC | AATAGTGTTG | TTGTTACTGA | GCTGACTATA | CGTGTTTTCA | 660 |
| TTTTCATCAT | CCTTCTATTT | TTTAAAACGA | TTTGAGGAAA | CAATAATCAA | TATGTCAATT | 720 |

| | GTAGCAACTG ATAAATTACT GAGTGATGAT GAGTGATTAT TTTAAGAATA TGTTTTTAAC | 840 |
|----|---|--------|
| | TTTTATTTAA AATTTGAAAG GAAGCATTTC AATTTCGAGG GTTAGTCAAA GTTGAATAAA | 900 |
| 5 | TTCTTTATGA AACAAGGAAA AGACATAGCT AATTTLATTG ATTAATTTCT TTAAAACTAA | 960 |
| | TGATTTGTTT GATTTAAAAA TGTAATCGAT TACAATATAA AAATACAAAT ATCTTAGAAT | . 1020 |
| 10 | TAAATCAATT AATTAACTAT TAAATAAAAA TTAACTATAT ATTAACTAGT GTAAATTAAT | 1080 |
| | AAATAGAAAT AGAGAAAAAG GGTATTAATT A | 1111 |
| | (2) INFORMATION FOR SEQ ID NO: 757: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 466 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757: | |
| | TATCTATTGT ATGTAACAAT AGGTACATAA TATTTTTAGG GTGGGTTATA TGAGCATAAT | 60 |
| 25 | TACAAGATTG TTTAATAACA GTGATTTTGA AAAATTAAAT CAACTATGTA AATTATATGA | 120 |
| | TGATCTAGGT TATCCAACAA ATGAGAATGA TTTAAAAAAG AGACTAAAGA AAATAACGAA | 180 |
| _ | TCATGATGAT TACTTCCTAC TGCTTTTGAT AAAAGAAAAT AAAATAATTG GTTTAAGTGG | 240 |
| 30 | TATGTGTAAA ATGATGTTTT ACGAAAWAAA TGCAGAGTAT ATGAGAATCC TTGCGTTTGT | 300 |
| | TATACATTCT GAATTTAGGA AAAAAGGTTA TGGAAAGAGA TTATTAGCTG ATTCTGAAGA | 360 |
| 35 | ATTTTCTAAA CGGTTGAATT GTAAAGCMAT AACACTAAAT AGTGGTAATA GAGATGANAG | 420 |
| | ACATCTGCAC ATAAACTATA TAGTGATAnT GGGTATGTTA GCAATA | 466 |
| | (2) INFORMATION FOR SEQ ID NO: 758: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 402 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758: | |
| | CGTACAGCAT AACCAAATAC ATATCTGCCA AAATCGCCAT ATGCCCCAGT TCCTCTTCCA | 60 |
| 50 | TATTCCGTTG TCATTGAGTT TTTAATTTTA TCGATAGAAA AATGTAAATG GCTATCTAAT | 120 |
| | TTGTTTTTTA AAGATTTTAT GTAATCECTA TATTTAAATT CGAATATTCT TTTTTATACC | 180 |

| | AACTAATATA TWCAATTGTA TGCCTAGCAT AATCTCTCAT TAAAATATGA GGATATACCA | 300 |
|----|---|-------|
| | TITCITTATC AAATATETCT TCATAAATAT AATTAGCAAT CTCTATATGT ATTECACAAA | 360 |
| 5 | TGTCGATTCG AAGTGTCGCC CCTAAAACAG rAGCATATAA TC | . 402 |
| | (2) INFORMATION FOR SEQ ID NO: 759: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 338 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759: | |
| | AAGTTACTCA ACAGCCATTT GACACGTCTC GATTAGAGCG ATTAGGTATA ACCGAGCGCC | 60 |
| 20 | AAACTAAAGA CATGTATCGT TTATTAGGAC TAGCCAAATA TGAAGATCGA TTTGTTATTC | 120 |
| | CAACATCACA CAAAGAAACC TATTTAGATA CGTATCACGC ACAAGGTAGT ACAGGATACA | 180 |
| | ATTACGGCGG CGAGCATTTT GGAGATAACT GTGAAGGCTG TGGCGTTGCA GTAGGTTCAG | 240 |
| 25 | GGAAAACTGG TCAAGAAATT TATAATGGAG AATTCTATGG AGGGATTTCC GTGGTTAATT | 300 |
| | TCGATAATTT AAAAAATATC CAAGAAAGTT TGGGTnnn | 338 |
| | (2) INFORMATION FOR SEQ ID NO: 760: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 35 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760: | |
| 40 | CTCTATTATA TTTAGAGTTA TAGCTATTGC AGTTGTTTAT TTATTGAAAA TAAATGTACT | 60 |
| | ATCATTAGET TTAGCAAGTG TATTAGGCAG TTTGGTATCL AGGCTACTAT TATCTATTAT | 120 |
| | TTTAAATTTA CCTGTGTGGG TAGTGTTGTT AAACGCGATT CCAGGCGTAA TATTCACTTT | 180 |
| 45 | AATTGTAGCT ATTCCTTTAT ATCTCACATT GAGAAAAAGA ATGGCAGTAT TACTAAGATA | 240 |
| | ATAAATCAAA ACACGGTCGT CACAATTACT GTTGGCGACC GTGTTTTACT AGCTATTTAT | 300 |
| | TGTTTTCAGT TTCTTTTGTA TCTAACAATT TCACTTTGTG ATTTTCCCAA TCAATTTCAT | 360 |
| 50 | ATGTTGATTT AAATGTTCTA GTTTTAAAGT TTTTATAAT | 399 |
| | (2) INFORMATION FOR SEC ID NO. 761 | |

| 5 | (A) LENGTH: 639 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|---|-------------|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761: | |
| 10 | GCATATHCAA AACAATAGCT GCTTTAGGTG CGGGGGCTAT TAGCGTTATT TCTGCACTAA | 60 |
| | CAGGAGGTTT AGTTGGCGCA GGTGTTGGTG GTTTCCTTGG ATCTATAGCT GCATCGAATA | 120 |
| | TTGATACTAG TAAGGGAATA TATATAAAAT TAAAAACTAA AAAGTATGCA GCCGGGGAAT | 180 |
| 15 | ACGTTCTGAC AGGAGAAAAA TGGGGATATC AGTAAGGGTG ATTTTATGGA TAGATTAAAA | 240 |
| | TATTCACTTA AAGTTGGAAT TTTAGCATTA TTATTATTTT GTACTTTAAA TTATTTAGTT | 300 |
| | CCAATGCAAA GCAATGCTTT TTCAATAATT ATATATTCGG CAATTTTTGC TGTGTTACTT | 360 |
| 20 | ATGCTTTTAG-TTTATATTT-TTTAGGAATT-TTAAAGAAAT-GACATGAAAC-AAATTAGCAT- | 420 |
| | TGGCTATGAA GAAATCTATG GGGATAGAAT TTTTCATAGC CATTTTTTAA AAGAGCATGA | 480 |
| 25 | AGTAAAAAT TGGAAAACCG TCAATCAAAT AATTGAAAAA GAACACTTGG ACAAAAATGA | 540 |
| 25 | ATATGRAAGC GGAACCGCCG TTATTTTCT TTTGCAGGAT CGTTAGATTA GATTRCGGTT | 600 |
| | GTATAGTATA ATGAAAAATA TTATAATAAA TTTATAAAA | 639 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 762: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 852 base pairs | a Sec. 1 |
| 35 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762: | • |
| | nTGTTCGTTG TCTGGATCCA ACGTAAACAG TCGCTTCATC TAATACAATG ATAGGCGCAT | 60 |
| | CTTTTAATAT CATTCTTGCA ATAGTGACTC GTTGTTTTTC ACCACCAGAC AATTTATCTC | 120 |
| 45 | CCACTGTACC AACATTCGTA TCATATCCAT CTGGCAACTT TTCAATAAAT TCATGACATT | 180 |
| | GTGCTAACTT GGCAGCTTTT TCAACTGCCT CATCCGTAGC TTCTGGATTG CCAAGTTTAA | 240 |
| | TATTTCTTT AAAAGTAAGA TTTAATAAAA AGTTATCTTG TCCAACAAAA CCAACTAAAT | ∴ 300 |
| 50 | CGTTAAGTTG TTTCGATTCA ATATCTTTTA TATTTATACC GCCAATCGTA ATTTCACCTG | 360 |
| | AAGTCACATC CCAGTATCGT GATATAAGCT TGGCAATGGT TGACTTACCG CTACCAGATG | 420 |
| | CCCCGACGAT AGCTGTGAAA TTATTTTCTG GTACTGTAAA TGATAAATGC TTAAAGACCA | 480 |
| <i>55</i> | | |

| | GAGGCTTCTT AAATTTTGTT GACAATACTA ACTCTTCTAG ACTTAATATT TGATTCACTT | 600 |
|----|---|------|
| | CAGTTAATGC GTATTGTATA GACTTTAAAT GATTTACATA ATTAGTAAAA TTCTTAATCG | 660 |
| 5 | GTGCTACTAC ACCTAAAGAT AATACGATGC ATAGGAAAAA TTCCGCATAG TTTAATTGGT | 720 |
| | TGATAGATAT CAAATACATG CCGACCGGTA AAATCCCTAA AAATGTTGAA GGTAATACAC | 780 |
| 10 | TAGCTCCTAA ATTCATATAC CCCCATGTAT TTTTAAACCA ATTCAAAGTG TGAATCTTAT | 840 |
| 10 | AATTATCTAC TG | 852 |
| | (2) INFORMATION FOR SEQ ID NO: 763: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 852 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763: | |
| | CTCTTCATGC GTCATACGTT GTGTCGATTG ATCAGTTGTT TTGTCTAAAT CACTAGCTTT | 60 |
| 25 | AAATTTAGAT TGATTTGATT GACGTGTCGT AAATnGTTGT TCCTTTTGTT GGCGTTTGCC | .120 |
| | TTTTTTCTT GATCTTATTA AAAATAAATT GATAACCCCA ACAATAATGA GCGCTAAAAT | 180 |
| 30 | AATGTAGCTA ATAATGAAGG TCGTAGTCAT TTAATGACCC CCTTAATTTT TATGGATTTT | 240 |
| | TACTTCAGCG TTCATTCCAG GAACAACTTG TTTAGACGGT TCTGATTCTA GAGTGATTTT | 300 |
| | AACAGGTATT ACTTGAGAAA CTTTAGTGTA GTTACCATCA CTATTTGATG ATGGCATTAA | 360 |
| 35 | TGAAAAgtTG CAGCAGTTGC TTTTCCAATA CTATCAACTT TACCTTTAAT AGAAGCTTTT | 420 |
| | TGACCGTCAA TAGTCACATC AACATCTTTA CCTACTTCAA CATCTTTAAT ATCTTTTTCG | 480 |
| | TCAATATTTG CTGTTACATA TAAATCATCT AAATTGTATG CATAAGCGAT TGGGTTACCA | 540 |
| 40 | GCTTGCACCA TTGAACCTTC CATACCATCT AATTTGGCAA TTGTACCTTT TTGAGGCATT | 600 |
| | TTAAGATCCA TATCTTTCGT TTCGCCATCT TGACCTTGTA CAGTAACAAT TGCTACTTTG | 660 |
| 45 | TCACCTTTAT CGAGTTTGTC ACCTTGTTTA ACATTAAGTG ATTTAATTTG TCCAGATGCA | 720 |
| | GGACTTGCTA TTTTAATTTG ATCGCCATTT ACTTTTGCAT TATCAGTTGT TACATAGCTT | 780 |
| | GTTGTTTTAT TCCAAAAATA AAAGCCAGCA ATCCCAATGG CTAACnGTAC AACAACCGTA | 840 |
| 50 | ATGACATTNA AT | 852 |
| | (2) INFORMATION FOR SEQ ID NO: 764: | |
| | (i) SECUENCE CHARACTERISTICS | |

(A) LENGTH: 747 base pairs

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

| 5 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764: | |
|--------------|-----|---|---------------------|
| | | ACATATTCGA CATTCATTTT AAATTGCATA TAACTACATT AACCATTCAT TGTGCAGCGC | 60 |
| 10 | | CTGTTGTTTA GATGATCATT TATTGACTTT TTGCTCTTAT nCCAngCAAT TTTTTGATTT | 120 |
| . 4 . | | ATTGCTTATA ATACATTTTA AGACAAATGT TTGTTTCAAC ATCGCATGCG ACATCATTAA | 180 |
| | | YTATTCATTT AAATTTATCC AGTTTCTATT TGTCTGCAAT TGCTGAAAAT TAAAGGAGCT | 240 |
| 15 | | TATTTTTAAT AATGGAACAA ATTATCACTG AATTTATTAG CCGTTTTGGG TATGCAGCCA | 300 |
| | | TTTTTATATT AATTTKATKA GAAAATGTAC TACCTATCGT ACCATCGGGA AATTATTCTG | 360 |
| | | ACATTTGCTG GTCTTATGTC TGTTAAATCA CATTTATCAA TTTTAACTTT ATTTATTATT | 420 |
| 20 | | GCAACTATCG-CATCGTTTAT-AGGGCTGTTA-ATTTTATATT_ATATCTGCCG_TTTGATTTCA | _4 B _. 0 |
| | | GAAGAACGTC TATATCGTTT TATTGATCGA CACGGTAAGT GGATTAAATT GAAAAGTAAG | 540 |
| 25 | | GATTTAAAGC GAGCAAATGA TTGGTTTAAA AAGTATGGCG TATGGGCTGT ATTKATCTGT | 600 |
| | | CGTTTCATAC CTGTATTACG TGTALTGATT ACCATTCCAG CTGGTGKAAA CCGCATGAAT | 660 |
| | | GTTGTGACAT TLACCGTTAT TTCATTAATA GGTACTACAA TCTGGAATTT CGGTTTAATT | 720 |
| 30 | | TTACTAGGAC GCACTTTGAG CGATAGC | 747 |
| | | (2) INFORMATION FOR SEQ ID NO: 765: | • . |
| 35 | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 820 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ¥. |
| | 144 | | |
| . 40 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765: | |
| | | TTTACCTTTT AACCAATCAT GCATTAATGC AATGTGTACT GTCTTAACAA ATGTTGCATA | 6 |
| 45 | | TECATOTTOT GCACTCCACT TTTTCAATTC CTGTTGATTA ATGGCATGTT TTTCTCCATT | 12 |
| , 4 3 | | TTCCAACATA TTGACATACA ATTTATAATG TTTTTCAACT GCCTGAATAA AAGCGAGTTG | 18 |
| | | ATTTTTATTT AAATGTGATT TTAACTTTTC TAAATCTGAA TTAATAAAGT CTTCTATAGT | 24 |
| 50 | | CGAATAAGAC ATATCTTGGT ATTCAACTAC TGCATTAATT TCATCTAATA ATTGCGATTG | 30 |
| | | TGATTTTAGC GTTATATAAC TCTCGTCTCC ATAAGATATT TCTGTAGTAG CTGCTGTAGT | 36 |
| 55 | | AGGATTTGGA GAACTGACTA AAATATGCTC GCCTAATAAT GCATTTATCA AACTACTTTT | 42 |
| | | | |

| | TGTTTCGTGG ATATCTTGCT TTGTACGCTT GAACAAAGGC ACATCCGAAA TTATATCAAG | 540 |
|--------------|---|-----|
| | CGCTTTTTGA ATATCTATAG ACATATTTGT TGTAGCTGTA TTTTGATTTA GCTGCTGATT | 600 |
| 5 | ATCACGATTA TCCTGAGCAT TATCAGTAGC CACTTGATAT GTTGTCTCTT GTCGACCTAT. | 660 |
| | TAATTTATCT AGAGATTCAT CTAAATGAAT ATAGTAGTGA CGATAATTCT TAGTCGTCAA | 720 |
| | TGACTGACGC AGCTCATTTA ATTCTGTATA ACGTTGATAT TCTTTTAAAT CATCACTTTC | 780 |
| 10 | TTCTGTTGGn AATTCATCTG CCTGCACATT TTCTATnATT | 820 |
| | (2) INFORMATION FOR SEQ ID NO: 766: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 672 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766: | |
| 25 | TCAACATGAC ATTAATTTAA TAGCGATGCA TACAAATTTA GATGTAAATC CGTATGGTGT | 60 |
| | CAATATGATG TTGGCGAAGG CGATGGGTTT GAAGAACATT TCAATAATAA ATAATCAACA | 120 |
| | AGATGTATAC TATAAAGTTC AAACATATAT ACCTAAGGAT AATGTTGGAC CATTTAAAGA | 180 |
| 30 | TAAGCTTAGT GAAAATGGAT TAGCGCAAGA AGGTAATTAT GAATATTGTT TCTTTGAAAG | 240 |
| | TGAAGGAAGA GGGCAATTCA AACCAGTTGG TGAAGCTAAT CCAACAATAG GACAAATTGA | 300 |
| | TAAAATTGAA TATGTAGATG AAGTTAAAAT TGAATTTATG ATAGATGCAT ATCAAAAGTC | 360 |
| 3 5 . | AAGGGCTGAG CAATTAATTA AACAATACCA TCCATATGAA ACACCGGTAT TTGATTTTAT | 420 |
| | TGAGATAAAA CAAACATCCC TTTATGGACT TGGCGTTATG GCAGAAGTGG ATAATCAAAT | 480 |
| | GACATTGGAA GATTTCGCAG CTGATATTAA ATCTAAATTA AATATCCCAA GTGTCCGTTT | 540 |
| 40 | TGTTGGTGAK TCTAATCAGA AAATTAAACG TATTGCAATT ATTGGTGGTT CAGGTATTGG | 600 |
| | ATATGAAKAT CAAGCtGTCC AACAAGGCGC AGATGTCTGT TACGGTGATA TTAAACATCA | 660 |
| 45 | GATGCCTAGA TG (2) INFORMATION FOR SEQ ID NO: 767: | 672 |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 403 base pairs (B) TYPE: nucleic acid (C) STRANDEDIES: double | |

| • | GAAAAAGTTA AACCTACTGT AACTACAACA AGCMAAGTTG AAGACMATCA CTCTACTAAA | 60 |
|------|---|-------|
| 5 | GTTGTmAGTA CTGACACAAC AAAAGATCAA ACTAAAACAC AAACTGCTCA TACAGTTAAA | 120 |
| 5 | ACAGCACAAA CTGCTCAAGA ACAAAATAAA GTTCAAACAC CTGTTAAAGA TGTTGCAACA | 180 |
| | GCGAAATCTG AAAGCAACAA TCAAGCTGTA AGTGATAATA AATCACAACA AACTAACAAA | 240 |
| 10 | GTTACAAAAC ATAACGAAAC GCCTAAACAA GCATCTAAAG CTAAAGAATT ACCAAAAACT | 300 |
| | GGTTTAACTT CAGTTGATAA CTTTATTAGC ACAGTLGCCT TCGCAACACT TGCCCTTTTA | 360 |
| | GGTTCATTAT CTTTATTACT TTTCAAAAGG AAGAATCTAA ATA | 403 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 768: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 483 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 7.4. | | * |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768: | |
| 25 | TTCAATGCTC GTTTTGCTTG CGTTAGTAAT TTCTAACATA TTCATTCACA TTTTGGAGCC | - 60 |
| | TAAACTATCA ATCACCACTC AAATCATCAT CGTTTTGATT TTAATTGAAG CACTAATTGG | 120 |
| 30 | ACTGCGTTTC TTGAAAGCGT ACGATGTTAA GCGTGGCAAA GATAAAGAAA ATAAGAAAAA | - 180 |
| | TAGTAAGGAT TTCGTTAAAC TAAAATCAAT TTTAGTAGCA ATTTTATTTA CATCATTGGC | 240 |
| | GCTGACAGCA GGTACTGTAG CTGATATATA CGGTTTCACT GACTTAGGAA ATACTAGAAG | 300 |
| 35 | TGATTTAATC GTTTGGAGCA TAGGTGGTAT TATATTTGGC CTCGTATGTT ACACAATGGA | 360 |
| | AGATAAAAGA TAACGATAAG GAGCTGGCGA TTATAAAGCT AGCTCCTTTT TTAACTTATA | 420 |
| | TATGTAAAGA aCTATCCTAA GGGKTTTTAA TCATATGTCA ATAATTTCTA TAATACATTA | 480 |
| 40 | TTA | 483 |
| • | (2) INFORMATION FOR SEQ ID NO: 769: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | *** |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769: | , |
| | ATTATATGTC TGATGTATTT CATGTCGTTA AAAATAAAGG TACGGAAGAT TTTAAAGAAG | 60 |

| | GGATGATGCT TGAAGGTGAA AAAATCAAAG CTTTTTATGA AGATATGCCA CCGTATCAGA | 180 |
|----|--|-----|
| - | CTGTCAAAAA AGGAACGATA CAAATTAAGC GTGATGGCAC ACCTATTATC CTATTAAATG | 240 |
| 5 | TCATTATACG CTnGTAGCTA CCCGCAAATC GGTACAATCG CAGTTATCAT TTACGAATTA | 300 |
| | GCACAAAACC GCAGGATCAC GTTGAATTCC ATTATAGTAT TTACGGCTGA AGACTGTAAG | 360 |
| 10 | nTANACTGGT AACCATATCA TGGATGATTG ATCATAGATG | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 770: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 750 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770: | |
| | ATCTCTTCTA CTTCTTTTAC AAATTGAGAA CGTCTTAAAA TGGCTTTCAC ACGGGCAACA | |
| | ACTICICAG GIKAAAAAGG CITAGTCATA TAGTCATCGG CACCTAATTC TAAACCTAAT | 60 |
| 25 | ACCCGATCAA ATTCATCATT TTTCGCCGTT AACATTAATA TAGGGACTAA ATTTTTATTT | 120 |
| • | GTTCTTACAG TCTTACATAC GTCAATGCCA TCTTTTTTAG GTAGCATAAC ATCTAAAATA | 180 |
| | ATTANATOTE GOTGTTCACT TTCTACCTTT TCTANAGCCT CATCACCATC ANATGCGACA | 240 |
| 30 | ACAACTTCAT AACCAGCTGK TTCtArGyTA TATTTAAGTA ATGGTTACGA TTGAATGETC | 300 |
| | | 360 |
| | GTCATCTACT WCCaACACTT TTTGCGACAT GGtATGCCTC CCTAACttak AATTATATTT | 420 |
| 35 | CATTATAACC GAACTATTTA TAAAAATAMC ATCCTACACA TTATCTTTAC ACATTTTTTA | 480 |
| | CATTACTTTA CATATAAATA AAATACTTCT TATATTTCCT TCTmTCATTT GCATGACTTA | 540 |
| 40 | CTCTGGGACA ACGAAATAAA TTTTGTAAAA ATAGCATTTC TATCCCACTA CCTATGCATG | 600 |
| | AGTITIACTC ATTIATTCCT AAGCITATGT ACATATTCGC TTTGTCTAAT GTGTAAGAAA | 660 |
| | CACTACATAA TCAATCATTG GTGACTCTTT ATTATTTCTA TCCTGTTGCC AACTTCAATT | 720 |
| 45 | CATITAAAA GGCGAACCTA GCAATTAAAG | 750 |
| | (2) INFORMATION FOR SEQ ID NO: 771: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

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| | TATTAATTA | TATTTTTCCA | AATCAATACG | ATATAATTTT | ATGTTTTTAT | CTTTTGGTGC | 60 |
|-----|------------|---------------------|------------|------------|------------|------------|------|
| | TGaGGCAAAT | TGATAAGtCG | TTTTGCCTTT | TTCAATATAT | CCAAAATTAC | CAGCAACTTT | 120 |
| 5 | GCTATATTCC | GTATGTGTTA | CTGCTTTGCC | AACATAATTT | TTAACAGCTT | GATATGTTGG | 180 |
| | ACCATTAGCA | TCATTATACA | TCATTGAAAT | ATGAGTTACT | TTACCATTGT | TTTTCTTACC | 240 |
| 10 | ATCAGTAGTT | ACTAATAACA | TACCTTTTTT | AGTATGGAAT | TCGTAATAAT | GTTCAGTTCC | 300 |
| | ATCITCATTG | TAAGAATACA | TCGGATTTTT | GTACTTAGTT | AAAACATCTT | TAATAGATTC | 360 |
| | GCCAATTTTC | ACATTTTCTA | ATGACTGATC | ACCCTTAATT | AATTGTTTAA | CAGTATCAAT | 420 |
| 15 | AGAGTTGCCA | CTTGCTGCTT | CGGCACTAGT | GTTCACTAAG | CCTACTCCCA | TTACAACAGA | 480 |
| | ACATGCAATT | ATACTTGCCG | TTAGTAGCTT | TTTCATAAGC | ACTCTCTCCT | TTTATTTATA | 540 |
| | TCGTCTTGTG | CTCACAACCA | TTATACAACA | ATCATTTCTA | AAACAACAGT | CATATTACAA | 600 |
| 20 | TTATATTACA | AATAATAATT | ACTACTTTTA | TATTTCACTT | ATCACTAAAA | ATTAAACATG | 660 |
| * . | CTTTTCATCG | TGATGTTTGT | TGATAAATGC | AGCTGTATCT | TCGACGAATC | TTTCTTGCTC | 720 |
| | TTCAACAAAT | GGGAATGCAC | TTGATTCTTG | ATATACTTCA | AAGTCCGCAT | TTTGGATTAA | 780 |
| 25 | ATCAGCTACT | TCTTTAGCTT | CTAATCTTGT | TGTTCTTTCA | CCGAATTCTC | CTGCAATAAT | 840 |
| • | TTTTGTCGGT | ACTACGACAT | TTCTATAAGT | TTGAGAAATA | TCAGCGTTTT | TGAATACCTC | 900 |
| 30 | TTTAACTGCT | TGAATTTCTT | CTTTAGTTGA | TATTTCATTT | GTATCTACGA | CATGTTTGAG | 960 |
| | GAATCGATTC | ATTTTTCTCG | GACGATAATA | CTTACGCTTA | TTTAAAAATT | TAWCYTGtTT | 1020 |
| | TTCaGGATCC | CaGTTtCGAA | TAATATGGGC | ATATTTTCTA | AATAAACGTT | CTTCCGGTAA | 1080 |
| 35 | TTCACCTTCA | ATAGATG TT G | GATTTACCAA | CGTAAGTGAT | GATGTAAATT | CAGGATAACG | 1140 |
| | TACTGAAATA | TCCGCACCAA | TGATTCCACC | CATTKCATGG | CATACAAATG | CAACTTCTTC | 1200 |
| | AATATATAA | TATTTAAGTA | ATTCAACAAT | GTCATCAGAA | AAATCTTTTA | TTTCAATGTG | 1260 |
| 40 | ACGAGGTTTA | TCAGAATAGC | CATGTCCACG | TAAATCAATT | AACACAACTT | GAAATGATTT | 1320 |
| | TGCTAATTCT | GCTGCTAATT | TATTAAACAC | AGAATAATTA | TCAAGTACAG | TATGAATCAA | 1380 |
| | TACGATAGGA | TAGCCTTCAC | CTAAnGTACT | GTAATGTATC | GATGTTCCAT | CTTTTCTAGT | 1440 |
| 45 | AAATAGATCC | ATAATTTTCT | CC | 4 | | • | 1462 |

(2) INFORMATION FOR SEQ ID NO: 772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772: | | | | | | | |
|------------|---|-----|--|--|--|--|--|--|
| | ATTATTATAA GGAGTTATCT TACATGTTAA ATCTTGAAAA CAAAACATAT GTCATCATGG | 60 | | | | | | |
| 5 | GAATCGCTAA TAAGCGTAGT ATTGCTTTTG GTGTCGCTAA AGTTTTAGAT CAATTmGGTG | 120 | | | | | | |
| | CTAAATTAGT ATTTACTTAC CGTAAAGAAC GTAGCCGTAA AGAGCTTGAA AAATTATTAG | 180 | | | | | | |
| 10 | AACAATTAAA TCAACCAGAA GCGCACTTAT ATCAAATTGA TGTTCAAAGC GATGAAGAGG | 240 | | | | | | |
| | TTATTAATGG TTTTGAGCAA ATTGGTAAAG ATGTTGGCAA TATTGATGGT GTATATCATT | 300 | | | | | | |
| | CAATCGCATT TGCTAATATG GAAGACTTAC GCGGACGCTT TTCTGAAACT TCACGTGAAG | 360 | | | | | | |
| 15 | GCTTCTTGTT AGCTCAAGAC ATTAGTTCTT ACTCATTAAC AATTGTGGCT CATGAAGCTA | 420 | | | | | | |
| | AAAAATTAAT GCCAGAAGGT GGTAGCATTG TTGCAACAAC ATATTTAGGT GGCGAATTCG | 480 | | | | | | |
| | CAGTTCAAAA CTATAATGTG ATGGGTGTTG CTAAAGCGAG CTTAGAAGCA AATGTTAAAT | 540 | | | | | | |
| 20 | ATTTAGCATT AGACTTAGGT CCAGATAATA TTCGCGTTAA TGCAATTTCA GCTAGTCCAA | 600 | | | | | | |
| | TCCGTACATT AAGTGCAAAA GGTGTGGGTG GTTTCAATAC AATTCTTAAA AGAAATCGAA | 660 | | | | | | |
| 05 | GAGCGTGCAC CTTTTAAAAC CGTAATGTTG ATCCAGTAGA AGTA | 704 | | | | | | |
| 2 5 | (2) INFORMATION FOR SEQ ID NO: 773: | | | | | | | |
| 3 <i>0</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 427 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | | | | | |
| | | | | | | | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773: | | | | | | | |
| | GACCACGACA CCACAAGCTA TGAAGAATGC CYTTGTTAAG CCGCCTTTGA ATtGCATAGA | 60 | | | | | | |
| | GATGAAAATA CCAATATTAA TAAAGAAGTT ACAGAAAATA CCTTTTGTAA AAATATTCAA | 120 | | | | | | |
| 40 | CCATGTTGAA TCAACAGTCT TTTTCTGAAC TAAAGCTGTT AAAGCTTGTG TCATTTCAGG | 180 | | | | | | |
| | TGTCATGACA TGCGCAAATT TCATTAAGAA AAATAACACA AACCCACCTA AAATATTTCC | 240 | | | | | | |
| 45 | TAAGAAACAA TATAATAAAA TCCAAGTCAT CTTCTTAACA GAAACGACTT TATAATACCA | 300 | | | | | | |
| | GCCTACTGTA AAGTACATGA AGTTACTTGT TAATAATTCA GAGTTAGTTA ATACAACTAA | 360 | | | | | | |
| | AATCAAACCT AAACTAAACG CAATGGCTCC CATTAAATTG ATAAGTCCAT CTACGTGAGT | 420 | | | | | | |
| 50 | ACtCGCA | 427 | | | | | | |
| | (2) INFORMATION FOR SEQ ID NO: 774: | | | | | | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs | | | | | | | |
| | | | | | | | | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|---|-------|
| 5 | (xi) SEQUENCE DESCRIPTION: SEO ID NO: 774: | |
| | AGGTGAGCAT TATTAAATAT TGCCAAGAAA TCAAAACTAA AAACTATGCA AAAGATGTAG | . 60 |
| | | |
| 10 | ATATATTATT TATTCTTGGC GGTGATGGCA CGGTTAACGA ACTTATAAAC GGTGTTATGA | 120 |
| | CACATGACCT TCAACTCCCT ATTGGCATTT TACCAGGCGG TACTTTTAAT GATTTTACAA | 180 |
| | AAACGCTAAA TATAGCACCT GAATCATAAA CAAGCTAGTG AACAAATGGA TTTCTGCACA | 240 |
| 15 | AGTTGGTACA TACGATGTAA TTGAAAATGA AATGAATCAA TATGCACTCA ACTTTGTGGG | 300 |
| • | CTTAGGTCTC ATGTTCAAAA CGCGGAAAAC GTACAAGAGG TTCAAAAGAT GTATTGGGTA | 360 |
| 20 | AATGGAGTTA TATTGGGTCC ACCGTCCAAA ACnCGGCnAA | 400 |
| | (2) INFORMATION_FOR_SEQ_ID_NO:_7.75: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 484 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . · . |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775: | |
| | AATTATTCCT CAATAGGAGC ATTACCCGCT CTCTCACCAA TTCCCAAAAA TGTAGTTTCT | 60 |
| | ATTTGCTTTG CACCATTTAA AATTGCAGCT AATGTATTTG CAGTAGCCAA CCCTAGATCG | 120 |
| 35 | TTATGACAAT GAGCAGAAAA AATTATGTTA GAATATTTTT TTACAAAGTA ATTAAAAATA | 180 |
| | TCTCCGTATT CTAATGGTGT CGAACATCCT ACAGTGTCCG CAAATGTAAC TGTTCTAACT | 240 |
| | TGATATTTTG AAATAATTTC CATGTATTCT TTCAATTTTT CTCTAGAAGT CCTTGTTCCA | 300 |
| 40 | TCTTCAAAAC AAATATCTAC TCCTTTTTTA TCTTTCTT | 360 |
| | ATTTTCTGAA TATAATATTT ATTTGAAAAA TTAAGCTTTT CTTTTATATG CAAGTCAGAT | 420 |
| 45 | ATTGGCAATA GTATTTLTAC CACTAAATTA TGAATTTLCA ATLTGACTAT TTTTGGTATG | 480 |
| 45 | TCnT | 484 |
| | (2) INFORMATION FOR SEQ ID NO: 776: | |
| <i>50</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 788 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776:

| | CGCAAGATGA AGTTAAAGAA CTTAATCGCT TATTAGGTAA AGTCATTCAT GCATTTGATG | 60 | | | | | |
|----|---|-----|--|--|--|--|--|
| 5 | AAACAAAGGA AAAATAATTA ACTTTTGTCA TGACAATTAA AGTAATGTTT AGAATTTATT | 120 | | | | | |
| | AAGAATAGAA AAACAATTAG CACGCGTAAC TTGTTAGTNA AAAAACTGCT TGAAAGGTTT | 180 | | | | | |
| | CTTAGCCTAT CAAGCAGTTT TTTTATGCAT TATATTGAAT CATATTCCAT AAAGCACCTT | 240 | | | | | |
| 10 | GATTAGCTAG TAATTGTTGA TAGTTTCCCT TTTCAACTAT TTTACCATTT ATCATCACAA | 300 | | | | | |
| | TGATGGTCTC AAAACGTGAC AATAAAGTTA AATCGTGTGT AGCAACAATT AATGTTTCTG | 360 | | | | | |
| 15 | CATGTGCTTC AATTAAATCC ATAACTTTTA AACTATTTTG TTTATCTAAT GCAGTTGTTG | 420 | | | | | |
| | GTTCATCTAA AATCCATGTT GATGCAGTAT CTTTTAATAA CATCCTCGTA ATCGCTAAAC | 480 | | | | | |
| | GCTGAATTTC TCCGCCAGAT AATGTATGAC CATCTAAGTC AATTTGACGT tCTAGTGCCA | 540 | | | | | |
| 20 | AATGTTCTAA ATCTAATTGC TTAAATATTG CTTGCACCGC TTCATCTTTT TCATCGGTAA | 600 | | | | | |
| | ATAAATTTTG ACGTATTGTA CCATCAAATA ATTGTTGAGA TTGTAGCAAG ACATTTAACG | 660 | | | | | |
| | ATTCAAACTT ATCTTTGTCA TCTATTTCAA ACATATCCAT ATTTTCGAAA CGAACAGAGC | 720 | | | | | |
| 25 | CACTATCTAA TTGATATAAC CCTGCCATAA TTTGTAGTAA TGTACTTTTT CCTGAACCAG | 780 | | | | | |
| | AAGGACCC | 788 | | | | | |
| | (2) INFORMATION FOR SEQ ID NO: 777: | | | | | | |
| 30 | (i) SEQUENCE CHARACTERISTICS: | | | | | | |
| | (A) LENGTH: 1145 base pairs (B) TYPE: nucleic acid | ė | | | | | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | | | | |
| 35 | (b) lorologi: linear | | | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEO ID NO: 777: | | | | | | |
| | | | | | | | |
| 40 | TTACAAAAGA AATGCAACAA AATTTTTGAA TCATTACATT TTTTTATAAA AATTTCACTT | 60 | | | | | |
| | TAGATTCACA ATAATTACTT ATTTTGTCAA TTTATTTAAT GTCAATATGT TGATTAATTA | 120 | | | | | |
| | ATAGTGTTGT CTAATGTATA TAATATTTAG GTCATCGTTA TAGTCAACAA TAATAAGGTA | 180 | | | | | |
| 45 | TTTCGAGTTG AAATTTATCT TATTATTTTT CCACTTTTAC GTGCTATCCC ATTACACAAA | 240 | | | | | |
| - | AACAAATAAG TAAAGATATT AAGTACAAAA AAGTGGAACA CCTTGTAGAT GCTCCACCTC | 300 | | | | | |
| | AATTATATA AGTTATATTA TTTTGCTGCT TGGTATAATT CATCAACTTT TTTCCAGTTA | 360 | | | | | |
| 50 | ACAATGTTCC AAAATGCAGT CATATAGTCT GGACGTTTAT TTTGATATTT CAGATAGTAG | 420 | | | | | |

1661

480

GCATGCTCCC AAACATCAAA TAGTAAGATT GGTGTTTTGC CTTCTGTTAA TGGATTATCT

| | GATCCAAATA | ATGTTGTTGC | TTTATTTGCA | AATTCATTTT | TAAATTCATC | TAAAGTGCCC | 600 |
|----------|------------|-------------|------------|------------|------------|------------|-------|
| | CACTGCGcTT | TGATGTCATC | TATTACGCCA | CCTTTTTCTT | CAGAATTAGG | TGATAGTATT | 660 |
| 5 | TCCCAGAATA | ATGAATGGTT | AAAATGACCA | CCGCCATTAT | TACGGACTGA | CATCCTCATC | 720 |
| | GCTTCCGGTA | ,CCTTGTCTAA | GTnAGCAATC | ATATCCGCTA | GTGATTGATG | CTCTAACTCT | 780 |
| | GTTCCTTCAA | CTGTTGCGTT | TAATTTCGTC | ACGTACGTAT | TGTGATGTTT | GTCGTGATGA | . 840 |
| o | AACTCCATTG | TTCTTTGATC | TATATATGGT | TCCAATGCAT | CATATGCATA | TGGTAAATTT | 900 |
| e * | GGTAATTTAA | ATGCCATAAG | TATATTCCTC | CTTTTATGAA | TATACTTTTA | TAATAATTAA | 9,60 |
| 5 | TTTTGGGTGT | GTTTTGCAAT | AATTATTATT | TATTTGTTAT | ATCCAATTAT | ATAAAATTTA | 1020 |
| | AATATTCGAA | ATTGATATAA | TATTTAATAT | TGAATGCAAA | AAGGCATTTA | ACTGCTTTTG | 1080 |
| • | TTTCCCGCTT | TTAAAGAGAA | TTAAAAAAGA | CAACTTCCAT | TTTTCAATAA | GAAATTGCCT | 1140 |
| 0 | TTTCT | | | | • | · | 1145 |

(2) INFORMATION FOR SEQ ID NO: 778:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 902 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778:

| AAAAGAGGTC | CAATATTATC | AATATACGGC | CGGAAGATTC | CCTTTTTCTT | CTCCACTTAC | 60 |
|------------|------------|-------------|------------|------------|------------|-------|
| TAAGCCCATC | AATGGTGTAT | GTTATCaATT | GGTGCTATCC | GCATTAAATA | ATTATCTTCA | . 120 |
| attgtggtai | CAAAGCTATT | CGCTTTTTCT | CCAATAATGT | CTTTACCATA | TTTATTGAAT | 180 |
| GCACCTACTA | AAATCAACAT | AAATGGAATT | AACAAGGTTA | CTACAATTGC | CATTCTTATA | 240 |
| AATTGTGGTA | TATAAGAAGG | TCGCCAATTT | AAAGCTTTAA | TACCTTCTTW | TCTAAATGGA | . 300 |
| GTTTCTATAA | AGCGATATGA | TAGCTCTGCA | AATATAATTG | TTAAACTTAT | ATCTATAAAG | 360 |
| TACACATATA | CAGGTATCTG | TCCGTCTACA | TAGTAACTAT | GTACGAAACT | AATTACTGCA | 420 |
| AAATGCCATA | AATATAAACT | ATAAGACCTT | TTCCCGATAA | ATACTAACAC | TGGATTTGAA | 480 |
| AATATCTTCG | CLATCCATGT | AGATGGATGA | ACGACACTAG | СААТААТААА | TAACGTTAAT | 540 |
| ATGGATATTA | AATAGAAACC | ACCATCATAT | ATCCAATTCG | TCTCATCATT | AATAATGAAA | 600 |
| AATAATAATA | TAAGTACTAT | AAATGATAAA | CTACCTATGC | TATCAATAAC | ATATTTTACA | 660 |
| | | C1150001110 | ~~~~~~~ | **** | | |

| | ATACTATAGA TAAACATCAT TAACCCTAAA GAAATTATTG ATACTCCCCA AAAAATAAAT | 840 |
|----|---|-------|
| | CCTATTTTGT ATCGCTTTTT AATTGTTAAC AATAATGTAA CCAAAATAAC TGGGAAAAAT | 900 |
| 5 | AT | 902 |
| | (2) INFORMATION FOR SEQ ID NO: 779: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779: | |
| | GGAATTAGTT TCCTAATGAT CAAACCATAA CCATTAGCTT TTAATGATGT TACGCCTTTA | 60 |
| 20 | AAGATTAGAG GATGATGACT AATAATAGTA TTATAACCTT TTTCGATTGC TTCATTTACT | 120 |
| | ACTTCCAACG TACAGTCTAA TGCTGTTAAA ACACCAGTAA CTTCAACATC TTCATCACCT | 180 |
| | ATTAACAATC CTACATTATC CCAAGATTCA GCAGTACTAA ATGGCACATG ATGATCTAAC | 240 |
| 25 | AATGTCATTA AATCAGCTAT TTTCATACTA TAACACCCTT TCAATTACAG CAATTTCGTC | 300 |
| | attaatttga gctaaacgtt gakgakgttg ttcagtawtg agettcgatt taatatgata | - 360 |
| | AAGTGCYTCL AACTCLCTTT GCCATTTLTT TATAAAATAT | 400 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 780: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 557 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780: | |
| | GTTCCTGTTT TAACATCAAT ATCTATCTTT TTAATATCTT GAACATAAAG CAGATTCAGT | 60 |
| | TGGCTAATAT TTGAATTTAT GTTAATCACT TTTTTCGTTC CATTTTTAAA ATGTACTGTG | 120 |
| 45 | TAAGTMGCTT TTTTTGCATA TTTTAATTCA CGTTCCCCGA TACCTCTATC ATGCTTCAAT | 180 |
| | ACTGATTTAA CTTTTTTAGA GATATCTTTG TAGCCTACAC GTGGGTCACC TGTAAATTTT | 240 |
| | AAATCTGATA AAATTGGTGT TGATGTGCCA TTTACTGCAA TTGTGTATGG TACATATCTG | 300 |
| 50 | TCTGCTTTCG CTTTAGTTCC TGTTTTAACA GTAATTTCAA TTCTCTTAAC ATCTTTCGCA | 360 |
| | TGAACTAAGT TTGCTGTGTA ATTTTTTGAA TTCAACTGTA AGATTCTTTT ACCACCATTT | 420 |

| | CTATCATGCT TCAGTACTGA TTTTATTTGA CTAGTTAAAT TTTTGTAATT TGTCCAAGGT | 540 |
|----|---|------|
| | TTATnTGAAA ATGAAAG | 557 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 781: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 475 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ** (|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781: | |
| 15 | TTCTGATAAC ACAACTTTCT TGGACCAAGT GACAATGGTA AAGTTGATAT TCTCAAAAAA | 60 |
| | TATATTTTAT TGAAAAGGTA ACTATATCGA CCGCTCTGTG CGACTTGCTG TGTAGAAACA | 120 |
| 20 | TCAAGCCCAG CTTGAAACTT CATATAAACT AATAACTTTT GATAAATGCT ATTCCCAATT | 180 |
| | TGTTCATACT GCTCCAAGTT ATCATTAATT CTAAATTTAA TACTTACTTC ATTTTTAACT | 240 |
| | GGAATAAAAT GTACATCACT CGCTTTCATT TCTATCGCTT TATTAATTAT TTCTTGAAAT | 300 |
| 25 | AGAATCTTCA AAAAAACACC TCCTACATAT AATCACGTAG GAGGTGTTTT TATTACTTCA | 360 |
| | ATTTAACCGT GTAAAAATGG ATTTAATTGT TCATCATCAA CCGTCGTATA TGGACCATGT | 420 |
| | CCAGGGAATA AAGGTAAATC GCCTTCTAAT TCAAATATTT TATCTTGAAT AGAAT | 475 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 782: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782: | |
| | ATGAATATCG GTGCAGGACG TATCGTTTAT CAAAGTTTAA CTCGAATCAA TAAATCAATT | 60 |
| | GAAGACGGTG ATTTCTTTGA AAATGATGTT TTAAATAATG CAATTGCACA CGTGAATTCA | 120 |
| 45 | CATGATTCAG CGTTACACAT CTTTGGTTTA TTGTCTGACG GTGGTGTACA CAGTCATTAC | 180 |
| | AAACATTTAT TTGCTTTGTT AGAACTTGCT AAAAAACAAG GnGTTGAAAA AGTTTACGTA | 240 |
| · | CACGCATTTT TAGATGGCCG TGACGTAGAT CAAAAATCCG CTTTGAAATA CATCGAAGAG | 300 |
| 50 | ACTGAAGCTA AATCCATGAA THAGGGCATH GGCCATTTGC ACCGGGCCCT GGCCGTAATA | 360 |
| | AGCCAAnGGA CCGGGCCAAC CGTTGGGACC GGGAAGAAAA | 400 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 810 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • | |
|----|---|--------|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783: | | |
| 10 | GATTAATGTA CTCGTGTACA TAACGTTTGA AGTATGATAA ATAGATATAG AAATAAAGTC | | 6 |
| | ATATGTGACA TCAATTAAAT GATGTTCAAA TGACAAGATA CAATAGAGGA ATGTTTGTAA | | 12 |
| 15 | TANAAACGCT TCATATAAAG GTCGAGTCAA TATATGATAC GACTTTATAT GAAGCGTTTT | | 18 |
| | ATTTGCTATG AGCTAGTATA TTTTATAATA ATTTTTCTAT TTCTCTTTCG ATTTGAACAG | | 24 |
| | GTTTTTTTG AGGTGCAAAT CGTTTAACAA CGTTACCYTC GCGATCCACT AAAAACTTAG | | 30 |
| 20 | TGAAATTCCA TTTGATTTTC TCATTAAAGA ATCCGTGTTG TGCCGCAGTC AAATATCTAA | | 36 |
| | ATAAAGGTAA TTGATGTTCC CCTTTTACGT CTATTTTTTG ATGCATAGGG AAGGTAACAC | | 42 |
| | CATAGTTTAA TTTACAGTTT TGAGCTGCTT CTTCGCCTGA ACCAGGTTCT TGGCCACCAA | | 48 |
| 25 | ATTGATTACA AGGGAAACCT AGAATTACAA ACCCTTGATC TTTGTATTTC TCGTATAATG | | 54 |
| | ATTGCAAACC TTCAAATTGT GAAGTAAAGC CACATTCGCT AGCTGTATTA ACAATTAGCA | | 60 |
| 30 | TAACGTCACC CTTATATGCA TCTAATTTGT AAGTAACACC TTTATTTGTT TCTACTACAA | | 66 |
| | AATCATAAAT TGTCTCCATT GTATCATCCT TTCGATTTAC TTAAAATGTA CCACAAAATC | | 72 |
| | GTGTAALAGT CTKTACTALA ACTCTATGAT AGAATACTTT GAGTAGGATT TTATTAAGGA | | 78 |
| 35 | GATGTATAAC ATGGNTCAGC AACAAATTCA | | 810 |
| | (2) INFORMATION FOR SEQ ID NO: 784: | · . | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 788 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 7 - 44 | |
| 45 | | . 0 | |
| 70 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784: | | |
| | AAATTCATTG CAGAAAACAT AGATAAATAA ACAAATTGAC TTTAAACGAG CGTTGCAACA | | 60 |
| 50 | TATCTCGAAT TGTAAAGGAG CTTGAAAATG AATAAAAATA TAGTCATTAA AAGCATGGCA | | 120 |
| | GCATTAGCCA TTCTAACCTC AGTAACTGGA ATAAATGCTG CAGTCGTTGA AGAGACACAA | | 180 |
| | CAAATAGCAA ATGCAGAGAA GAATGTTACG CAAGTTAAAG ATACAAATAT TTTTCCATAT | | 240 |

| | ACCAATAAAC | ATGTATCAAA | AGATTATAAA | GTTGGCGATA | GAATTACTGC | CCATCCAAAC | 360 |
|---|------------|------------|------------|------------|------------|------------|-----|
| | GGTGACAAAG | GAAATGGTGG | TATATATAAA | ATTAAAAGCA | TTTCTGATTA | TCCGGGTGAT | 420 |
| ÷ | GAAGACATCT | CTGTCATGAA | TATTGAAGAA | CAAGCAGTCG | AACGTGGACC | AAAAGGCTTT | 480 |
| | AATTTTAATG | AAAATGTCCA | AGCATTCAAT | TTTGCGAAAG | ATGCTAAAGT | TGATGACAAA | 540 |
| | ATTAAAGTTA | TTGGTTACCC | ATTACCTGCT | CAAAATAGTT | TTAAACAGTT | TGAATCTACA | 600 |
| | GGAACTATAA | AAAGAATSAA | AGACAATATT | TTAAATTTTG | GATGCCATAC | ATTGGAACCC | 660 |
| | GGGGAATTCA | GGGATCACCA | GTTCTAAATT | CTAACAATGA | GGTCATAGGT | GTGGTGGTAT | 720 |
| | GGGCGGGTAT | TGGGAAAAAT | TGGGTTCTGG | AATAATAATG | GGTGGCCGTA | TACTTTACGC | 780 |
| | CTCCAnAT | | | | | | 788 |
| | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 785:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1023 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785:

| CAATATTTTA | GAAACAATAA | TTAACTTGCG | ATGAACAAAC | TATTAACAAT | AATCTTGAGT | 60 |
|------------|------------|------------|------------|------------|------------|-----|
| ATTATATTTA | TCTTAATTAA | TAATATATTT | ATTTAAGATT | ATGTTACTTC | CAACTTTCAA | 120 |
| agtagaaaaa | CGGTATAATT | TGTTGATGGG | TGTTTATTGA | TAAACTGCAA | AAAATACAGC | 180 |
| CTACAACCAC | ATAGATTGTA | GACTATATTT | AAAATAATAG | GTATTTATCA | TATCTCGTAA | 240 |
| ACTTAGTGCC | AATTTTTATA | CTCGTGGTGC | TGGTAAGCTA | CCCTTAAATT | CAGGAACGTA | 300 |
| GTGTGTaGGG | CTATAACTTG | GAACAGCATA | TTGATAATTT | ACATTTTTGA | TATTTAATGA | 360 |
| TGGTTTCCCA | ATTTTATAAC | CATTTGATTG | TGAAAATGAG | AAATAKTTCT | TCACACCTTT | 420 |
| AACTACTTTA | TAAGAATAGA | AGTATTTATA | GTCATATGCT | TTATTTACTT | TAGCATTTTG | 480 |
| ATGTGTTGCT | GTTGTGTTAT | TTTGGAAACT | TGGTACATGC | ATACGATGTG | AATTGTGACC | 540 |
| ATATGGTGGA | ATTACCTTGA | AACTATTTAT | TTGTGGCACA | ACACAAAAGT | GATTAATTTT | 600 |
| AATGCTAGCA | TGCCCTGGTG | TAACAAATTT | ATGCGCGTGA | TATCCAGGAA | CTGCAAAATG | 660 |
| ATGCTTGATA | ATTAAAGATT | gAGATGGATG | TGTATATCTA | GGCGATTCTG | ATGGTTTAAC | 720 |
| AATAAAGTGT | TTATTAATAG | AATCCTTTGC | ATGATTTACA | TGTTTATGTA | CATGTGTTGA | 780 |
| TTTGTATGAA | GTAATAACTT | TCTTGTAGTG | GGTTTGCGTA | GTAATGAAGT | GGTGGTTTAC | 840 |

| | TIGHT OF STREET THE THE THE THE THE THE THE THE THE | 960 |
|----|---|------|
| | TGGCACAATG TTTCCTAACT TTGATTCTGG NACGACAAAG TTTTTATCTA CAATTTTACT | 1020 |
| 5 | AGC | 1023 |
| | (2) INFORMATION FOR SEQ ID NO: 786: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 487 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| * | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786: | |
| | TCAAGTTTAT TCGCTTGTTG GAAAGCTTTA ACTTGATTTT CTAAAGCTTT ATCAAATTGC | 60 |
| 20 | GTTGATTCAT TATCAACTTT ATAACCTAAA GCTGATAAAC CAATTTTAAT AGTTTTAATA | 120 |
| | TTTTTATCAT CGTCTCCAAC TTTAAATGTT TTCGTATTAG GAATGACATT TAAAGATTGA | 180 |
| | TATTTAGGTG TGTCAATAGT AACGTCTGGT TTAATGCCTT TACCGTGAAT ATAATGACCA | 240 |
| 25 | TCTGGCGTTA ACCATTTCAT TTCAGTATAT TTTAACAATG AACCATCCTT AAACTCTCTT | 300 |
| | GTAGTTTGTA CGACACCTTT GCCGAATGTT TTTGACCCAT AAACTTTAGC TTTATTATAG | 360 |
| 30 | TCTTTTAGCG CACCAGTAAA CACTTCAGAA GCGCTAGCTG AACCTTCATT CACTAAGATG | 420 |
| | GATATATCCA TGTCTTTCGC TTCTTTTAAC GCATCATTAG AAGTEGAATT GCTCAGTACT | 480 |
| | TTACCTT | 487 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 787: | * |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 803 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787: | ٠ |
| | GNAAACNATA TTTANAATTA AGTGTTCGAT TTGCAGTAAA TTCATACAGA AAAGCTAAAA | 60 |
| | TTAAAATGAT ACAGTGGAAT AATGTCACAT TCTCCATAAA TAATTGACCG AAGAAGCATA | 120 |
| 50 | AAACATAGAA TAGTACAGTA ACACTTACCG GCTGCTTTTC TTTATATATA ATTGCATTAA | 180 |
| | TACAATAATA AATAATAAAG AGTGAAATTA GTGTTGATGT CGCATAATTA TAAAATCCTG | 240 |
| | CAAACCAGCC ATATGTATCT GCATAAATAG CACTTGGTAA AATTAACATT AAAGAAAATG | 300 |
| 55 | | |

| | TGCCCATACT AATGAGGCCA TATGAAAGCC AACGTAACCA GCT | TACATGT | ACAGCTATAA | 420 |
|----|---|--|----------------|-------|
| | TTTCAAAGAT ATTTCCGATA TAGCGACCAT TAAGTGATGC AAA | ATCCTACT | TTTAAAATAT | 480 |
| 5 | CAGTATTATA ATTGCTAAAC CATTGTAAAT CATCGTGCAT GAG | STGGTAGT | AAGATACCCA | 540 |
| ٠ | TAAAAGTATA AAACAATAAT ATCGCAATTA ATATCAAAGT TGT | CTTGTGT | AATTGAATTG | 600 |
| | TTTTCACTTT GCTAATCCTC AAATCTAGTT AAATTTTCCT CAA | ACTTGTAG | GTCGAAAAAT | 660 |
| 10 | TAATTCAATA TTTTTAATGT ATTTCTAATT TTCACCTATG CAT | GTTTCCT | CAATCAAATT | 720 |
| | AGATAAACAA GGTATTTAAT ATTACTTTCA ACAATTTATC TAA | ATCGCCC | CTCGTCTTTT | 780 |
| 15 | TCTATGaCGA ATGATTACAC TTG | • | | 803 |
| | (2) INFORMATION FOR SEQ ID NO: 788: | | · · | . 6. |
| | (i) SEQUENCE CHARACTERISTICS: | | • | • |
| 20 | (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid | | | "7 |
| | (C) STRANDEDNESS: double | -1 | `- | |
| | (D) TOPOLOGY: linear | | | 4. |
| | | | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788: | | • | |
| | GAAAAGTTGT ATTATGAATA AAGTTAATCA AGGTGCTCAG GAA | GAGGCAA | TGGAAGAGTT | 60 |
| 30 | ATTAGTGACT TITCAAAAAT TGATTAAAGA CTAAAGGAGT TTA | AGATGAT | ACATCAAAAT | 120 |
| 00 | ACGATTTACA CAGCGGGAAT TGAAACAGAA GAACAAGTAA GTC | AATTGAC | AGAACGCATT | 180 |
| | TCAAATATGA TAGGTGTTCA TCAAGTGAAT ATTAATATAA TAG | SATGGTCA | AGTAACTGTA | . 240 |
| 35 | TCGTATGAGA CACCAGCAAA TTTGAATAGT ATTGAAAAAG AAA | TCTATGA | TGAAGGATAC | 300 |
| | AAAATTGTAT TTTAGGGTAT AATGTAGAGT GCGCTATAGA TTT | TAATTT | GAAAATAAAT | 360 |
| | TAAAAATTTT GTAAATGATG TAGTAAAGGT ATGTCGAATA | | | 400 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 789: | | | |
| | (i) SEQUENCE CHARACTERISTICS: | | | |
| | (A) LENGTH: 762 base pairs(B) TYPE: nucleic acid | • | | |
| 45 | (C) STRANDEDNESS: double | | | |
| | (D) TOPOLOGY: linear | | | |
| | | • * | | |
| | | . • | | • |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789: | | | |
| | GTTTAAAGAT GGAGAGATTA TTGATTTTTC AGCTGGAAAA GGT | GAAGCGG ' | TATTGAAAGA | 60 |
| | TTTAATCAAT ACTGATGAAG GTTCAAGAAG ATTAGGTGAA GTA | GCATTAG | TACCTGATGA | 120 |
| 55 | · | | | |

| | ATGTCATTTA GCGATTGGAT CTGCTTACGC CTTTAATATT CAAGGTGGAA CGGAAATGAC | 240 |
|----|--|-----|
| | TGTTGAGGAA AAGATTGCAA GCGGATTAAA TGATTCAAAT GTACATGTCG ATTTCATGAT | 300 |
| 5 | TGGTAGTAGT GATTTGACTA TTTATGGCAT ATTCGAAGAT GGTTCAAAAG AACTAGTATT | 360 |
| | TGAAAATGGA AATTGGGCAT CAACATTTTA ATAAATGTTA TTTTGAGGTG CTGAGTAGGA | 420 |
| 10 | AATGAAACAT GTATTTAAAG GTCAAATACG TGATTAAAGT ATAGATTGGG AGATAAAATA | 480 |
| | ATGACAAATC AGGACAGACC AATGAAATCT ATGTCAGAAT CAAAATGTTA TAAAAATAGA | 540 |
| | CAAGTTTTCC CTCAAGATAC GAATCACCAT CATACAATGT TTGGTGGTAC ATTGATGGCT | 600 |
| 15 | AATATTGATG AAATTGCAGC AATCACAGCT ATGAAACATG CTGGTGCGCA AGTAGTTACC | 660 |
| | GCATCTACAG ACTCAGTAGA TTTCTTAAAG CCGATTAAAA CAGGGGACAT ATTACAATAC | 720 |
| | GTAGCGATGG TTTCATACGC TGGGACTAGT TCAATGGAAG TG | 762 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 790: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790: | |
| 30 | | |
| | TTTAATTTTA TCTTTTGGAT ATCACATAGA TGCTACTTTT CTATACTGTT CTAAATCTAT | 60 |
| | TATTTCGTCA CATTGATTTG CAATAGCCAT ATCATGTGTT GCTAAAATCA GCACTTTATT | 120 |
| 35 | TTCATCGACC AAACCAAATA ATGATTGAAT AATCATCTGT CCTGTTTTAG GATCTAACGC | 180 |
| | ACCCGTTGGT TCATCAGCTA ACATAACAAT CGGATCTTTT AACATCATTC TAATTAAAGC | 240 |
| | GACACGTTGT TGTTCACCTC CACTTAGCGT ATGAACTTTT CTTTTTAAAC TGTTTGACAG | 300 |
| 40 | ACCAAACTGT TCLATATAAC GLATCTLLAT TTGTnCTTTT TCTTTCTTAC TTATTTTTTT | 360 |
| | ATATGCTAAT CCAATATCTA AATTTTCATT TACTGnCAAA | 400 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 791: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: dcuble (D) TOPOLOGY: linear | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791:

55

| | AACGIAAAGC GGAAGIIGGG AIGGIIGAAG AIGCIGAAIT ICAIGCGCAA CIACAICGII | 120 |
|------------|---|-------|
| | ATAATGCTTT TCTAGAGCAA CATCAAGATG ATAAAGTGTT GTATTTmGAA ATTGGAATTG | 180 |
| 5 | GTTATACTAC ACCACAATTT GTGAAGCATC CTTTTCAGCG TTGACACGTA AAAATGAAAA | 240 |
| | TGCCCTTTAT ATGACGATGA ATAAAAAGGC TTCGCATTCC GAATTCAATT CAGGACGTAC | , 300 |
| | CATACTTTAA CTGAGATTCT CAACTTGTTC AGCAGACTCC GGACGCAGCA CACGAAATAC | 360 |
| 10 | ACATGGGGGC AGAGTNACTT ATGGACCGTT GAATGNGATA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 792: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 678 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| : : | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792: | |
| | GTTCCGTTTG ATACAGAGAA GCGAATGTAA GCATAATCTT TAACAGTATC GTATGATALA | 60 |
| 25 | ALTTAATTGG CAACTTTTTG TCACCTTCAT AAACTTCAAA TTTTCTCCAA AATTGACCTG | 120 |
| | ATTGTAATCC TAATTCAATT TCTGGTTTTG AATCAGTGAA AATAACTCTA GCAGGTTTAA | 180 |
| 30 | CAGAACTTGC ATAATGATAA AACTGTTGAG TTCCATCTTT CTTTTTCATT TCAAAATCAA | 240 |
| | TTGGACGAGA GTTTGGTGCG CTATGATCTT TGTCTTTTAT TGCAGGGTTT TTAATCGCTT | 300 |
| | CTCTAAGTTC CTGATTCAAA ATAGGATATG TATTGTTAGT GGCYTTTGCT GCTGGTTTAA | 360 |
| 35 | CTTCTTTGT TTCCTTAGGG GCTTTAACTT CTTTAACTTC TTTAGCTTCT TTTGTTTCAG | 420 |
| | AAGTAGGGGC CTCAACTTCT TTATTAGATA CTGAGACAGC ATTAGCTACT GGTTTAGTTT | 480 |
| | CTGGAGCTTT TTCAGATGTT GTTGTTGGAC TTGCAACTGC TTCAGTTTTT GGTTGTGCTT | 540 |
| 40 | CTGTATTTGT ACCACCTGTT TCTTCAGCTG CTGCTTGTGT TCGCCATTTG ACATTAATAA | 600 |
| | TAAAAGTGTA CTAATTGCTA CAGATGCAAC GCCTAGTGAT GACTTTCTAA TTGAATAAAA | 660 |
| | TGATTTAAAT TCTTTTTG | 678 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 793: | |
| 5 0 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | - |

| | ACTGGCGGAT CCACGATGGC ATGTGTTAGT GAAGCAATTC ATTTATTACC ATATAATGTA | 60 |
|---------|---|-----|
| | TTCTTCGTAC CAGCCAGAGG TGGACTAGGC GAAANTGTTG TCTTTCAGGC AAACACAATT | 120 |
| 5 | GCAGCCAGTA TGGCACAACA AGCTGGCGGT TATTATACGA CGATGTATGT ACCTGGATAA | 180 |
| | TGTCAGTGAA ACAACATATA ATACATTGTT GTTAnGAGCC ATCAGTCATT AAACACTTTA | 240 |
| 10 | GGACAAAATT AAACCAAGCA AACGTTAATA TTACACGGGC CTTTGGTGAT GCGCTGGAAG | 300 |
| ,,, | ATRIGGCCCT CGGACGTCCA ATCACCTGGA AAAGGTCCTT GGAACCACTT C | 351 |
| | (2) INFORMATION FOR SEQ ID NO: 794: | |
| 15 - | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794: | |
| 25 | GGGCGAGGCG TTCGCGCACC GGCCGAGCAG CAAATAGGCC GGGATGTCGC GTCTTGCTGC | 60 |
| 20 | AGGTCCGAAA AATATCAACT TGAAGAGGTA ACACCGnTAG ATATGTTTCC ACAAACAACA | 120 |
| | CATGITGAGA CAGTGGCATT ATTCAATTTG AAATAGCGCA CATGATTTGA GATAAAATTT | 180 |
| 30 | CGCCTTAATA AGTGAAGAAA GAAGTCGTAT ATTAAAATTT TATTACAGCC AATTTACTTT | 240 |
| | CTTGATATGA ACTITITAAA TTAAATGTGA CATTGTATAC TATATTTAAA GAAGAATAAG | 300 |
| | AATGTCATGA TCGGGAGGGT TGGTAATGCA TAAAATTGAT TTAACGACAA ATAATTTTCA | 360 |
| 35 | AATGCGAGGT TTATTATCCT GGCAACCTGG TTATTGCGTT | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 795: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 407 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795: | |
| | ATGTTCCAGG AACGTATTTT TACAACCGAC AATTAGCATA TGTCATAATG AGTTTTATAA | 60 |
| 50 | TTGTATTTTT TATTGCATTT TTAATGAATG TTAAATTACT GAGTAATATT AAAGTGCAAA | 120 |
| | AAGGTATGAT TATAACTATC GTCTCACTAT TATTACTGAC GTTAGTAATA GGTAAAGATA. | 180 |
| | TTAATGGTTC TAAAAGTTGG ATAAACTTAG GATTTATGAA CTTACAGGCA TCTGAGTTAT | 240 |

| | TANGTANACC AMAGITANTE TTANGTCCTA TTGTATTAGC ATTAGGTTGT ACGTTTTTAG | 360 |
|----|---|------|
| 5 | TTTTCCTACA AAAAGACGTG GGCAACATTA CTAATATTAA TNATNIT | 407 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 796: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 10 | (A) LENGTH: 1053 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796: | |
| | CAGTAGGTAC ACTTGCAGCA TTTGTTGGAT ACTTAGAGTT ATTGTTCGGG CCTTTACGTC | 60 |
| | GTTTAGTCGC ATCATTTACA ACTTTAACGC AAAGTTTTGC TTCAATGGAC CGTGTATTCC | 120 |
| 20 | AATTAATTGA TGAAGATTAT GACATCAAAA ATGGTGTTGG TGCTCAACCT ATTGAAATTA | 180 |
| • | AACAAGGTCG TATTGATATT GATCATGTTA GTTTTCAATA TAACGATAAC GAAGCTCCAA | 240 |
| 25 | TTTTAAAAGA TATTAATTTG AGTATTGAAA AAGGAGAAAC AGTTGCTTTC GTAGGTATGA | 300 |
| | GTGGTGGTGG TAAATCAACA TTAATTAACT TAATACCGAG ATTTTACGAT GTAACTTCTG | 360 |
| | GGCAAATTTT AATAGATGGT CACAACmTTA AAGATTTTTT AACGGGAAGT TTAAGAAATC | 420 |
| 30 | AAATAGGATT GGTGCAACAG GATAATATTT TATTCTCTGA TACAGTTAAG GAAAATATTT | 480 |
| | TaCTTGGTCg TCCaACAGCa ACAGATGAAG AAGTAGTTGA AGCGGCGAAA ATGGCTAATG | 540 |
| | CACATGACTT TATTATGAAC TTGCCACAGG GATATGACAC TGAAGTAGGT GAACGAGGTG | 600 |
| 35 | TTAAATTATC AGGTGGTCAA AAACAAAGAT TATCGATTGC TAGAATATTT TTAAATAATC | 660 |
| | CGCCAATTCT TATCTTGGAT GAAGCAACAA GTGCACTTGA TTTAGAAAGT GAATCCATTA | 720 |
| 40 | TTCAAGAAGC ATTAGATGTG TTGAGTAAAG ATCGAACGAC ACTTATCGTA GCGCATCGCT | 780 |
| | TGTCCACTAT TACACATGCT GACAAAATTG TCGTAATTGA AAATGGACAT ATTGTTGAAA | 840 |
| | CAGGTACGCA TCGTGAATTG ATTGCAAAAC AAGGTGCTTA CGAGCATTTA TATAGCATTC | 900 |
| 45 | AAAACTTATA AAGTATTAGT TGTTTGACTT CAGTACAATC TTGAAGAGAA AATTTGTAAC | 960 |
| | AGGATGGTGG GGTCATAACA TAGAAAAAGC AGTAAGAGAT TTTCTTAGTT GAAAATAATC | 1020 |
| | TTnCTGCTTT TTTAAATTTA ATTTCGnGAT TCA | 1053 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 797: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 544 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | * |
| | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797: | |
|------------|--|-----|
| _ | AAGAGTGACT CCTGAAGTGA AAGAAGGGGA CCGTGTCGTG TTCCAACAAT ATGCTGGTAC | 60 |
| 5 | AGAAGTTAAA CGAGATAATG AAACATATCT GGTATTAAAT GAAGAAGATA TTTTAGCAGT | 120 |
| | TATTGAATAA TACAGAACTT AATTCATAAA TAAATTAAAT | 180 |
| 10 | CTAAACAAAT GGAGGTTTAT CATTTATGGT TAAACAATTG AAATTCTCTG AAGATGCACG | 240 |
| | TCAAGCAATG TTACGTGGTG TTGACCAACT TGCAAATGCA GTTAAAGTAA CGATTGGTCC | 300 |
| | TAAAGGACGT AATGTTGTAT TAGATAAAGA GTTTACAGCA CCTTTAATTA CGAATGATGG | 360 |
| 15 | TGTGACGATT GCYAAAGAAA TCGAATTAGA AGATCCATAT GAAAATATGG GGGCTAAACT | 420 |
| | AGTTCAAGAA GTCGCAAATA AGACAAATGA AATTGCTGGT GACGGTACGA CAACTGCAAC | 480 |
| | AGTATTAGCT CAAGCAATGA TTCAAGAAGG CTTGAAAAAT GTTACAAGTG GTGCGAACCC | 540 |
| 20 | AGTT | 544 |
| • | (2) INFORMATION FOR SEQ ID NO: 798: | |
| 2 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 372 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | ٠., |
| | (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798: | ٠ |
| | CAATTGCATA GATATTGCTG ATAGACGTAC GGCTTTGTTT ATCAACTTCT AATAATCCAC | 60 |
| 35 | GGTCAGCGAA TTTAACACCT AATTTCGTCT GTGTTTGGAC GACGACCTAC AGTTACTAAT | 120 |
| | ACATAATCAG CTTCGATTGT TTTCTCTTCG CCTTTAGCTT CATAAGTAAC TTTAACTCCG | 180 |
| • | TTATCTGTTT CTTCAGCTGA TTTAGCCATA GCTTCAGTAA CGATTTCAAC ACCTTTTCT | 240 |
| 10 | TTCATACCTT TTTTAACAGG TTGTGTGCAT TTGnTTTTTC GAGGCCACCT AAGATATCTT | 300 |
| | TAGCACCTTC AAGGGATGGG GTACTTTCTG NAACCAAAGT TAGCAAATGC TGTACCTAAT | 360 |
| 15 | nctggtccaa tg | 372 |
| | (2) INFORMATION FOR SEQ ID NO: 799: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1182 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

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| 5 | AAACGACATT TGTTTAATTG GAAGAATTAG CACCATTTTT TGAGGCGGGT ATAGALTCAT | 60 |
|----|---|------|
| | TTAAAATCGA TGGTATTCTA CAAACGGAAG AATATATTAA TGTGGTAACG GAACAGTATC | 120 |
| | GTCAAGCGAT AGATTTGTAC AATGAAGATC CTGAAATCTA TGAAGATGAG AAATTTATGT | 180 |
| 10 | TGATGGATCC AATTGAAGAA ATTCAACCTG ATCATCGACC ATTTGACGAA GGTTTCTTAT | 240 |
| | ATAAACAAAC AGTATATTAA GGAGGTTAAT CATGAAGACA ATAGAAGAGA TTAAATCAAC | 300 |
| | TCCTAAAACA GTTATGAAGA AACCAGAATT ATTAGCACCT GCTGGAAACT TAGAAAAGTT | 360 |
| 15 | AAAAATAGCA GTACATTATG GCGCTGATGC CGTATTTTTA GGTGGTCAAG AATATGGATT | 420 |
| | ACGTTCaAAT GCTGaTaATT TCaCGATGGA AGAAATAGCT GAAGGTGTTG AATTTGCGAA | 480 |
| - | CCGTTACGGT GCCAAAATTT ATGTTACGAC AAATATTATT GCACATGATG AGAATATTGA | 540 |
| 20 | AGGTCTAGAA TCATATTTGC GTAATTTGGA AAAGACTGGT GCGACAGGTA TCATTGTTGC | 600 |
| • | AGATCCTTTA ATTATCGAAA CATGTAAAGA AGTTGCGCCA AAACTTGAAA TTCATTTATC | 660 |
| 25 | TACTCAACAA TCACTTTCTA ATTACAAAGC TGTAGAATAT TGGAAAGAAG AAGGATTGGA | 720 |
| 25 | TCGTGTTGTA TTAGCACGTG AGACCGGCGC GATGGAAATG CGTGAAATGA AGGAAAAAGT | 780 |
| | AGATATTGAA ATCGAAGCAT TTATTCATGG TGCTATGTGT ATCGCCTATT CAGGTAGATG | 840 |
| 30 | TACATTAAGT AATCATATGA CTGCAAGGGA TTCCAACAGA GGCGGTTGCT GTCAAAGTTG | 900 |
| | CCGTTGGGAT TATGAATTAT TAGAAGTTGA TGATAATGGT GAACTTGATG TTTTTTATAA | 960 |
| | TCAAGGTGAA GTTACACCGT TTGCGATGAG TCCTAAAGAT TTAAAATTAA TCGAATCAAT | 1020 |
| 35 | TCCTCAAATG ATGGATATTG GTGTGGACTC ATTAAAAATT GAAGGACGTA TGAAGTCAAT | 1080 |
| | TCATTATATT GCAACAGTTG TCTCAGTATA TCGTAAAGTC ATTGATGCGT ATGCGGCAGA | 1140 |
| | TCCTGACACT TTAAGATTAA TCCGGAATGG TTAATAGAGT TA | 1182 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 800: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 989 base pairs | |
| 45 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800: | |
| | GTATTCTTCC AATAACACCT TŢCATTTGGA AACCGTTTAG AAAGAATACA GTTACTTCAG | 60 |
| | TTTCCTTTCC TTTAAAATTC TCTACTCCTT TCTCTTCCAT CTTTTCC+TC CAATCATCTC | |

| GCATATTGGC GTGAATGTTG CTTTAAATCA TTGACAGCAT CTTCATAAAT CATT | CCGTTTT 240 |
|---|---|
| | TTGTCCG 300 |
| TTAATCACAG GTATTAATTC TTTATATCCA ATAGCTTGCA TACTTTGGCA AGAT | TTCATAG 360 |
| CCTTGTTCAA CAAGTTGTTG CACTTCTCTA AATAATCCGT GATCCAACAT AATA | ATCAACA 420 |
| CGTTTATTTA TTCTTGAATA TAATGTTTTA CGCGACATTT CAATCCCTAA TAAT | TAATGTA 480 |
| TCATAATTT CAGTAAATTG TTGCACTTTC TTGCGATTAC TCAAAAGTTT TTTT | GTTTT 540 |
| AAATAATATT CAATAGCGCG CAACACTCTT TGGCGGTTGT TAGGGTGAAT ATTT | TTCTGaC 600 |
| AGAAACCGAC ATCAAATTGA GCTAAATAAT CGTGTAGTTG CTGATTATCT AAAT | GTTCTA 660 |
| ATGCAGATAA CTTTTGTTTA ACTATGGATA ATTGTGCAGG TGTACTGTTT CATC | TTCTAA 720 |
| TTCATAATTA TATATTAATG ATTGAATATA TAAGCCTGTT CCACCTGCTA TGAT | TGGaAC 780 |
| 20 TTTACCTCTA TTCGTLATAT CAGTAATTAA ATCTTCTGCT AATCGCTTGA ATTC | ATATGC 840 |
| TGAAAATGTA TCATCAGGAT TCAAGATATC AATTAAATGA TGTGGAATAC CATC | CATTIC 900 |
| TTCAGGTGTn ACTTTTGCAG TTCCAATATT CATATGTCTG TAGACTTGCA TAGA | GTCACC 960 |
| 25 GCTTATGATT TCACCATTGA TACGCTTCG | 989 |
| | |
| (2) INFORMATION FOR SEQ ID NO: 801: | , |
| (i) SEQUENCE CHARACTERISTICS: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | * |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | CTGCAG 60 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801: CGTTAGATAT AGAATTAAAA GATAATATTA AATTTCAAAA CGGTCAAAAA TTGA | ATTCAT 120 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801: CGTTAGATAT AGAATTAAAA GATAATATTA AATTTCAAAA CGGTCAAAAA TTGA AAAAAGTGAA ATCTAGCCTT GAAAATAGCA TGAAAAAAAG CGACTTGGTC AAAT. | ATTCAT 120 CCGCTT 180 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801: CGTTAGATAT AGAATTAAAA GATAATATTA AATTTCAAAA CGGTCAAAAA TTGA AAAAAGTGAA ATCTAGCCTT GAAAATAGCA TGAAAAAAAG CGACTTGGTC AAAT TACCAATATC ATCAATTACC GCTAAAGGTC AAAAACTGAC AATTAAAACC AACTA | ATTCAT 120 CCGCTT 180 ATGCTA 240 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801: CGTTAGATAT AGAATTAAAA GATAATATTA AATTTCAAAA CGGTCAAAAA TTGA AAAAAGTGAA ATCTAGCCTT GAAAATAGCA TGAAAAAAAAG CGACTTGGTC AAAT TACCAATATC ATCAATTACC GCTAAAGGTC AAAAACTGAC AATTAAAACC AACTAACCAATATC ATCAATTACC GCTAAAGGTC CTTTTATGGC AATTATGAT ACAG | ATTCAT 120 CCGCTT 180 ATGCTA 240 ATAAGC 300 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801: CGTTAGATAT AGAATTAAAA GATAATATTA AATTTCAAAA CGGTCAAAAA TTGA AAAAAGTGAA ATCTAGCCTT GAAAATAGCA TGAAAAAAAG CGACTTGGTC AAAT TACCAATATC ATCAATTACC GCTAAAGGTC AAAAACTGAC AATTAAAACC AACT ACCCTGAACT TGTATCTGAA TTAGCTAATC CTTTTATGGC AATTTATGAT ACAG AATCAGATGT TAATCAAACT CCTGTTGGTA CAGGCCCTTA CCAAATAAAA GATTAAAACT CCTGTTGGTA CAGGCCCTTA CCAAATAAAA GATTAAAACT CCTGTTGGTA CAGGCCCTTA CCAAATAAAA GATTAAAACT CCTGTTGGTA CAGGCCCTTA CCAAATAAAA CCGAAATCCCCAAATAAAA CCGAAATCCCCCCCAAATAAAA CCCGAAATCCCCCCCCCC | ATTCAT 120 CCGCTT 180 ATGCTA 240 ATAAGC 300 AACTTG 360 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801: CGTTAGATAT AGAATTAAAA GATAATATTA AATTTCAAAA CGGTCAAAAA TTGA AAAAAGTGAA ATCTAGCCTT GAAAATAGCA TGAAAAAAAG CGACTTGGTC AAAT TACCAATATC ATCAATTACC GCTAAAGGTC AAAAACTGAC AATTAAAACC AACT ACCCTGAACT TGTATCTGAA TTAGCTAATC CTTTTATGGC AATTTATGAT ACAG AATCAGATGT TAATCAAACT CCTGTTGGTA CAGGCCCTTA CCAAATAAAA GATTTAATCAAAACT CCTGTTGGTA CAGGCCCTTA CCAAATAAAA GATTTAATCAAAACT CCTGTTGGTA CAGGCCCTTA CCAAATAAAA GATTTAATCAAAACT CCTGTTGGTA CAGGCCCTTA CCAAATAAAA GATTTAATCAAAAAAAAAA | ATTCAT 120 CCGCTT 180 ATGCTA 240 ATAAGC 300 AACTTG 360 AATCTC 420 |

(2) INFORMATION FOR SEQ ID NO: 802:

| (I) SEQUENCE CHARACTERISTIC | (i) | SEQUENCE | CHARACTERISTICS | : |
|-----------------------------|-----|----------|-----------------|---|
|-----------------------------|-----|----------|-----------------|---|

- (A) LENGTH: 1139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802:

| - | GCGAATTCGT | ACACACATAT | ACACAAAGAT | AATCATAGTT | TTACATTGAA | GCACATGAAA | 60 |
|----|------------|------------|------------|-------------|------------|------------|------|
| 15 | GATAATTCAT | TTAAAGGAAG | GTATTATCAA | TGACTAAAAA | AATGGGATTA | TTAGTTATGG | 120 |
| | CTTATGGCAC | ACCTTATAAA | GAAAGTGACA | TAGAGCCATA | TTATACAGAT | ATTAGACATG | 180 |
| | GTAAACGTCC | ATCTGAAGAA | GAACTTCAAG | ATTTGAAAGA | TAGATATGAA | TTTATAGGTG | 240 |
| 20 | GTTTATCACC | ATTAGCAGGT | ACAACAGATG | _ACCAGGCTGA | TGCGCTAGTT | TCAGCATTAA | 300 |
| | ATAAAGCATA | TGCAGATGTT | GAATTTAAAC | TATACTTAGG | ATTAAAACAC | ATTTCACCAT | 360 |
| 25 | TTATCGAAGA | TGCGGTTGAA | CAAATGCACA | ATGATGGCAT | TACTGAAGCA | ATCACGGTAG | 420 |
| | TACTAGCACC | ACATTATTCT | TCATTTTCAG | TAGGATCATA | TGACAAACGT | GCTGATGAAG | 480 |
| | AAGCTGCAAA | ATATGGTATT | CAACTTACAC | ATGTGAAACA | TTATTATGAA | CAACCTAAAT | 540 |
| 30 | TTATTGAATA | TTGGACGAAT | AAAGTCAACG | AAACATTAGC | TCAAATACCG | GAAGAGGAAC | 600 |
| | ATAAAGACAC | GGTATTAGTT | GTTTCGGCAC | ATAGTTTGCC | AAAAGGTTTA | ATCGAAAAGA | 660 |
| | ATAATGATCC | ATATCCACAA | GAACTAGAAC | ATACTGCGCT | TTTAATTAAA | GAACAATCTA | 720 |
| 35 | ATATTGAACA | TATCGCGATT | GGTTGGCAAT | CTGAAGGTAA | TACAGGTACA | CCTTGGTTAG | 780 |
| | GGCCAGATGT | ACAAGATTTA | ACACGTGATT | TATATGAAAA | ACATCAGTAT | AAAAACTTTA | 840 |
| | TATATACGCC | AGTAGGTTTT | GTATGTGAGC | ATTTAGAGGT | GCTTTATGAC | AATGATTATG | 900 |
| 40 | AATGTAAAGT | AGTTTGCGAT | GATATTGGTG | CGAATTATTA | TCGTCCAAAA | ATGCCGAATA | 960 |
| | CACATCCATT | ATTTATCGGT | GCAATTATTG | ATGAAATCAA | GTCTATATTT | TAATGACGAA | 1020 |
| | AGAAGCGTGA | AACGTTGTGA | CTAAATCAGT | GGCTATTATA | GGAGCGGGGA | TAACAGGTTT | 1080 |
| 45 | ATCAAGTGCA | TATTTTTTAA | AACAGCAAGA | TCCTAATATT | GATGTAACCA | TCTTTGAAG | 1139 |
| | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

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| | ALL SEGUENCE DESCRIPTION: SEQ ID NO: 803: | |
|----|---|-----|
| _ | TATCCHAAAT AHAAATGTGC GCATTTATCA AAACCTTACA TACAATAGAG TTTTCCCTAA | 60 |
| 5 | CAGTAAATTA GATATTATTA CACCTGTTGA TATGTCTTCT AATGCCAAAC TGCCAGTTAT | 120 |
| | TTTTTGGATG CACGGTGGTG GTTATATTGC GGGTGATAAG CAGTATAAAA ACCCATTATT | 180 |
| 10 | AGCGAAAATT GCTGAACAAG GGTACATTGT TGTGAATGTA AATTATGCAT TGGCGCCACA | 240 |
| | ATATAAATAT CCCACACCAT TAATTCAAAT GAATCAAGCA ACTCAATTCA TTAAAGAAAA | 300 |
| | TAAAATGAAT TTACCTATTG ATTTTAATCA AGTAATTATT GGCGGTGAYT CTGCAGGTGC | 360 |
| 15 | TCAATTAGCT AGCCAATTTA CGGCAATACA GACGAATGAT CGCTTAAGAG AAGCCATGAA | 420 |
| | ATTTGATCAG TCATTCAAAC CATCGCAAAT TAAAGGTGCT ATACTATTTG GTGGTTTTTA | 480 |
| | TAATATGCAA ACAGTTAGAG AAACTGAGTT TCCAAGAATA CAGTTATTTA TGAAAAGTTA | 540 |
| 20 | TACTGGCGAA GAAGATTGGG AAAAGAGTTT TAAAAACATT TCACAAATGT CGACAGTAAA | 600 |
| | ACAATCGACA AAAAATTATC CACCAACATT TTTATCTGTT GGAGATAGCG ATCCATTCGA | 660 |
| | AAGTCAAAAT ATAGAATTCA GTAAGAAATT ACAAGAATTG AATGTACCAG TAGATACTTT | 720 |
| 25 | GTTTTATGAT GGTACGCATC ATTTACATCA TCAGTATCAA TTTCACCTTA ATAAACCTGA | 780 |
| | ATCGATAGAT AATATCAAAA AAGTGTTACT TTTCTTAAGT CGTAATACAT CCTCTAGTGG | 840 |
| 30 | TATTCAAACT GAAGAGAAAC CACAAATAGA AAATCCGAGT AATGAATTAC CGTTAAATCC | 900 |
| | TTTAAACTAA TGATAAACAG TAGTAATTTA TTACTTAAGC AACATTTAAG ATTTTCAAAT | 960 |
| | TAAAAACGAG AATTTAAAAC ATGTGGTGC | 989 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 804: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 711 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804: | |
| | TAAHCCCTGG TTTAATGATT TTGATTACGT GTTTTTATAA TAAAAACATA TCGAACATTG | 60 |
| | ACTACGTTAT TAAGCTGCTT TTTTGTACAC TTTATAACCA ATAGCTTAAG ATTTAAAACT | 120 |
| io | AATCGGAAAG AACAATGATT CACCANAAAA ATATTTATGT TGCTATTAAA AATCAGTTAA | 180 |
| | TACGAATGTT AAAATACGTT TGATTTTCAT TAATAATGAT TCAAGTTTAT TTAAATGAGC | 240 |
| | GTTAATGTCA GTCTGTTTTG ATGCACCTTA TAATAAAGAC AGATAGTTCA AATTACGTAA | 300 |

| | | AAAGCAACAT TAGCATTAGG AATATTAACT ACAGGTGTGT TTACAGCAGA AAGTCAAACT | 420 |
|-----|---|---|-----|
| • • | | GGTCACGCGA AAGTAGAACT TGATGAGACA CAACGCAAAT ATTATATCAA TATGCTACAT | 480 |
| 5 | | CAATACTATT CTGAAGAAG TTTTGAACCA ACAAACATTA GTGTTAAAAG TGAAGATTAC | 540 |
| | | TATGGCTCTA ACGTTTTAAA CTTTAAACAA CGAAATAAAG CTTTTAAAGT ATTTTTACTT | 600 |
| | | GGTGACGATA AAAATAAATA TAAAGAAAAA ACACATGGCC TTGATGTCTT TGCAGTACCT | 660 |
| 10 | | GAATTAATAG ATATAAAAGG TGGCATATAT AGCGTTGGCG GTATAACAAA G | 711 |
| | | (2) INFORMATION FOR SEQ ID NO: 805: | |
| 15 | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 680 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | | • |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805: | |
| | | ATCAGGAAAA ACAGAATAAT GTAAATCAAG CTGTTCAGCC TCAAAATAAT ACTAATGAAA | 60 |
| 25 | | CATCAAAAGT ACCGGCTAAT TTTGTCAAAT TGAATGATAT TAAACCAGGT GATACTTCTA | 120 |
| ٠. | | TACAAGGAAC AACTITACCA AATCAATITA TACTATTAAC TATTGATAAA AAAGATGTGA | 180 |
| 30 | | GCTCAGTTGA AGATTCTGAC AGCAGCTTTG TTATGTCTGA TAAAGATGGG AATTTTAAGT | 240 |
| ,,, | | ATGACTTAAA TGGTCGCAAA ATTGTTCATA ATCAAGAAAT TGAAGTGTCT TCATCAGATC | 300 |
| | | CCTATTTAGG TGACGATGAA GAAGATGAAG AAGTAGAAGA AACTTCAACT GAAGAAGTTG | 360 |
| 35 | | GTGCTGAGGA AGAAAGTACA GAAGCTAAAG CTACATATAC AACACCGCGA TATGAAAAAG | 420 |
| | | CGTATGAAAT ACCGAAAGAA CAGCTAAAAG AAAAAGATGG ACATCACCAA GTTTTTATCG | 480 |
| | - | AACCTATTAC TGAAGGTTCA GGTATTATTA AAGGCCATAC CTCTGTAAAA GGTAAAGTTG | 540 |
| 10 | | CTCTATCTAT TAATAAAA TTWATTAACT TTGAGACAAA TGCTALGGTG GLCCAAATAA | 600 |
| | | AGAAGAAGCG AAATCTGGAT CAGAAGGAAT CTGGATGCCT ATTGATGACC AAGGATACTT | 660 |
| | | TAATTTTGAC TTCCAAACGA | 680 |
| 15 | 4 | (2) INFORMATION FOR SEQ ID NO: 806: | • |
| 0 | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 950 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |

| | GTATTTCATT | AGCCATTGGC | AATTGACATC | TGACAATGAG | GAATGGCTTT | TGCATTGGAA | 60 | |
|----|-------------|-------------|-------------|------------|------------|------------|-----|------|
| | TTCACAGTTG | GAGTGCATTT | ACTGGTTATT | TTGGAGGTCA | TTGTTGATAC | ATTATTAATG | 120 | |
| 5 | GAGAATAACC | GAATTTGTTA | TGTTATTTCC | ATTTTTAATA | TTTGCAATTG | TATTAAATGC | 180 | |
| | TGCACTTGGA | GATAAAATTA | AAAATCCTTA | TGGATCTGCC | ATAATTCTTG | TTCTAGTTAT | 240 | |
| | TATCGTATTA | AGTTGGGGAG | GTATTGACAA | GACTTGTTCG | TGGTAAAGTA | CTTCAAGAAA | 300 | |
| 10 | AAGAAAATGA | ATACTTTTTG | GCAGCAAAAT | CAATTGGTAC | ACCCACATAT | TTTATTAAAA | 360 | |
| | TGAAACATCT | TTTGCCGAAT | ATATTAAGTG | TAGTTATCGT | ACAAGCAACA | TTGTTATTTG | 420 | |
| 15 | CCGGTATGAT | TGTAGTGGAA | TCAGGTTTGA | GCTTTTTAGG | ATTCGGAATT | AGTAAAGCAA | 480 | |
| | TACCATCTTG | GGGTAATATG | TTGAGTGATG | CTCAAGAAGG | GGATGTTATA | AGTGGTAAAC | 540 | |
| | CGTGGATATG | GATGCCACCT | GCTATAATGA | TTACATTAAC | TATATTAAGT | ATAAACTTTG | 600 | |
| 20 | TAGGGGAAGG | GATTAAAGAT | GCTTTTAATC | CTAGAGGTAG | ACGTTAAATA | ATAAAAGAGG | 660 | |
| | CACTAGTTAA | TTCTAGTACC | TCTTTATTTT | ATCTCTTACG | TCCTAAACCC | ATCGCTTTTT | 720 | |
| | CCATTTTTTT | GACAGTTTTA | AATGAÄACTT | TGTGTGCTyT | ATCTCTACCT | TGATCTAAAA | 780 | |
| 25 | TATCAYCAAG | TTTATCTGAG | TTATAGAAAC | TTTCGTATTT | TTCTTGGAAT | TCTACTAAAA | 840 | وليد |
| | ATGCTTTAAC | TATTTCAGCA | AGGTCACCTT | TAAATTTACC | ATAACCTTCG | CCCTCATATT | 900 | 12 |
| | TTGCCTCAAT | ATCTTTAATT | GGCATGTCTG | TTAATCCAGC | GTATATTGAA | | 950 | * ; |
| 30 | (2) INFORMA | TION FOR SE | O TD NO. 90 | .7. | | | | |

(2) INFORMATION FOR SEQ ID NO: 807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807: 40

| GTTACCAGTC | GAAGCTTTAC | GACCTGTTAC | GAAACATTGT | TTACCCATAT | GAGTACCTCC | 60 |
|------------|------------|------------|------------|------------|------------|-----|
| TTTAATAAAT | ATAAATACAC | ATAACTACTT | ATATACTTAA | TTAAGATAGC | ATAGTTTCAT | 120 |
| TTGAAAAACA | ATGAATAATT | TTCACATAAA | AGTCAAAAAT | ACTGAGTTTT | GTGATATAAT | 180 |
| TGTAGACTGT | GAAGTTATGT | AGTATGATAT | TTTAGAGAAA | TAAGTGAATG | AAACATTTAA | 240 |
| AATTTTTATT | Tratgatact | ACATCTATTA | AAAGAAAACG | CCTATAGATA | ATCGTCaTGA | 300 |
| GTGTAAATTC | AGTTTACTCA | AcAtATAaTA | GGkGaTTTAA | gCgTAAGtCa | TTCTGATAAG | 360 |
| TTGTACCATT | GATATTTTAT | GAAATAnTCn | ATGAACTTAA | AGCGTTTATG | CTACACTA | 418 |

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| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 842 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-------|
| | | , . |
| - | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808: | |
| 10 | AATGGChATT AATCTTTAAT ACGATGCTTG AGGATTTTTC CTAATAAAAC CTTGATTTCm | 60 |
| | AAAAGGGTTT AAATCmAATG AAACAATAAT AAAAAAATGW CGCAATATAA TAATAAGTAC | 120 |
| ٠, | AAATTTAATT AAGAAATTAA ATTGATTGTA TATGTATATT TTGGTAACGT AAAAGAGANA | 180 |
| 15 | TATACAAAAT AATTAATTAT TTATATGAAA AGAGAATATA AATGAAGTAT AAAACAGAGA | 240 |
| | GACGTGAAGC GATGGGATAT TTAAMAAGGT TTGCATTGTA CATAAGCGTT ATGAYTTTAA | 300 |
| 20 | TATTTGCGAT AGCAGGTTGT GGCAAAGGTA ATGAAACAAA AGAAGATTCA AAGGAAGAAC | 360 |
| -% | AAATCAAAAA GAGCTTTGCG AAAACATTAG ATATGTATCC AATTAAGAAT CTCGAGGACT | 420 |
| | TATACGACAA AGAAGGATAC CGAGATGGCG AATTTAAAAA GGGTGATAAA GGGATGTGGA | 480 |
| 25 | CGATATATAC AGATTTCGCC AAAAGTAATA AACAAGGTGG ATTGAGTAAT GAAGGTATGG | 540 |
| - | TCTTATACTT AGATAGAAAT ACACGGACTG CAAAGGGACA TTATTTTGTT AAGACATTCT | - 600 |
| | ATAATAAGGG CAAATTCCCA GATAGAAAAA ATTATAAAGT TGAAATGAAA | 660 |
| 30 | TTATCTTATT AGATAAAGTA GAAGATACAA ATCTAAAAAA GAGAATAGAA AACTTTAAAT | 720 |
| | TTTTTGGACA ATATGCAAAC CTTAAAGAAT TGAAAAACTA CAACAATGGT GATGTCYCAA | 780 |
| | TTAATGAGAA TGTTCCAAGT TATGACGCAA AATTTAAAAT GAGCAATAAA GATGAAAATG | 840 |
| 35 | TT | 842 |
| | (2) INFORMATION FOR SEQ ID NO: 809: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 451 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809: | |
| | TAAGACTATG CCATCTTGGC AACGCGTTGT CGCATATTCA TTATTAGTAA GTATATGCAA | 60 |
| 50 | GCATGATTTT GCCATAACLT TACCLCLTTC TATATTTAAG TACCACTTTT ATCATTCCCT | 120 |
| | ATAATATTA ACTTATTAA TTAAACGTAA ATTTAACACA ATACGAATAC CAAATCAAAA | 180 |
| | | |

| AAAAATAGAT GTAGTCAGTT TAATTAAACT ATCCAATTGA AAACACACTA CTTTTTAGTA | | 300 |
|---|---|-----|
| TITTCAAAAT AATTTTAAAT GACCACATCT ACAACGTATT ACTATTATCT TTTGTTAGTT | 3 | 360 |
| ATATATTCAT TTTCAATTTA FAAATAAACA CTTAETTAAA TCACATTCTA CTTTTGAGAT | 4 | 420 |
| GAGCTCAAAC TAACATTAAA TTGTTTATAT T | 4 | 451 |
| (2) INFORMATION FOR SEQ ID NO: 810: | | |
| (i) SEQUENCE CHARACTERISTICS: | | |

- (A) LENGTH: 1499 base pai (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810:

| | ACATTITGTG | CTTGTTGTCC | AATCCAATTT | CTACTTTGTT | GAACAGTATG | AGTTGCTTGA | 60 |
|---|------------|------------|------------|------------|------------|------------|------|
| | CCACGCATGT | TACTCAGCAT | TTGTCCAACA | TGAGTATTTT | GAGCAAAGTT | ACGAGATTGA | 120 |
| | TTCAACACAC | TGTTTTTCAT | CATTnCCATT | TTAGGTGAAA | TACGACTAAC | TGCTTGTTGC | 180 |
| | ATTGTCTTTT | GCAATCCTGT | TTTAACTGCA | AATTTTTCTC | CGCCTTTGAA | GCCTAATTTC | 240 |
| | ATTAAACTTT | TCCCAGCACC | TTTGAGGAAG | CCCATACCTG | GCAATGGAAT | AAGCGAAAGT | 300 |
| | CCTTCCATGA | TTCGTTCTTC | TTTAGATAGC | TTTCTTCCAG | TTACAATATT | TTTTCCTGTG | 360 |
| | GCTGCATTTG | CTGCTGAATA | AGCGGAATAA | GCACCAATAG | CTACTGCTCC | AGCAACAGGA | 420 |
| | TTAATACAAG | ATAAAACTAC | CATACCAGCT | AGTGCTGCAA | TCTCTATAGC | TTCTTCTTTT | .480 |
| • | TTCTTTTGCT | CCTCTAGcTC | TTCCGCTTCA | GCTACTGTCA | TGTAATCACA | AGAAGCGCCC | 540 |
| | TGAGTCATCA | TTTTTTCAAA | ATCACTTTTA | GATAATTTCT | TATCTTCTTT | TTTCATTTCT | 600 |
| | TTGTAATGCT | GATCAATTAC | TTTTACAAAT | TCTTGATCCG | ATTITAATAT | TTCATCGATG | 660 |
| | CTATAAACAT | CGCTGTCACT | TTTCTTGGCA | TCTCCCTTTG | CAATTTTCCC | AGAAGCCCCA | 720 |
| | TAGGTATCTC | TACCATGTCC | ACCACCATTT | TTAATTAGTA | TATTTTCCAA | TTTAACATTC | 780 |
| | GTTATACCTT | TGAATGCTTT | ATCTATATCT | TCTATAAATG | GCGTGTCAAT | AATTTCTTTC | 840 |
| | ATTTTCGAAT | CTAATTGAGA | TGCATAATCA | TATAACTCAT | TTTGATAATA | CCCCATTAAT | 900 |
| | TTAGATCCTT | GTGGACCTAC | TACACTACTT | GTTAATGATA | TTGCGCCATC | TTCGTCTAAA | 960 |
| | GAACTGACAT | CGCTTACCGC | ATCATCCATT | GTTGTATCTA | CATCTAAGAA | GTCTTGACCC | 1020 |
| | TCTATTGCAT | CTATTACACT | TTGGATAGAT | GACTTTTCAT | TGTCATAATC | AGCTGTTAGA | 1080 |
| | TATTCAATAT | CTTTTGTCAT | GTCATGCACC | TATCCCTCAA | TATTATAGTA | AAGCTTGGCA | 1140 |

| | CCACCGAGTG TACTCAATGG ACCTTTGAGA CCACTAATGA CTGTTGCAGC ACTACTATAG | 1260. |
|------|--|-------|
| | CCATTTTCCA TAGAATGTGC AGCTTTTTCA CTACTGTAGT AATTTAATTG CGCTATTTTT | 1320 |
| 5 | CCAAAGTTTT GAGCTATTTC ATCATACTTT TGACTTATGC TTTCCAATTC TTTTACAACA | 1380 |
| | TGTGCAATCG TTTCAGCTTT AACACTAATT TTTCCACTCA ACGTCATTAC TCCTCtGGTt | 1440 |
| | TATLAATATG ATTTTCATCA GTATCGAATC CAAATAATTC TCGTGATAAA nGTATTGAA | 1499 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 811: | |
| | (i) SEQUENCE CHARACTERISTICS: | 3. |
| | (A) LENGTH: 620 base pairs | ٠. |
| 15 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| | | • |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811: | |
| | CNCGCTGCAC -CGAAGAATGC TTTTGGTTTG TGTAAAGATG CAGGATCTAA ACCACCTGAT | 60 |
| | AATGTACGAC CACTTGGTGG AATAACYAAG TTATAAGCGC GTGCTAATCT CGTTATAGAA | 100 |
| | | 120 |
| 25 | TCCATTAAAA TAATGACATC TTCCCCAATT TCTACTAAAC GCTTTGCACG TTCAAGTAAT | 180 |
| | AATTCAGCTA CTTTAACATG GTGTTCTGGT GGTTCGTCAA ACGTTGAATG AACGACTTCA | 240 |
| | GCAGCTTCTA CTGAGCGTTC TAAATCTGTT ACCTCTTCAG GACGCTCGCC AACTAACAAA | 300 |
| 30 | ATAAATAGCT TTGCATCTGG TTTGTTCGTA CTGATTGCAT TCGCTATTTC TTTTAATAAC | 360 |
| | GATGTTTTAC CTGCTTTAGG TGGCGCCACT ATTAAACCAC GTTGACCTAA ACCAATCGGT | 420 |
| | GTTACTAAAT CCATGATGCG CGTTGAATAA TTTTGTATTT CTGTCTCTAA TTTAATACGC | 480 |
| 35 | TCATCTGGAT AAAGTGGTGT CAAAGCTTGG AAATGCGGAC GTTTCTTCAC TTCTTCTGCG | 540 |
| | TTATGGTCAT GACAAAGTCA ACTTGTAATA AGCCATAATA TTTTTCGTTA TCTTTAGGTT | 600 |
| | TTCTAACTTT CCCAGTTACT | 620 |
| 40 , | (2) INFORMATION FOR SEQ ID NO: 812: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 1094 base pairs | |
| 45 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812: | |
| | CCGGCTGAAA TTAAGTTCTT GTTATATTTC GCAAAAATGA CAAAGAAAGA TAAAAATAAA | 60 |

| | TGAACTATTT | GCAATTAGAG | AATTGTTAGA | GAAAGGTTTG | ATTGGTGATT | GTATTCAACC | 180 |
|----|------------|------------|------------|------------|------------|------------|------|
| 5 | TATAATTGAA | CCAATTAAAT | ATACAACCAC | TAAAAATTTA | ACTTTGCAAT | ACTGTGGTGA | 240 |
| 5 | AAAAGCATTC | TCTATAAATT | TAGTAGTAAA | TTCAAAGTTA | ACTGAAGAAG | AGATTAGTAA | 300 |
| | CGAAaCTGTt | GCACATTTAA | CTGAAATAAT | AACAAAAAAC | AAAAGTGTTA | TTCAAAAAGC | 360 |
| 10 | TTACTTGGGT | CCTTCTGATG | AAGGCAATGA | TAGGTTGAAA | CAGCAATTTT | CAAGTAATAG | 420 |
| | TTTAGCTATT | TTAACAAGTG | TAGATGATTG | GGAAATGTTT | GGAGATAAAA | ATAAACTTGA | 480 |
| | AATGGTTTTT | GTACCAGATG | ATAGACACAT | TAAACGTAAA | TTGCGTAATA | TTCCAAACAA | 540 |
| 15 | AGGCATSATT | ATGGATCCTT | TTAATAAACT | AAGTCGTAAT | GTTGATTATT | TAGATAATGA | 600 |
| | TGACGAGTTT | TATAGCGACG | ATCACCTTTA | TTATAAGGAA | GATGGATACG | TAGCATTTTC | 660 |
| | AGACTATTCT | GTTATAGGTG | GAGAATÁTGT | AGACGGTGGC | TTTTCGCCAT | TAGCLATTGC | 720 |
| 20 | GrTACATATT | GTCTATTTTG | ATGAGGCTAA | TGAGCTAAGA | GTTAAGCATT | TtGTCTCTGa | 780 |
| | TTCTAATAAT | GATAGATCAA | ATCCAGGTAA | AAnGTTTTTT | GAGGCTGTAG | ATAAATTAGT | 840 |
| 25 | AACATGGTCA | AAAAACTTAG | ATATTAAAAA | TAGATCTTAT | GCGCTTGGAC | AATTTGAAGA | 900 |
| , | ATTAAATGAA | AATAATAAGT | ATCCAGGATT | AGGTTTAATT | AAAnGTTATC | TATCAGCATC | 960 |
| | ACCTAGAAAT | TATGAATAGA | TACTGGGTCT | CAAAGAAATA | GGAAAAGTTT | ATATCGAACT | 1020 |
| 30 | GAACTGCAAG | AATGCATTGA | CATGGATGAA | CACACGGGTA | AAATGATCGC | AGCTGAAATG | 1080 |
| | ACTATGGTAT | TAGC | | | | | 1094 |
| | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813:

| | CTTAAAGATG GACATCACTT CAAAGAATTT TCAACGAATA TTATGCCACC GAAATTCCGA | 480 |
|----|---|-----|
| - | AAAGATTTTC ATGATCTACT TGAAAAAATG AGTGTTCAAG TTGGTTCATA CATTCAAGGA | 540 |
| 5 | CAAATTATCG TTTCATTCTG TATCGGTATA CTGTTGTTTA TCGGTTATTC GGTTATCGGG | 600 |
| | TTGAAATATA GCTTAGTATT AGCTAGTATT GCGGCAGTTA CAAGTGTTGT ACCATATTTA | 660 |
| 10 | GGGCCTACTA TAGCGATTTC TCCAGCTATT GTAATHGCTG CTATAACAYC GCCGTGGATG | 720 |
| 2. | CTCTTAAAAT TAGCAGTAGT ATGGACTTTA GTACAATTTG TTGAAGGGCA CTTCATTTCA | 780 |
| | CCAAATATCA TGGGTAAAAC ACTTAAGATT CATCCACTTA CAATCATTTT CATTTTACTG | 840 |
| 15 | TGTGCAGGCA AATTGCTTGG TATTGTAGGC GTTATTTTAG GTATTCCGGG ATATGCTATT | 900 |
| | TTAAAAGTAT TLAGTTACTC ATTTATTCCA | 930 |
| | (2) INFORMATION FOR SEQ ID NO: 814: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | • |
| | (A) LENGTH: 461 base pairs | |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 25 | (2) 101020011 2211002 | |
| | | |
| | | |
| * | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814: | |
| 30 | GTATGATTGC TGTTTTAATA CCAGATGATG GCAGTGGCAA ATCTTATGAC TATATGCTTG | 60 |
| | TGAACCCAAA AATTGTAAGT CATAGCGTTC AAGAAGCTTA TTTACCAACT GGTGAAGGTT | 120 |
| | GCCTTAGTGT CGATGATAAT GTTGCTGGTC TAGTTCACCG TCATAATAGA ATTACAATTA | 180 |
| 35 | AAGCCAAAGA CATCGAAGGT AATGATATAC AATTACGACT AAMAGGATAT CCAGCAATTG | 240 |
| | TTTTCCAACA TGAAATTGAC CATTTAAATG GTGTAATGTT CTATGATCAC ATTGACAAAG | 300 |
| | ATCACCCATT ACAACCACAT ACAGATGCAG TAGAAGTTAA AACACATTTT CTAATTATCA | 360 |
| 40 | AAGCTTAGGA TAALATGATG LCCTAAGCTT TCCTTTACAA CTTTTCGGAT AACCAACAGT | 420 |
| | TAATATATCA CCTTCTAACC AAACTTTTAA TCCCTCATTA A | 461 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 815: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815:

| A | ACGATATAA TA | GAATTGAA | TAAAGTGGGT | GATAATGTGA | CTAAAAATGA | GATTAGAAAA | 120 |
|--|--|---|---|--|--|--|--|
| T | ACATITIAC AT | AAAATGAA | GAATTTTAAT | AAAGCTGAAA | AGCGAAAAGC | AGACACATGG | 180 |
| ⁵ T | TAAGAAATC AA | TTTTTGC . | AACTGAAGAA | TACAAAGAAG | CAAACGCAAT | TGCGCTAGTT | 240 |
| С | TTTCTTTTA AT | CATGAAGT | AGATACTTTT | TCTATTATTG | AACAAGCCTT | AATGGATCAT | 300 |
| | AACGTATTT TTO | GTACCGAA | AATGGATTAT | TTAAATCATC | AAATGACTTT | TAAAGAGATA | 360 |
| 10 T | TTAATCTCA AAG | GATATTGA | TGTCGATAAT | AAGGGGATTT | ACTATCCAAC | TTCAAAAGGT | 420 |
| G. | AAACAACGA ATI | AACCTAGA | TTTAATTGTT | GTTCCTGGTG | TTGGATTTCA | AGACGATGGA | 480 |
| 15 T. | ATAGAATTG GG | TATGGTGG | TGGCTATTAC | GACAGGTTTT | TAGCTÄATTA | TCAGACAAAG | 540 |
| A | CAATAAGCT TAT | TTATACGA | TTTTCAAATA | ACA | | | 573 |
| (: | 2) INFORMATIO | ON FOR SE | Q ID NO: 81 | .6 : | | | |
| 20 | | | ACTERISTICS | | | | |
| | (B) | TYPE: nuc | 3989 base p cleic acid | | | | |
| | (0) | | NESS: doubl | . e | | | |
| | | TOPOLOGY | : linear | | | | |
| 25 | | | : linear | | | | |
| 25 | (D) | TOPOLOGY | : linear CRIPTION: S | SEQ ID NO: 8 | 116: | | |
| | (D) | TOPOLOGY | CRIPTION: S | _ | | ATTCACTAAA | 60 |
| T. | (D) | TOPOLOGY JENCE DESC | CRIPTION: S | TGTCCAACTA | AATGTAGACG | | 60 120 |
| T: 30 | (D) (xi) SEQU AGTTTAACA ATO | TOPOLOGY JENCE DESC STCTATTC TAAACCCC TAAACCCC | CRIPTION: S ICATAGAATT AAATTATAAT | TGTCCAACTA AGTCTCAATA | AATGTAGACG TTAATATATT | ACAATTTATT | |
| T: 30 C: | (D) (xi) SEQU AGTTTAACA ATO | TOPOLOGY JENCE DESC FTCTATTC TAAACCCC ATCATTTC | CRIPTION: S ICATAGAATT AAATTATAAT AATTAATAGG | TGTCCAACTA AGTCTCAATA TTGTTATCAG | AATGTAGACG TTAATATATT GGTTAAATAA | ACAATTTATT | 120 |
| T: 30 C: C: 35 | (xi) SEQU AGTTTAACA ATO TTCTAAAAA AAT ATAGGATTT TTA | TOPOLOGY JENCE DESC GTCTATTC TAAACCCC ATCATTTC TTTACGTT C | CRIPTION: S ICATAGAATT AAATTATAAT AATTAATAGG CTTTTAATAA | TGTCCAACTA AGTCTCAATA TTGTTATCAG CTCAATTCTA | AATGTAGACG TTAATATATT GGTTAAATAA TTCATTTGAT | ACAATTTATT ACATTTTTTG TATTCATTTT | 120 180 |
| T. C. C. C. T. S. S. A. | (xi) SEQUAGTTTAACA ATO TTCTAAAAA AAT ATAGGATTT TTA | TOPOLOGY JENCE DESC GTCTATTC TAAACCCC ATCATTTC TTTACGTT TTTTAACA | CRIPTION: S ICATAGAATT AAATTATAAT AATTAATAGG CTTTTAATAA | TGTCCAACTA AGTCTCAATA TTGTTATCAG CTCAATTCTA TTTATCYTGT | AATGTAGACG TTAATATATT GGTTAAATAA TTCATTTGAT TCAGTGAGAC | ACAATTTATT ACATTTTTTG TATTCATTTT AAGGTATTTT | 120 180 240 |
| Ti 30 Ci 35 Ti Ai | (xi) SEQUAGTTTAACA ATO TTCTAAAAA AAT ATAGGATTT TTA AATAGTCCT TTT | TOPOLOGY JENCE DESC GTCTATTC TAAACCCC ATCATTTC TTTACGTT GTTTAACA GCATAAGT | CRIPTION: S ICATAGAATT AAATTATAAT AATTAATAGG CTTTTAATAA ATGCACTTAC ICGCATGAGT | TGTCCAACTA AGTCTCAATA TTGTTATCAG CTCAATTCTA TTTATCYTGT TAATTTAGCT | AATGTAGACG TTAATATATT GGTTAAATAA TTCATTTGAT TCAGTGAGAC GGTGCATTAC | ACATTTATT ACATTTTTG TATTCATTTT AAGGTATTTT CTGTGACAAA | 120 180 240 300 |
| T: 30 C: C: 35 T: A: A: 40 T: | (xi) SEQUAGTTTAACA ATO TTCTAAAAA AAT ATAGGATTT TTA AATAGTCCT TTT TTGTCTATA GAT AGATTTATA TTC | JENCE DESC GTCTATTC OF TAAACCCC OF ATCATTTC OF TTTACGTT OF TTTAACA OF GCATAAGT OF TTTAAAAAT OF | CRIPTION: S ICATAGAATT AAATTATAAT AATTAATAGG CTTTTAATAA ATGCACTTAC ICGCATGAGT ITAAATAATA | TGTCCAACTA AGTCTCAATA TTGTTATCAG CTCAATTCTA TTTATCYTGT TAATTTAGCT ATTCATAAAA | AATGTAGACG TTAATATATT GGTTAAATAA TTCATTTGAT TCAGTGAGAC GGTGCATTAC AACAAATTAT | ACAATTTATT ACATTTTTG TATTCATTTT AAGGTATTTT CTGTGACAAA GATCATTACT | 120 180 240 300 360 |
| 75 Ti | (xi) SEQUAGTTAACA ATO TTCTAAAAA AAT ATAGGATTT TTA AATAGTCCT TTT TTGTCTATA GAT AGATTTATA TTC | JENCE DESC STCTATTC : TAAACCCC : ATCATTTC : TTTACGTT : TTTTAACA : SCATAAGT : TTTAAAAT : | CRIPTION: S ICATAGAATT AAATTATAAT AATTAATAAA ATGCACTTAC ICGCATGAGT ITAAATAATA | TGTCCAACTA AGTCTCAATA TTGTTATCAG CTCAATTCTA TTTATCYTGT TAATTTAGCT ATTCATAAAA GTATTGCCCA | AATGTAGACG TTAATATATT GGTTAAATAA TTCATTTGAT TCAGTGAGAC GGTGCATTAC AACAAATTAT TTAGCAATAA | ACAATTTATT ACATTTTTG TATTCATTTT AAGGTATTTT CTGTGACAAA GATCATTACT AGCTACTCGT | 120 180 240 300 360 420 |
| 77 30 C1 35 T1 A1 A1 T1 | (xi) SEQUAGITTAACA ATO TTCTAAAAA AAT ATAGGATTT TTA AATAGTCCT TTTTTGTCTATA GAT AGATTTATA TTC GCTCGTAGT TCT | TOPOLOGY JENCE DESC STCTATTC TAAACCCC ATCATTTC ATTTAACA SCATAAGT TTTAAAAT CGCATGAT CCATTTTG | CRIPTION: S ICATAGAATT AAATTATAAT AATTAATAAG CTTTTAATAA ATGCACTTAC ICGCATGAGT ITAAATAATA IATTTACCCA CACCATCTTC | TGTCCAACTA AGTCTCAATA TTGTTATCAG CTCAATTCTA TTTATCYTGT TAATTTAGCT ATTCATAAAA GTATTGCCCA TCCTATTAGT | AATGTAGACG TTAATATATT GGTTAAATAA TTCATTTGAT TCAGTGAGAC GGTGCATTAC AACAAATTAT TTAGCAATAA AATCGTTCTT | ACAATTTATT ACATTTTTG TATTCATTTT AAGGTATTTT CTGTGACAAA GATCATTACT AGCTACTCGT | 120 180 240 300 360 420 480 |
| 77 C1 35 A1 A2 40 T1 C1 55 | (xi) SEQUENCE (x | TOPOLOGY JENCE DESC STCTATTC TAAACCCC ATCATTTC ATTACGTT GCATAAGT CCGTTTTG CCATTTTG | CRIPTION: S ICATAGAATT AAATTATAAT AATTAATAA ATGCACTTAC ICGCATGAGT ITAAATAATA IATTTACCCA CACCATCTTC | TGTCCAACTA AGTCTCAATA TTGTTATCAG CTCAATTCTA TTTATCYTGT TAATTTAGCT ATTCATAAAA GTATTGCCCA TCCTATTAGT AGTTGCACCA | AATGTAGACG TTAATATATT GGTTAAATAA TTCATTTGAT TCAGTGAGAC GGTGCATTAC AACAAATTAT TTAGCAATAA AATCGTTCTT TAGTAAGGGT | ACAATTTATT ACATTTTTG TATTCATTTT AAGGTATTTT CTGTGACAAA GATCATTACT AGCTACTCGT CATTATTGAA ATAACCCCTT | 120 180 240 300 360 420 480 540 |
| 77 730 735 740 75 75 75 | (xi) SEQUENCE (x | TOPOLOGY JENCE DESC GTCTATTC TAAACCCC ATCATTTC ATTACGTT GTTTAAAAT GCATAAGT CCATTTTG TACGTTATC TACGTTATC TACGTTATC TACGTTATC TACGTTATC TACGTTATC TACGTTATC TACGTTATC TACGTTATAC TACGTAAT TACGTAAT TACGTAAT | CRIPTION: S ICATAGAATT AAATTATAAT AATTAATAGG CTTTTAATAA ATGCACTTAC ICGCATGAGT ITAAATAATA IATTTACCCA CACCATCTTC CAATAATTCC | TGTCCAACTA AGTCTCAATA TTGTTATCAG CTCAATTCTA TTTATCYTGT TAATTTAGCT ATTCATAAAA GTATTGCCCA TCCTATTAGT AGTTGCACCA TCTATTATTT | AATGTAGACG TTAATATATT GGTTAAATAA TTCATTTGAT TCAGTGAGAC GGTGCATTAC AACAAATTAT TTAGCAATAA AATCGTTCTT TAGTAAGGGT TCAAAGATAA | ACAATTTATT ACATTTTTG TATTCATTTT AAGGTATTTT CTGTGACAAA GATCATTACT AGCTACTCGT CATTATTGAA ATAACCCCTT AGATGTCTTT | 120 180 240 300 360 420 480 540 |

1685

TTCTTCTAAT TCAATTTGTC GGTCGAGTTT GCTGAAGAAC TTGCCTATTT TTTGCTGTTC

| ٠ | | TCGACTACCT | CCACTTTGTG | CAAGGAAAAT | TTTCCTTTTA | CCTTTTCTTG | ATAATAGATA | 960 |
|----|---------|------------|------------|------------|------------|------------|--------------|------|
| | | CTGTCCAAAA | AAATTATAAT | AATACTCTTT | TTTCAATCTA | ATAATACATA | CATGTTGATT | 1020 |
| 5 | | TAAATTAGCA | TGCGTTTCAA | CTATCGAATT | AATGGCTGTT | CTACCTATTG | ATGCTCCTGT | 1080 |
| | | AATATTTAAA | AGAACATCAC | CATAGTACGT | TCTACTATTT | TTCATCTCAT | CATCTATATC | 1140 |
| | | TTTACTAATA | TAAACTAAGT | CATTAAGATT | TAATTTACCA | TTTCTAATAT | TTTGACTCCT | 1200 |
| 10 | · 1 · · | TAAAAATGGT | ATGCCTTTGT | TTGTATAGTT | TTCACTTCCA | CCTTTGGGAG | TCTTTCCACT | 1260 |
| | | ACCTATTTTG | GTAGTAAGAT | TCCCTAACTT | CTTCTCTTCC | CATTCGCCTT | CAAATCCTGG | 1320 |
| 15 | ; | GAATCTCAAC | TCTGGCACAT | TTTTCGTTTG | TGTATTACTC | ATCTTTCAAC | ACCCCAAGTT | 1380 |
| | | CTTTCAGGTA | TGCATTGATT | TCTTGTTCAA | TTTCTGCGAT | TTCTTTGTCG | ATATTTTCA | 1440 |
| | | AATCTTGTTG | GACTTGATCT | AAATCAATTG | GTGCTTCTTC | TTCGAATGTA | TCAACATATC | 1500 |
| 20 |) | GCGGTATGTT | TAAGTTGTAA | TCGTTATCGG | CGATCTCTTG | TAATGTCGCG | CTGTAGCTAT | 1560 |
| | | ATTTATCAAT | CGTTGCTTTA | CGCTTATATG | TGTCTATAAT | ACGTTCGACT | TGGGCATCGC | 1620 |
| | | TTAAATGGTT | TTGATTTTTT | CCTTTTTCAA | AATCATTGGA | TGCATCGATA | AATAGTACGT | 1680 |
| 25 | ; | TGTCGTCTTG | TTGGCGACAT | TTTTTAAATA | CTAAAATACA | TGTTGGAATA | CTTGTCCCAT | 1740 |
| | : | AGAAAATATT | GGCTGGTAAC | CCAATCACGG | CTTCTAAGTA | GTTCTTTTCT | TCTATTAAAT | 1800 |
| 30 | | AGCGACGAAT | CACACCTTCT | GCGGCACCAC | GGAATAATAC | ACCATGTGGG | . agtacgactg | 1860 |
| - | | CCATGGTACC | TTCATCGTCT | AGGTAATGTA | CCATGTGTTG | AATAAAGGCA | AAGTCTGCTT | 1920 |
| | | TGGaTTTTGG | CGCAAgCTTG | CCGTAACCAC | TGAATCGTTC | ATCATTTTCA | AATTTTGAAT | 1980 |
| 35 | ; | CTGCTGTCCA | TTTCGCACTG | TATGGTGGGT | TCGCAATAAC | CGCATCAAAT | GTATTGCCTA | 2040 |
| | ٠ | AAAAGGCTGG | ATTTTCCAAT | GTGTCATCAT | TACGGATCTC | GAAGTTCTCA | TAACGCACAT | 2100 |
| | | CATGTAATAA | CATATTCATG | CGTGCTAAGT | TGTATGTAGT | ATTGTTACGT | TCTTGTCCGA | 2160 |
| 40 |) | AATAACGATA | CACTTGCGTT | TCTTTACCAA | CACGTAACAA | CAATGAACCG | GAACCACATG | 2220 |
| | | TTGGGTCGTA | CACGTGACGT | AATTTATCTT | TACCGTCTGT | GACAATCTTC | GCCAGTATCT | 2280 |
| | | TAGATACTTG | TTGTGGTGTA | TAGAACTCGC | CTGCTTTTTT | ACCCGCTGTC | GCCGCAAAGC | 2340 |
| 45 | | GCCCGATTAG | GAATTCATAT | GCATCACCTA | ACATATCAAT | TTCCATGTCA | CTGTGAACGA | 2400 |
| | | ATGGTAAGTC | GTCAAGATTA | ACCATGACTT | TAGAGATTAA | AGCAGTACGT | TCTTTGACAT | 2460 |
| 50 |) | TGTTACCTAG | TCGCGTTGAA | CTCAAATCCA | TATCGCTGAA | CAGCCCGATA | AAGTCATTTT | 2520 |
| | | CACTTTCTTC | ACCTAATGTA | GATGTTTCAA | CTTTGCGAAT | CGCCGTCGCT | AGATGTTCTA | 2580 |
| | | TATCGAAATC | TTGCGTTTCA | ATTTCACGAA | TCATCGCACT | GAATAAATCT | TGTGGCTCAA | 2640 |

| | CCCATGCTTC | TTGATACGTG | ATGTCTTCAC | CTGACAAGGC | ATCTGCATAT | TCTTGTTCGG | 2760 |
|----|------------|------------|------------|------------|---|------------|--------|
| | CTTTTTCAGA | TAAGAAGCGA | TAGAAAATCA | AGCCTAAAAT | GTAATTACGG | AATTCACTCG | 2820 |
| 5 | CATCCATGTT | CCCTCTTAAA | TCATTCGCAA | TCGACCATAA | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | AATTCAGCTT | 2880 |
| | GTTGCTGACG | TTGTTTTTCA | GTAATAGACA | TGTGATTCCT | CCGCCTTTGC | ATAAGTAATT | 2940 |
| | TATCTCTTTG | TGTAATAGAT | TTATTATAAC | ATTTGGTTAT | GTTGCGATGT | TGATAATTTG | 3000 |
| 10 | GATGTTGGTG | GTGGAAATTT | TGAGTTTTAG | TGGCGCAATT | GTTATTGAAA | AATTTTATAG | 3060 ° |
| | AAATGTTGTA | GCTTTCAAAT | GCTTTCAAAA | TCATTTATAT | TCTTAATGAT | GTCAAAAAGT | 3120 |
| 15 | TGTTCATTCA | TACATAAATA | AAACCAATCA | ACAATTGAGT | TGGTGAAAAT | CAATCGTTGA | 3180 |
| | TTGGCTTTGA | TGCATATTAA | ATAATGCAAT | ATATATTAAT | AAATGTTAGT | TATAGTATAT | 3240 |
| | TTTGTCAGGA | TTGGGTGAAT | GTCTAAGTTT | TAATTATTTA | TCTAAATTAT | CTGCAATGAA | 3300 |
| 20 | TTTCTTAATT | TCAGGAGAGA | AATAAACAGC | AAATCCTCTT | GTGCTTTCAC | CTGATGGCTT | 3360 |
| | ATTACCGGCA | TAGATTACAC | CAATAGCTTC | GTGTTTACTA | TTTAATATAG | GTGAACCAGA | 342Ô |
| • | GCTACCAGGC | TGAATAATTG | CATCCGATGA | CACTATATTC | CCATTCACTG | ATAATACTTT | 3480 |
| 25 | ACCAGTTGAT | TCATACATTT | GTAGTTTATT | TCCATTAGGA | TTTGGATAAC | CAATGACTGA | 3540 |
| | TATAGGTTCA | TTTTCTTTAG | CTTCTGATGC | TATATTAAAT | TTACTAGTGA | AATCTTTGAA | 3600 |
| 00 | TTTTCTACCT | TTTGGTTGTG | TTGATTTTTC | TTCAACTTGT | ACAACCGCAA | TATCTTCTTT | 3660 |
| 30 | ACCAGGATAA | TCTACAATCT | TAGTAACTTT | ATAAAGTCCA | CCACCGTTAT | TATAAAAACC | 3720 |
| | ATTAGGATGT | GCTTTGATTT | CATCACCGAC | TTTCATGTGA | TAGGTAAČAT | GTTTATTGGT | 3780 |
| 35 | AATGATTGTA | TGATTTCCAA | CTACAAATCC | TGTTCCAGCG | CCCATCCATG | TAACACCACT | 3840 |
| | GTATGGTGCA | ACATTTGTAT | TTGTAATTTG | TTTAACAGTA | TTTTCGGCTT | TGGCTGTTTG | 3900 |
| | TTGAATACCT | TCAACCATTG | TTGTGCCGAC | ACCAGTTATT | GATGTTAAAA | TCGTCAATGC | 3960 |
| 40 | TGCAATACTT | TTGATGATTA | TATTTTTAT | | | | 3989 |

(2) INFORMATION FOR SEQ ID NO: 817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817:

CGTTGAGCAC AGTTTTAGAT AATAGATAAT CTTGCCCTAG TTGTTGCAAT GTCTGCGATT

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| | TATGCGTGTA | ACGTTCAGTT | ATCGTTTCTA | AGGTATACTG | AGATGTATTT | AATTGATATC | . 180 |
|----|------------|-----------------------------|-------------|---------------------------------------|------------|------------|-------|
| | CTTTAGATTT | AATACTTACG | ATGATATCAT | CCATAAAATT | GCTATTGATA | ACATGGATAT | 240 |
| 5 | CATTGCGAAC | TGTGCGGTTT | GAAACATTGA | CATGTTTAGC | AATTTCATTA | GAACTAATGT | 300 |
| | GCTTTGATGG | ATTTTTAATA | AAAAACTGGA | GTAGTTTTAA | GTGTCTATCA | AGCATTTAAC | 360 |
| | ATGTACCTCC | TTTCTAAATT | TTTCGTGTAA | GCGTTTTTAA | GGGTGTATTA | ATATTATTAA | 420 |
| 10 | ACATGAGAGC | TTATACATAC | GTCAATGACA | TTAAAGCGAA | CTTTTATATG | ATTTTAACAG | 480 |
| | AGTGCGAATT | ATGCAAATAA | AGAACAGCAG | TAAGATATTT | CAAATAGAAA | AATATCTCAC | 540 |
| 15 | TGCTGTTTTT | CTGAATTTAT | GCATCTGGTA | CTTGTGGACG | TATCAGGCAA | ATGATTAATT | 600 |
| | TTTAGGTGAT | TGTGCTTGAG | GTGTTTGTTT | AGAAGGCGTA | TTGGTATTAT | TTGATTTATT | . 660 |
| | AGCAGGTGGT | GTGTTCTGTT | GTTGATTATT | TTGGTTGTTT | GTTGACGATT | GACTGCCACC | 720 |
| 20 | ACCGTGAGTA | TTATTTTTAT | TTGAATTTGA | GTCTTTTGGC | TGAGCTGGTT | GCGTATTCGA | 780 |
| - | TGGTACTGTT | GAATGGTTGT | TAGGAACATT | TGACGGTGAA | GATGGTTGAT | TGTCATTAGT | 840 |
| | AACGTTATTG | CCATTATTTT | GATTLTTATC | TGTTTTGTCT | GCACTATCAT | CTTGTTGATC | 900 |
| 25 | ATTT | | | | | | 904 |
| | (2) INFORM | ATION FOR SI | EQ ID NO: 8 | 18: | | | |
| | • • - | EQUENCE CHAI | | | , | | |
| 30 | | (B) TYPE: no (C) STRANDE | ucleic acid | • | | | |
| | | (D) TOPOLOGY | | , , , , , , , , , , , , , , , , , , , | • | | |
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| | | | | | | | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818:

TTTAACALGA TAATAAAAAA TCTTTTGTTA TATCATTAGG AATATTTGAT GAACTTGATA 60 TTAAGGTTAC ATTITGAGAA ATGGACTTAG GGATATTTCC ACTATTATTT AGTAAGAAAT 120 CTTTAGCTAA TAAAGATTTT CCTACACCAT TTTTACCAAC AATGTGATTG ATCTGACCAA 180. GATAGAAATT TAAATCACAA TTGTCAACTA GTTGTTTGTT TTTAACTTTT AAAGAATAGT 240 TATTTAGTTT CATGTATACA ACTCCTATGT ATAAAGGGAT TTATTACACC GATATTTAAT 300 TGTATTTTTA AAAATTCLTT CACATTATGT ATAGAWGTTA TAAATTAGTA TATCACACTA 360 TATTTEGECT AAATGATAAA TATATCGTTA TATTTTTACA ATATTCTGAA ATTTATGTTC 420 GCCTCTGAAT GCTATATCCA GTGTAATGTG TTTTGCATAT ATGAAAGCAA TTTCAAAATG 480 TGAATATAGG TTCATTGTGG TATGACAAAC TTCATTGCTT GTCATGAGAT GGATATAATG 540

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| | GACGGGACGT | TTTTAGATTC | AAAAAAGACA | TATGATAAAC | TTAGATTTGA | AGCGATTTTT | 660 |
|----|------------|------------|------------|------------|------------|------------|------|
| | ACTGAACTTA | gaaatagaga | TATTACATTT | ATTGCTGCGA | GTGGCAATCA | ATATGCGAAG | 720 |
| 5 | TTGAAGTCTA | TTTTCGGGGA | TAGAGATATG | TATTTTATTT | CTGAAAATGG | TGCAGTTATT | 780 |
| | TATAATGGCA | ATGAGTTATA | TAATTATAAA | AGCTTTAATC | GTCAGGTGTT | TCAACAGGTT | 840 |
| 10 | GTCGATTACT | TAAATATGAA | GCAAAGTATT | GATCAACTCG | TCATCTGTGG | TTTGAAAAGC | 900 |
| 10 | GCGTATATTT | TAAAACATAC | TTCTGAAGCG | TTTAAAGAAG | ATACGAGATT | TTATTATCAT | 960 |
| | CAGTTAAAAG | AAATTGACAG | TCTACAGCAA | TTACCTGAGG | ATGATTATGT | CAAAATAGCA | 1020 |
| 15 | TTTAATATTA | ATCGTGAGAC | GCATCCGAAT | GTTGACGAAG | AAGTAGCAAC | GCAATTCAGC | 1080 |
| | AATGATATTA | AACTTGTCTC | AAGT | | | | 1104 |
| | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819:

| CCCTTTTTAC | GGATTAAnGG | CTTTTTCCTA | TTTAAAACCT | ACGGCATTTT | CTTTTCAACC | 60 |
|------------|------------|------------|------------|------------|------------|-----|
| ACGGCGGCTC | CCATATGGAT | GGTATnGGĠA | TTGGGGTTTA | TAAAATGGGG | ATTGGAAATG | 120 |
| GTCCATCCTA | AATACTCAGT | TTAGTGCTTA | TTTCCTTTAG | TGCTGACGAA | TAAATATGAT | 180 |
| CTAACTCTAC | GAAACCTAAT | AACGTATCAA | ATGCTTCATC | ACCATTTTCA | AATTTACTTA | 240 |
| AACTATTTTT | AAAATCATGT | CGCAAATCCT | CTAAATATAG | TGATGGTTTT | CGATCTACAT | 300 |
| ACATTTTTAT | ACTAACCTCC | GATATATAAT | CATCTTTATT | GTACCTAACA | TTTTATTAAG | 360 |
| ATAATACTAA | TACACTATCG | AACTTTGGGC | TGATACTGAA | ACAGCACAAA | GAAACTCAAA | 420 |
| CAATTCGAAT | TATGTATCAA | AACCTTCAAT | TACAGGAAGT | GATTTTAAAA | TGATTTAACG | 480 |
| CAAAAAAACA | CCTGTTACCG | TTATATAGGT | ACAAGTGCTT | AATTGATAGA | GATGTTATAC | 540 |
| GTCTTTAAAT | GATTCCACAA | CTTTTGGATG | TGGACCATCC | ATAAGCGGTT | CTCTTTGTCG | 600 |
| AACGCCACCA | CTTTGGTTGC | CAATTGATTC | GCTATCAAAG | TACGATTTAT | CTTGATTTGA | 660 |
| TTGTTCTTGA | ATATGTTCTT | CATTATCAGT | TGTTGCATAT | TCACTATCCA | CCTCTGTTTT | 720 |
| TTCCATTGTT | GCTGTATGGA | ATTGTACGAA | GTTCTCTTCT | TCTAATGCTT | TGATTTCTTC | 780 |
| TTTCGATAAC | GCTCGATACC | AATCTTTCGC | TTTTTTCGCC | GCAaTAGGAa | CAaCAtCTTT | 840 |

| TACTTCAAAT | TCTTTCCATT | TTTCGGGGTA | ACCTTTCATT | GTAAAGGGCA | TTCCCTTAAC | 960 |
|------------|------------|--------------|------------|------------|------------|--------|
| CTCCAATATG | TTATAATTCA | TGTTATATAC | CACCATAATT | ATAAAATGAA | ACATATTAAA | 1020 |
| CACAATTTTT | TAGACTCCCG | TCATAATAAC | TTCAGACAAA | CGTTAGTCTG | ACCTGATAAA | 1080 |
| TATTTAATTT | TAAACGTTCT | тстстстстс | ACGAAAACCA | TTGTGTTGAA | TATTCATCAT | 1140 |
| TGCTGATTGA | ATATAATTAT | ACTGTGGTAA | ATCTGGTAAT | ATCTTTATTT | CTAATTCTGT | 1200 |
| ATTTAATTCG | AAATGCTTAG | CGATGTTTTC | AAATATTGCT | AAATACTCGC | CCATTAATTG | . 1260 |
| TTCATTTATT | GTAAGTCTAT | CTTCATTAGC | CATGGCTCTA | TTTAACATAA | AGCTAATTTC | 1320 |
| TTCTAATGCG | AATAAGCTAG | GATAATAATT | TTGAATCAAT | GTCTTATCAC | TAAATAATTC | 1380 |
| ACCATTAGCT | GCATTATAAA | CTTGCGTGCA | TGTTATTTAA | TTTGC | 111 | 142 |
| | | 10 11 111 11 | | * | | |

(2) INFORMATION FOR SEQ ID NO: 820:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1165 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820:

| nCGnCCTTAT | ATATGTTTTT | CATGTCCTAC | AAAAAACGAA | ATATTCCAAT | TGCCTATATA | 60 |
|----------------|------------|------------|-------------|-------------|------------|-----|
| CAGATATTCA | TTAATGACAC | ACTCAATAGC | AACCATnACA | ATATTATGTT | ACCTATTTAA | 120 |
| ATGAAATAGT | TCTTTTAAAG | AAATACATTT | TTCACATATT. | AATCTATAAT. | CAAAATCAAC | 180 |
| TGACCGATAT | TCTATAATTT | ATGATTAAAA | TAAGTTATAA | TATAATAGTA | AAGATAAAGA | 240 |
| TAGAGGTGGC | TATAATGTGT | GGACTTAGAA | GTATAACATT | AGGTACAACA | AATATAGAAC | 300 |
| AGACaAAACa | TTTCATGGTT | GACATATTAG | GATTAAATTA | TGAAGAACTT | CTTGAAAACT | 360 |
| CAATTCGTTT | CGGCGATGCA | GATATAAGCC | CAGGAACAAG | ACTTCAATTT | ATACAAGTTC | 420 |
| CAAGTGAGCA | ATTAGAAGAA | TCTCACTTTG | TGGGTATTGG | ATTACGTACA | CCAACTGACT | 480 |
| CAGGTTTAGA | GGAGTATGCG | GAAATATTAT | CGAATAAGGA | TATTCCATTT | ACAACAGTTA | 540 |
| AAGAATTAAA | TGGCAATAAA | TATTTCAGTC | TCGAAGATAA | CAATGGTCAT | ATTTTCTCAA | 600 |
| TATATTCAAA | CGAGAATAAT | TATGGCGTTG | GTTTAGGTAT | GCCTTCTTyT | GAGAGTGCGG | 660 |
| TCAATCCGTT | ACATCAAGTG | CAAGGTTTAG | GACCAGTGAT | TCTTAAAGTG | AATCATGTAG | 720 |
| ATATTACAGG | TCAAATTTTA | ACAAATATAT | TCGGACTTGA | AGTATTTGCA | GAATACCAAC | 780 |
| CCTTCGACAA | TGCTGACTAT | CATGTCCAAG | TATTCAAAGT | TGGAACGGGT | GGTCTAGGTG | 840 |

| | ATCAAGTTGA GTTTGAAACG AAAGATGCAG ATTTCTTTAA TCAAGCGAAA TCGCGCTTAG | 960 |
|---------|---|------|
| | ATGAAGTGGA AATACCATAT CAAACGCTTG AGCAAGATGA TATTGAATCA ATTAGAATTA | 1020 |
| 5 | CTGAAAACAG TGGATTATCG TTTATATTCA CTTTACAAAA ATAATTTTTT TACGATAGCG | 1080 |
| | AGGACAAAAT TTATGTTACA TGAAACTTGG AAAGAACGTA CACCAATCAA GAAAGTAGAA | 1140 |
| | GTCATTAATA CAGATGCAAA GAAAT | 1165 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 821: | , |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821: | |
| | TCGCCCAATT ATTATGAAAT ATTCAATACA GTTTATTGAT CAAAAAACAA AAATCCATTA | 60 |
| | TGAACCTTGT CATCACGAAT ATTAACTGAC GTTAGATGGA CCTCTTTAAT GATAGAACAA | 120 |
| 25 | TTAATAAATA ATGCACTTAA GTATGCGAGA GGTAAAGATA TATGGATTGA ATTTGATGAG | 180 |
| | CAATCCAATC AATTACACGT AAAAGATAAT GGTATCGGTA TTAGTGAAGG NACTTGCCTA | 240 |
| 30 | AAATATTTGA TAAGGGCTAT TCAGGTTATA ATGGCCAGCG CCAAAGTAAC TCAAGTGGGA | 300 |
| 30 | TTGGTTTATT TATCGTAAAA CCAATTTTCA ACACACAA ACCATCCGTT TCCGTCGTAT | 360 |
| | CTAAACAAAT GAGGGTACAA CCNTTACGAN TNCCATTTCC | 400 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 822: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 760 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822: | * |
| 45 | TGATATAATA CTTTTGTAAA GAAAAGCATG TGTGGGAGGT ATGACCTGTA TGTCGAACGA | 60 |
| | AATACTTATC GTAGATGATG AGGATAGAAT CAGAAGATTA CTTAAAATGT ATTTAGAAAG | 120 |
| | AGAATCTTTT GAAATCCATG AAGCAAGTAA TGGCCAAGAG GCTTATGAAC TTGCAATGGA | 180 |
| 50 , | GAATAATTAT GCTTGCATAC TACTAGATTT AATGTTGCCT GAAATGGATG GTATCCAGGT | 240 |
| | CCCAACTAAA TTCCCCTCAAC ATAAACAAAC ACCCATTATT ATCCCACCACTATAA | 200 |

| | TTCACCAAGA GAAGTAGTCT TAAGAGTTAA AGCACTTCTA AGAAGAACGC AATCTACAAC | 420 |
|------|---|-----|
| | TGTAGAACAA AGCGAACCTC ACGCACGTGA TGTGATTGAA TTTAAACATT TAGAAATAGA | 480 |
| 5 | TAATGATGCA CATCGCGTAC TTGCTGATAA TCAAGAAGTT AATTTGACTC CTAAAGAGTA | 540 |
| | CGAATTATTA ATATATTTAG CTAAAACACC AAATAAAGTA TTTGACCGTG AACAATTATT | 600 |
| | AAAAGAAGTT TGGCATTATG AATTCTATGG TGATTTAAGA ACAGTTGATA CTCATGTTAA | 660 |
| 10 | ACGCTTAGAG AAAAGTTAAA TCGTGTGTCT AGTGAAGCTG CGCATATGAT TCAAACAGTC | 720 |
| | TGGGGCGTTG GGTATAAATT TGAGGTTAAA TCTAATGATG | 760 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 823: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 465 base pairs (B) TYPE: nucleic acid | |
| 20 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | ·· |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823: | |
| 25 | CAAAGGAAAT TGCACAATTA GAAGACCGAT TACGTTCACG CTTTGAATGG GGGCTAATTG | .60 |
| | TTGATATTAC GCCACCAGAT TATGAAACTC GAATGCCAAT TTTGCAGAAG AAAATTGAAG | 120 |
| | AAGAAAAATT AGATATTCCA CCAGAAGCTT TAAATTATAT AGCAAATCAA ATTCAATCTA | 180 |
| 30 . | ATATTCGTGA ATTAGAAGGT GCATTAACAC GTTTACTTGC ATATTCACAA TTATTAGGAA | 240 |
| | AACCAATTAC AACTGAATTA ACTGCTGAAG CTTTAAAAGA TATCATTCAA GCACCAAAAT | 300 |
| 35 | CTAAAAAGAT TACCATCCAA GATATLCAAA AAATTGTAGG CCAGTACTAT AATGTTAGAA | 360 |
| | TTGAAGATTT CAGTGCAAAA MAACGTACAA AGTCAATTGC ATATCCGCGT CAAATAGCTA | 420 |
| | TGTcTTGTCY AGAGAGCTTA CAGATTTCTC ATTACCTAAA AATTG | 465 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 824: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 355 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 45 | (D) TOPOLOGY: linear | ٠ |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824: | |
| 50 | CACCGCGGTG GCGGACGCTC TAGAACTAGT GGATCCCCCG GGCTGCAGGA ATTCGGCACG | 60 |
| | AGGTAAGGAG GTCTCTGTAC CATGGCTCGT ACAAAGCAGA CTGCCCGCAA ATCGACCGGT | 120 |

240

GGAGGGGTGA AGAAACCTCA TCGTTACAGG CCTGGTACTG TGGCGCTCCG TGAAATTAGA

| | CGTTATCAGA AGTCCACTGA ACTTCTGATT CGCAAACTTC CCTTCCArCG TCTnGTGCGA | 300 |
|----|--|------------------|
| 5 | GAAATTGCTC AGGACTTTaa AACAGATCTG CGCTTCCAnA GCGCACTATC GGTGG | 355 |
| | (2) INFORMATION FOR SEQ ID NO: 825: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1099 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | , |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825: | |
| | TTCACTTGGC TTGTTGACTG ACTTGTALAT GATGATGTGC TTTGTGAATC GGATTCGCTC | 60 |
| 20 | GTGCTTGTAC TTGTTGAGTT TGAGGCACTT TGGCTTGCTG AGTTTGAGTC TACTCCGCTT | 120 |
| | TGATTCATTG AGGCACTTAG TGACAATGAT GTACTCGTTG AGTCAGACAA ACTTGTACTC | 180 |
| | GTTGACGTAC TTGTACTTCC TGATGTTGAT TGAGACATAC TTATGCTCAT TGATGTTGAA | 240 |
| 25 | TCGGATTTAC TTTCACTTGA TGATGTTGAG TCGGATTCAC TTTCACTTGT AGAACCACTT | 300 |
| | AATGATGTGG ATGTACTAAT GGAATCAGAT TTACTTGTAC TGATTGAATC ACTTGTCGAC | 360 |
| | ATTGATGTAC TTAATGAATC AGACTTACTA TCACTTGTGG AATCACTTAA TGATGTTGAC | 420 [‡] |
| 30 | AAACTTGTAG AGTCAGACAA ACTTGTACTC GTTGACATAC TCAGTGATGT TGAAACACTC | 480 |
| | TCGCTCTTAA ACGTTGACGT TGATTCACTG ATACTTGTCG ATGTTGAAAT GGACGTACTA | 540 |
| | CCACTTGTTG AATTACTTAA TGATGTTGAT GTGCTACCAG ATTCTGATGT ACTGTCTGAT | 600 |
| 35 | AATGACGTAC TCTCACTTGT CGAACTACTC ACTGACTCTG ATGTTGATTC AGACGTACTT | 660 |
| | TCACTTAATG ATTCACTTAA AAAGGCAGAT GCACTTTGTG ATTCTGAATC GCTAGTACTA | 720 |
| 10 | TTTGATTCAC TTAATGATAT AAACGTGCTC TCTGAAGCAG ATATTGCTTC ACTTATAGAG | 780 |
| | TCGCTCGTTG ACGTTGATTC ACTTATTGAA TCAGACTCTG ATGTACTTAA GCTTGTGGAA | 840 |
| | TCACTCATAG ATGTTGATGT ACGTTCTGAA TTACTTGTAC TTAACGATGT CGAAGTACTT | 900 |
| 15 | ACCGAACCAG ATGTGCTCGT AGAAGCACTT TGTGATATTG ATTCACTTGA TGCAGTTGAT | 960 |
| | GCTGATTTGC TATCACTCGT TGAATCACTA AACGACGTTG ATATGCTCAL TGAATCGGAT | 1020 |
| | TGACTTGCAC TCAnTGAACC AGACGTACTT TGTGATTCCG AAGTACGTAC TGAAGCACTT | 1080 |
| 50 | GTCGACGTTG ATGTACTTG | 1099 |
| | (2) INFORMATION FOR SEO ID NO: 826: | |

| , <i>5</i> | (A) LENGTH: 338 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|------------|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826: | • |
| | | |
| 10 | TATGCGTATC CTGATAGTCA CTTTGATTTT GATATGGAAT TAGCGAAAGA GCAATCTCAA | 60 |
| | GACAATCCAG TTTACTATGC TCAATATGCA CATGCGCGTA TTTGTTCAAT TTTAAAACAA | 120 |
| | GCGAAAGAGC AAGGTATTGA AGTGACTGCT GCGAATGATT TTACAACGAT TACTAATGAA | 180 |
| 15 | AAAGCGATTG ANTTGTTGAA AAAAGTAGCT GATTCGGANC CTACAATTGA AAGTGCTGCT | 240 |
| | GAGCATAGAT CGGCACATAG AATTACTAAT TATATCCAAG ATTTAGCCTT CTCATTCCAT | 300 |
| | AAATTCnATA ATGCTGAAAA GTGTACCAGT TGGTATTG | 338 |
| 20 | -(2)-INFORMATION-FOR-SEQ-ID-NO:-827: | · . |
| - | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 838 base pairs | |
| 25 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| ٠, | (D) TOPOLOGY: linear | |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827: | |
| | GTATTTTCTT TCGCGAATGA TTTTATTACT TGAATACCAC GAATAACCTC CAATACCTTT | 60 |
| | TCCACTAATT GGTTTTGTAC ATTATGATAC GCTGGGGGCAT TTTGTCGACT CTTTCTTTCT | |
| 35 | | 120 |
| 35 | AATAATTGAA TCGCAAAAAA TGATAGTAAT ACGCCAATGC ATGCTAATAA TGATACTTGC | 180 |
| | CACGAAACTA CAAGTAGAGA CAATATGAGT ACTGTAATTA ATATGTATCC ATTAACAACA | 240 |
| | ACGTCCACCA TTTTCATAGC AAAGTTTTCT AAAAAGGTTA AATCTGTTGT TACTATTGTT | 300 |
| 40 | GTTAACTCAT TTGAATGATG CGAATTAAAA TAACCTAACC | 360 |
| • | CCTATATCTA AACGTTCTTT CGCACTCATT TCATAAGCGA TGCTCTCATG GCTTTTGCTT | 420 |
| 45 | TTGAAATATG CTGTAATAAA TCGTCCAATC ACTAATAAAA CCATGATAAT TACAACATTC | 480 |
| | AATATATCTT TCATATAAAT AGGTTTATGA GATAGCACAT TATTAAATAT TTTTGCAGCT | 540 |
| | AAAAAGATAG GTAACGCAAT AAAAATAGCA TTTAAAAATG ACATGCTAAA TCCTAAAATC | 600 |
| 50 | ATTCTTGCTT TATATGGTCT TATCCAGTTT AAAATTTTAA ATGTAATTTG AAACATATTT | 660 |
| | · | |

780

ATGTGCGTAT CCCACATTTT CTTATAATTA CCGTTTAATT TTAGCAATAA GTGATGTGAC

| | (2) INFORMATION FOR SEQ ID NO: 828: | |
|----|---|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 898 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ÷ |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828: | |
| | TCCnAAAGAA GAAATAaCAT TATCATaAAA TCCATTGAAT ATAAATTCAG TCATCCCCTC | 60 |
| 15 | TGAACTECTC CATAAATATA ATGGTGAATA AGTATTTGTA ATGCAATTAG TAGTTGTTTG | 120 |
| | ACTTATTAAA TAAGCTTTTA TAATTAAATT TTTAAATCCA TCAGTCTTAT AACCATTTAA | 180 |
| | TCGAACTCTA TCTCTAATTA TTTCCATATT GTAATCACTA GGCAACTTAA CATGATATTG | 240 |
| 20 | CATTGCATGC ATTTAGCATA CCCCCTTTTA TAAAAAGGAT AGCAATAATA AGTAAAATCT | 300 |
| | CATATTATCC AATTGTGATA TAGTTATCAT AAAAAGTGAT AGGTGATTAA ATTGAACTTT | 360 |
| | AATGATTTGG AAATTTTTAT AACTGTATGT GAAGAAGCAT CTATCAATAA AGCTGCAATT | 420 |
| 25 | AAACTTAGAT ATGCACAATC TAATATATCT CAAAGAATTA GCAAGCTTGA AAATGAATTA | 480 |
| | GGTGTAGTTT TGCTTTTTAG AAATCAAAAA GGTGCTAAGG CAACTAAAGC AGGCGAAGAA | 540 |
| 30 | TTCTTAGCGT ATAGCAAAAA AGTATTAAGA GATACAGAGA CTATAAAAAA TAAAATGAAA | 600 |
| 00 | AATAATACTA TGTCTATTTT ATGCTCAGAA CTGTTATTTA ATTATTTATC TGAGAGCGAA | 660 |
| | GAAATTATGA TGTCGAATAA CTCAATTAAT TTTATTTCTA GTGGAAATAT TAGAAAAGCT | 720 |
| 35 | ATAGAAAAA ATAATTATGA TAAGGTTATT TCATTCATAA AAATTAACGA CTCAAATTAT | 780 |
| | AGACTTAGTA ATGTTGATAC TATGAAAGTA ACGCTTTACA GTAATGGAAG TAATTATGAT | 840 |
| | AAAGAGGCTT TACTAATAAA TAAAGATGAG TTTGGTCCTT TAAGGNAAAT AACTTTAG | 898 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 829: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 798 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829: | |

AGTAGGAGTC ATAAAATCGN ATTTCAAAAG CAATTAATGC AAAATACTGA GTCTACAGTG

CTATTTGCGA AAGCGTCCAT ACGAAGTTGA GCAATGCTAA TAATAATGGT CTATCAAAAA

| | AATATGTTGA TAGTTACACT GATTCTCTTA CTGGAGTAAC AACTTCTGCT TTTTTAAATA | 240 |
|------------|---|------|
| | AAGATACAGG CAAAGTAACT CTCGGGATGA CTGGGACTAA TTTACAAGAC GAAGCCTTTA | 300 |
| . 5 | AAAAGTTAAA AGAAGGTGAA TTTTCAAGAC AAAATGTTAC CAATGCTTTG GAAACAGTTA | 360 |
| | AAGATGGATA TGCAGATCTT AAAATATTAT ATTCTCCTGC ATCTGATCAA AACTATAGAT | 420 |
| | ATGCGAATAC ACAAGAATTT ATAAATAAAA TAAAAAGTAA GTATGACATT GATTTTATTA | 480 |
| 10 | CTGGACATTC ACTAGGTGGA AGAGATGCGG TAGTTCTAGG AATGAGTAAT GGTATTCCGA | 540 |
| | ACATTGTGGT TTATAATCCA GCTCCTATTT CTATAACTAG TTTGAATCCT AATTCCCCAG | 600 |
| 15 | ATGGAAAACG TTTATTAGAA TTATATAAAA ATTATAAAGG TAATATTACT AGGTTTGTTG | 660 |
| | CAGAAAATGA TGCATTGACA GAAAATCTGA AGAAATATAA GCATTATGTT TTTTTCGGTA | 720 |
| | ATGATAAAGT CTTTAAAAAT GGTAAAGGTC ATGAAATGKA AGGCLTTCTG ACCGAAGAAG | 780 |
| 20 | AACAAAAAGC tATAAAAn | 798 |
| • | (2) INFORMATION FOR SEQ ID NO: 830: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830: | ** |
| | AATATCAATC TCTTCATAAG CTGAATTATT TTCATGCACT TCTTGATGTG ATGATTTGTC | . 60 |
| 35 | ACGAACHGCT ACAACTAACA TTTTATCGTC TAAAATAAGT TGTTTATATT TTTCTAATTC | 120 |
| | ATCAGGCGCT AAGTTGTAGC GTGATAAAAC TGCATGTTCA CCATCTTCTC CTGTTAACAG | 180 |
| | TTTAGTCATT CTATCACTAA ATGTTCCACT TGTTGAGATA AGGGGAGATT TCAGAGTCGT | 240 |
| 40 - | GTAAGTCATT AGGTGTAATT TACTTTACT AATAATTGTT AGCCTGATCT AAATAACTTC | 300 |
| | AGATTCTTTG ATTGATANGT GNATAATCGC AGTGCATTAC ACAGAATACT GCCAAGTGCG | -360 |
| 45 | CCCTTAAAAT TGTTATTAnC TTACCTCTAT ATAAGAACCC (2) INFORMATION FOR SEQ ID NO: 831: | 400 |
| 5 <i>0</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 475 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | AAGTCIGCAT GACTTTATT IGCAAGTTCG ACTGCTTGAT CAAAAGCGCG ATGATCTTCA | 60 |
|----|---|-----|
| | GGATLAGCAC TTTGAACTGA GCTGAAATTC GGATCAGGTT TACATTGTGC TTCTACAAGA | 120 |
| 5 | TTAAATTGAT TGAAATTCAA AGATTGTAAT AACTCAGGTA CAATCGGAAC ACTTGTACCA | 180 |
| | TGCAAACTAG TGAACACAAC TTGTAAATCA GATTTAGGAA TATAGCCAAT CATATTTTGA | 240 |
| 10 | ATGTGTTTCA TATAGTCATC AGTTACAGAT TTCGGAAAAG GCTTGATATA AGATGTATTT | 300 |
| 10 | TGTTTAGAAA LAGGTATATC AATCTGTAAT GGATCGCCAA CTTCTTCGAT ATAACGACTT | 360 |
| | GCAAGCTCAG ATGCATCAGT CGATAATTGC GCACCATCAG AACCATATAC TTTGATGCCG | 420 |
| 15 | TTATAGTCTT TCGGATTATG ACTTGCLGTA ATCATAATGC CAGCAGTAGT ATTAA | 475 |
| | (2) INFORMATION FOR SEQ ID NO: 832: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 724 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832: | |
| | CTTGAATTGA AGGATACGCA AATGATGCAT AATCAGCTTC TGTATAAAGC TGTAATGTAA | 60 |
| 30 | TGTCATCAAG GTCACCTTTT CTAACAAGCA CCTTATTAAT AGAAGTATGA TTCGCTTGCC | 120 |
| | AAGTACCTTG ATTATTTTGT TCTAAATGAA TGACTTCGCC TAACGATTTC AACGTAATAT | 180 |
| | CTGCACGCTC GTCTTCGCTA ATAGTATATG TCTTACCATC TCGCAAATTG AGCATCTTCA | 240 |
| 35 | ATTGTTTGTT ATATTTTATA ATCAATTTAT GCATTGTCTT TGCCTCAGTC CTATACTATT | 300 |
| | TITTTCTTC AGCITCTTGG CGTITTTCTT TATCTTTTTG TGCTTGTTCT TTTTGTTTCT | 360 |
| | TTTCGTTCTC TTCTTGTTGC TTTAATTTCT CATCTTTCGC TTTTGCTTTC TCTTCTTCAG | 420 |
| 40 | ATTTCGCTTT TTCATCTTTA ACTTGTTTTT CTTTGTCTAA AATATCTTGC AATTTATCGT | 480 |
| | TATACTTTTT CGTTTCTTCA GAACGTTTAT CATTCGATAA ATCTCCGTTA TTTTTAATCT | 540 |
| 45 | CATTTAATTT ATTAATCAAC GCTAACTTTG TAATATCGTT ATCATCTAAA TAAGTGGCAA | 600 |
| | TATTAATCGC TTCATCAAGA TGTCCTTGTC CTAATTCCAT CCAATATAAT AAGTAGTCTT | 660 |
| | TGTTTGAATT TGGTGTCACA TTATTAAGTA AATTTTCTTT CGTATCTGTn TCTAAACCnT | 720 |
| 50 | GTTn | 724 |

(2) INFORMATION FOR SEQ ID NO: 833:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 994 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

| • | | | |
|-----------------|---|------------|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833: | • | |
| | AGCAGTTTGG CTCGTAGAAA TCTCCCGTCT CTATTCTATG TATTAACTTT | TATTATATTT | 60 |
| 10 | GTTATGATAC TATCGATATG AAAGCGTTGT CAATGGTTTT TGTAAAAATT | TTGTCAAATT | 120 |
| | TAATTTTTCA AGTCTTTATA AAAGTAGTTT AATTTGAAAA CTAGAAATAC | CAATCCTAAC | 180 |
| | TAATTTATTT ATGACGCTCT TTTGTTTAAT TGACATTCTT CAGCCATATT | TTTTATGACT | 240 |
| 15 | AGTTGCATTT TTTACTAATA AACACCTCTA AAACTTTAAT GATTTTAATC | GTTTTAGAGG | 300 |
| | TGCTAATTAT TTTATTTGAT TATTTTTTGT TTGATACCTA CTGCATATCC | CATATGAAAA | 360 |
| | CGGCTTTTTT ATTATGTTAT ATGACTAAAT CTCGTGAAAA ATGAAATTTT | IGCAGACTTA | 420 |
| 20 | TGATTTACCA-AAGTTTATCA-TAACTAGTAG-TTACATATTT-CGCTCCATTT- | TTAACAGCTT | 480 |
| | CATTGACTTC ATCTATTGTA TTAATTAGGC CACCTGCAAT GACTTGTGTG | PTTGTTTCTT | 540 |
| 25 | TCTGAATATG ATGAATCGCT TTACTCGCAA CACCTGGAAG TACTTCAACA | AAATCAGGTT | 600 |
| 2 ⁸⁷ | CAACTTTTT TATCAAATCT ATACTGCGTT TCAATGCTTG ACTATCAATA | ATAAATACTC | 660 |
| | TAAAAATCGT TAAAGTATTT AATGATTTAG CTTTTTTTAT TACTTTAGAT | TTAGTCGATA | 720 |
| 30 | CGATACCTTT TGGCTTGTAT TGCTGAATAA TAAATTCACT TGCAAATTCA | rcgtggctta | 780 |
| | AACCTTTTAT CAAATCTATA TGAATAAAAC ACTCTATATG ATTTTGCTTC | AGCAATTCCA | 840 |
| | TAATACTTTT TATATGTCCT ATATGCATAT CTAGAAGCAC ACACATTTTA | PAGTCTGTnT | 900 |
| 35 | TAATCCAGTT TCTCTAAATC nTTAATGTTT CCTATAAGCA GGCAATATGT | TGTTAATTCA | 960 |
| | CTnGATCCAT CCTCTCTACA TCACACGCTT AAAT | | 994 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 834: | | |
| | (i) SEQUENCE CHARACTERISTICS: | G. | |
| | (A) LENGTH: 783 base pairs (B) TYPE: nucleic acid | | |
| 45 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834: | | |
| 50 | TCnACAAAGT CGGTATTAGG CTATGGGCCA TTTnACTATT ATAACTAATC | GGAAATATAC | 60 |
| | CACATAACAT CATTATTGAG TTGATTCTAT CATTTGGCTT ATTAGGGTTT | TTTATCATAA | 120 |
| | TGATTTGCAT TTTGCTACTA GTTTATAAAA TGATTAGGAA CTATGATCCA | AACACTATAG | 180 |
| 55 | | | |

| | ATTTAGTTGT AAGTGAATTT TGGTTTGTGT TGTTCTATTT TATTACAAAA GGACGGCGTC | 30(|
|----|--|-----|
| | ATCATGGCTA AGAAAGTTTT TATTATGGAT AGCGTAAAGA CAATAATTGG TACGTTGCTT | 360 |
| 5 | ATAGCTTTAG GATTACAATT TITAGCTTAT CCAATTATTA ATCAACGAGT AGGTAATGAA | 420 |
| | GCGTTCGGTT CTATTTTAAC GATTTATACA ATAATAACAA TCACGAGTGT TGTATTAGGC | 480 |
| 10 | AATACGCTTA ACAATATACG mTTGATTAAT ATGAATCTAT ACAAATCCAA TCATTACTAC | 540 |
| 10 | TGGAAATTTG CATCGATACT TTTAATCTCA ATTCTGATTG AGAGTATAGC TTTAATTATT | 600 |
| | GTATTTCTTT ACTTTTTAA TTTGAACATC ATCGATATTA TCTTTTTAAT TCTACTTAAT | 660 |
| 15 | ATTTTAATGT GTTTAAGGAT TTATCTGAAT GTATTTTTTA GGATGACTTT AAAATATAAT | 720 |
| | CAGATTTTGT ATATTGCTCT TATTCAATTT TTAGGTTTGC TGATAGGACT ATTTCTATAT | 780 |
| | nAT | 783 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 835: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 794 base pairs | |
| 25 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | , |
| | | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835:

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TTACCTAATT TTTCAAtCaT AAGATTCCCC CTATTGTTTA AACATAAAAA TATTATACGA 60 TTAAGCACGA GMCACTTCAA TATATTTTTC AGAATATTCT TATAAATATT AATATGATCA 120 TTTCACTATT TAAACACGTT TAATATTAAA ATAAGTTATT CATATAAACT GGTGCTGTTT 180 GATCCAATTG CAGACTTACG AGTCATTGAA AAGTCTCACA AACTATTGMA AGTAAAALATC 240 TTAAAATAGA AAGTGAATGG TTAATTTAAG TATATTTMAA AAATATTAAC CTTTTTAAGC 300 ACTGCTATTT AGGATATACT AAATAATAAC TAAGTTTAGA AAAATAGGAG GAACATCGTT 360 TATGTTAAAC AAGGTTTGGT TCCGAACTGG CATCGCTCTG ATTATGCTGT TCATTCTCAT 420 CAAACTATTT ATGGAAGTGC ACGAAGTATT TACTCCAATA GCTACAATCA TCGGTTCTGT 480 ATTTCTTCCA TTTTTAATTA GTGGTTTTTT ATTTTATATC TGTCTACCTT TTCAAAACTT 540 ACTTGAAAAA GTCGGTTTTC CAAGATGGGC TAGTATAACA ACAATCATGT TAGCTTTGTT 600 TGCTATTATC GGCTTAATTG TTGCGTTTGT TGCACCAATC ATCATTTCAA ATATCAACAA 660 TTTAATTAGT CAGACACCTG GCCCTACAAA AAGGAAGCAG AGCAAATTAT TAAATTCGCA 720 CTGGCTCAAA TGGnTAAATT ACCTGGAGGA TGTAACCANG TGGATTACCA ATATGGTAAA 780

(2) INFORMATION FOR SEQ ID NO: 836:

(i) SEQUENCE CHARACTERISTICS:

| 5 | (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · |
|----|---|------|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836: | |
| | TGTTTATACT GTGCCTGAAT TAGAAGAGGT TTTAACACCT ATGAGACAAG ATGGAACTCG | 60 |
| 15 | TGATATTTAT GTTAATTTAG AAAATGTGAG TLATATGGAT TCGACAGGTT TAGGTTTATT | 120 |
| | CGTAGGTACA TTAAAAGCAT TAAACCAAAA TGATAAAGAA CTATACATTT TAGGTGTGTC | 180 |
| | AGATCGTATC GGTAGACTAT TTGAAATTAC TGGTCTTAAG GATTTAATGC ATGTTAATGA | 240 |
| 20 | AGGAACGGAG GTCGAATAAC ATGCAATCTA AAGAAGATTT TATCGAAATG CGCGTGCCaG | 300 |
| - | CATCGGCAGA GTATGTAAGT TLAATTCSTT TAACACTTTC tGGCGTTTTT TCGAGACTGG | 360 |
| | TGCCACATAT GATGATATTG AAGATGCCAA GATTGCAGnT | 400 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 837: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 433 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837: | |
| | ATTGATCCAT TTTGCGGTTC GGGTACAATA GCTATAGAAG CTTGTTTAAT TGCTCAAAAT | . 60 |
| | ATCGCACCTG GTTTTAATCG CGAGTTCGTA TCAGAGCAAT GGAACATCAT GCCAGCAAAT | 120 |
| 40 | ATTTATGATG ATTACCGTGA TGAAGCGGAT AAGATGGCTG ATTATGATAA AGAAATCGAA | 180 |
| | GTATATGCTT CTGATATCGA TCCAGAAATG GTAGAGATTG CTAAGCGTAA CGCTGAAGAA | 240 |
| 45 | GTTGGGTTGT CTGATATTAT TAAATTTAGT GTAAAAGATG TCAATACATT AACAATTGAT | 300 |
| 45 | ACAGAAGAAC CGGTGGCGTT AATTGGAAAT CCTCCATATG GTGAACGTAT TGGTGATCGT | 360 |
| • | GAAGAAGTEG AAGAAATGTA CCGTTATATT GGTAAACTAA TGAAACAACA TCCATTTTTA | 420 |
| 50 | TCTACATACA TTT | 433 |
| | (2) INFORMATION FOR SEQ ID NO: 838: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 926 base pairs | |

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

| 5 | (wi) CECUENCE DECEDEDATOR OF TO WE ARE | |
|----|--|------|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838: | |
| | ATTGGGCCAA CTAATCCTGT ATATCCAAAT CCAGCAGACA ATGGTGTTCC TTTAACCTGA | 60 |
| 10 | AGAACGTAAG CAATGATTCC AGTAATTATT CCATTTATAG TCAATGGTAT CGAAATAATT | 120 |
| | AAATTTTCA AGTAAACTGG GATCATCATT TTTGCAGCTC CTATGAGTAA AACTGCATTT | 180 |
| | ACACCAATAG AATTGACACG CAATGAGCCA AATAAGAAAG TAACACAGGC AGCCACTATA | 240 |
| 15 | CCTAGGTTTG CTGCTCCACT TCCTAGTCCG TTTAAACTAA TCGCAGTTGC AATCGCTACT | 300 |
| | AACGATATTG GTGTTACCAT TAATAATGAA AATGCCACAC TAATAAGTAT AGACATTAAC | 360 |
| | AACGGATTTA AGTCTGTAAA AGAATGAATT ACATTTCCAA TTGCTTGAGT AATTTTTCGA | 420 |
| 20 | ATGTAAGGTA ATGTGATTAG ACCGATACCC CCACTAACGA TAGGTACTAA AACTGGTAAT | 480 |
| | ATAATTAATT CAAAAGATCC AAGTTTGTTT TGTAATACCA TATATATAAG ACATGCAATA | 540 |
| 25 | ATAACAACCA AACTCGTATT TATAATGtCa CCTATACCTT TTAACATAAA ACTATTATTG | 600 |
| 25 | CTATATACAA CAGCACCTGA ACCAATCATA GCTGATGTAC CTACTATAGC AGCACCTGCA | 660 |
| | CCATTAAATT TAAATTGATG AGCAGCTAAA ACCCCAATAA TAAATGCCAT AAATGATTGA | 720 |
| 30 | ATTAGTATCA CTAACTGATA CGTTAATTCT AAAATTTCAT TACCACTTTT AAATATTTTt | 780 |
| | AATACTTCAC CTAATAAAGC ATTCGGAACA AGTGCAATAA CAACACCAGC ACCAATAGAA | 840 |
| | TTTAAAATCT TACTGAAAAA CTGTTTATTA TCAGCATTAT TTGCGTTACT CATAAACGAC | 900 |
| 35 | CTCCAATTTG AACATTANAC TCATCA | 926 |
| | (2) INFORMATION FOR SEQ ID NO: 839: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 40 | (A) LENGTH: 400 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839: | |
| | CTTCGAAACG TACTTGGTCA TTCCCTTTAC CAGTACAACC ATGTGCAATA CCTACTGAAT | 60 |
| 50 | TTGTTTTCTC AGCAATCTCT ACTAATTTTT TAGCGATTAA TGGTCTTGAT AAAGCTGAAA | 120 |
| | CTAATGGATA TGCATTTCA TACATTAAAT TTCCTTTGAT TGCATAACTT ACATACTCAT | 180 |
| | CACTAAATTC TTTTGTTGCA TCAATAATAT GACATTCAAC TGCTCCCATA TCTAAAGCTT | 240 |
| == | The state of the s | 2-10 |

CGTATCCLTT GTCGATAAGC CATTGAACGG CCACACTTGT aTCTAGtCCt CCkGAATATG

| | CTAAAACAAT TTTCTCTTTC ATAAAATTCA CCTCATTGTA | 400 |
|-----|---|------|
| 5 | (2) INFORMATION FOR SEQ ID NO: 840: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1043 base pairs (B) TYPE: nucleic acid | |
| 10 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840: | |
| ٠ | GGATCGCGGT GTTGTGCTTG ATATACTTTG TAGCGATAAC GTTTACCTAC ACAATCATAA | 60 |
| | CGACAATGAA AATCGTCATC GACTGTAACT ACATTGTTGA CATAAATATC ATCAGGTAAC | 120 |
| 20 | GTTCGGTTCA TTGCATATTG CCATTGTGAC ATAGGTATAT TCAGCTCTGT GTCGAAATGA | 180 |
| | AAGTATTGCT GTATCGCATG TACACCTCTA TCAGTCCTAC TTGAAGGATG GATTCTCACA | 240 |
| | TGTCTTTTAT GCATGCGTTG TAATAGCTTT TCAAATTGTT GCTGTACCGT TCGACCATTT | 300 |
| 25 | TGTTGAATTT GAAAACCTAG AAAATTATTT CCTTGATACG CAATTTCTAC TAATATACGC | 360 |
| . • | ATGAATTTAC ACTCCTGAAT ATTTTAATAC GAATAAAATA ATTGCAATTG GGATAATCAT | 420 |
| 30 | GGTTAAAGAT ATCGTATCTC TCAATTGCCA TTTAAGCTGT CTGTAGCTCG TTCTCTTAAC | 480 |
| | ATTGGCATCA TAACCCCTAA CTTCCATTGC GACCGCTAAT TCTTCGGCGC GTTGGAAAGC | 540 |
| | TGAGATGAAT AGTGGCACTA GTAATGGAAT AAATGATTTA ATACGTGTTG CAATGTTCCC | 600 |
| 35 | TGAACTTATT TCAGAACCAC GCGACTTTTG CGCCAAAATG ATTTTATCTA ACTCATCCAT | 660 |
| | TAACGTCGGG ATGAATCGTA ACGCAATGGA CATTATCATA CTTAATTGAT GAACTGGTAA | 720 |
| | TTTAAACATC tTTAGTGGTG CAAGTAATCT TTCAAACGCA TCTGTTAAAT CAATTGGACT | 780 |
| 40 | TGTAGATAGT GTCATAATTG TTGCAATCAT TACAATCCCA ATTAAACGCA GTGrTATATA | 840 |
| | TAGCCCTTCT AAAATACCAT TAGTTTCAAT CGTGATGCCA TGCCATTCAA CTAATACATA | 900 |
| | TCCACCTTTA GTTAAAAATA TATGCATCAT TAATGTGAAG ATTAAAAAGA AAAATATTGG | 960 |
| 45 | TGTTAAACCT TTGATTAGGA ACCATAATTG AATTTTTGCT AATCTCATAA TGAANANGAT | 1020 |
| | AAGTGCAAAC ACCCAAAGAT ATG | 1043 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 841: | • |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 343 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| cc | | |

| | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 841: | |
|----|---|-----|
| 5 | TCGAAATCAA ATTATAATAG ACAATTTTAG GAGGTGGACT TTCGATGACC AAAGGAATCT | 60 |
| | TAGGAAGAAA AATTGGGATG ACACAAGTAT TCGGAGAAAA CGGTGAATTA ATCCCTGTAA | 120 |
| | CAGTAGTAGA AGCTAAAGAA AATGTTGTAT TACAAAAGAA AACTGTAGAA GTTGATGGAT | 180 |
| 10 | ACAACGCAAT CCAAGTTGGA TTTGAAGACA AAAAAGCATA CAAAAAAGAT GCAAAATCTA | 240 |
| | ATAAATATGC TAATAAACCA GCTGAAGGTC ACGCTAAAAA AGCTGACGCn GCACTGAGAG | 300 |
| 15 | nTCCCCTCAT AATTTCCCCA AnCGTAACCA TGTGTGAATA AAT | 343 |
| | (2) INFORMATION FOR SEQ ID NO: 842: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 430 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842: | |
| | ATGAGTATTT TAATGATGCG CTACGAGCGT ATGGTCTTAC TGTGANAACA GGTGAATTTG | 60 |
| | GAACACACAT GAATGTTAGC ATAAATAATG wtGGwCagTC TCTGGTAGTT TAGAATTAGA | 120 |
| 30 | AGAATTAAAG CAATTTAGAC AATGGGGTTC TAAAACACCA GGTCATCCTG AATACAGACA | 180 |
| | TACAGATGGT GTAGAAGTTA CTACCGGACC ACTTGGACAA GGTTTTGCTA TGTCmGTAGG | 240 |
| 35 | ATTMGCTTTA GCAGrAGATC ACCTAGCAGG GAAATTTAAT AAAGAAGGAT ATAATGTTGT | 300 |
| | AGATCATTAC ACATATGTAT TAGCTTCTGA CGGTGATTTA ATGGAAGGTA TATCGCATGA | 360 |
| | AGCAGCTTCA TTTGCTGGAC ATAATAAATT AAGTAAATTA GTTGTTTTAT ACGATTCAAA | 420 |
| 40 | TGGATATTTC | 430 |
| | (2) INFORMATION FOR SEQ ID NO: 843: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . · |
| 50 | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843: | |
| | GGACTGCCCG ATGATTTGAC AAATGAATTG CTGATTTGAT TTATATATTA TCTGNAATTA | 60 |

| TAAATCTCAA CCTTACTATA TTAATATATA ATCAAATCTT AGATTAACTA GTGTAAATGAT ACAGATGGAT AATTGAGTAC AAATTTAAAA CCCTGAGATT TTCGCTTTAA TTTGAAAACC 300 TCAGGGATTA TTTGATTTT ATATAATGA (2) INFORMATION FOR SEQ ID NO: 844: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844: AGATGAGAA AGTGTTTCAT CGATTATCTT AACAGTGTT GCTTTATATA CTACAATTCT TCCTAGACTC TGTACCGTTG AAAAGAGACC TGGTTGTAAA ATCTCTATATG ACATTTTCAA 25 ATTTCTGTTC ATCTATIGCA TAAAATGAC TGCATTATA ATCTCTTTCG ATTTGTATAA (GTACACCCC GCCATACAACA TTAAAATTGA TCCATTCCC TGCTTGGTAC ATTGACATTG (GTACACGCC GCTGATAAAA ACTTTTAACG GTGTGGGTCC AATAATTTGC CATCCGCCAG (GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG (2) INFORMATION FOR SEQ ID NO: 845: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCC CATCTTTAGT TCCAAATATA TCAACGTATT 60 TATTCTTAA CTGGATATAGT TTCCCCAAC TCTCGGATC AAACACTTGA ATATGACTAT 120 ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTCC CATAACCATT 180 TCCCAGATAA TGAAAAATGG GGCTGAGTGT AATATTTGAT TAGTCCATTG ATATTGGTCAT 180 TCCCAGATAA TGAAAAATGG GGCTGAGTGT AATATTTGAT TAGTCATTG ATATTGGTC 180 TTCCAGATAA TGAAAAATGG GGCTGAGTGT AATATTTGAT TAGTCATTG ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGAGAAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 301 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 301 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 302 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 303 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 304 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 306 | | TCATCTATCC AACAATATGT CTTATCAATG GTATAGTCTT TGCACACCAA TGGAGGNAAA | 180 |
|---|-------------|--|-----|
| TCAGGGNTTA TTTGATTTT ATATATGA (2) INFORMATION FOR SEQ ID NO: 844: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDMESS: double (C) STRANDEDMESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844: 20 AGATGAAGAA AGTGTTTCAT CGATTATCTT AACAGTTGTT GCTTTATATA CTACANTTCT 60 TCCTAGATCT TGTACCGTTG AAAAGAGAC TGGTTGTAAA ATCTTAATTG ACATTTTCAA 120 TCACCACCCA GTCATCAACA TTAAAGTTGC CATCTGATAT ATCTCTTTCG ATTTGTATAAA 180 ATTTCTGTTC ATCTATTGCA TAAAATTGTA TCCATTCTCC TGCTTCGTAC ATTGACATTG 240 GGAAATCTGA TGGGATATAA ACTTTTAACG GTGTGCGTCC AATAATTTGC CATCCGCCAG 360 GGAAATCTGA TGGGATATA ACTTTTAACG GTGTGGGTCC AATAATTTGC CATCCGCCAG 360 AATTTTTTAA CCTTGGGCNG ATTACCGTCTA NGGNGTATGT 400 (2) INFORMATION FOR SEQ ID NO: 845: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDMESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT 120 ACCAAACCCA GTATTAATG TTTCCCCAAC TCTCGGATCC AAACACTGA ATATGACTAT 120 ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTGC CATAACCATT 180 TCCCAGATAA TGAAAAATCG GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTTTTGA TAAAACTAAT TTATTCATGA 360 | ` , | TARATCTCAR CCTTACTATA TTARTATATA ATCARATCTT AGATTARCTA GTGTARTGAT | 240 |
| (2) INFORMATION FOR SEQ ID NO: 844: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDENDESS: double (C) STRANDENDESS: double (C) STRANDENDESS: double (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844: (Xi) SEQUENCE ANAGAGACC TEGITGTANA ATCTEATTA CTACANTTCT 60 TCCTAGATCT TGTACCGTTG ANAGAGACC TEGITGTANA ATCTEATTG ACATTITCAM 120 TCACCACCCA GTCATCAACA TTANAGTTGC CATCTGATAT ATCTCTTTCG ATTIGTATAM 180 GTTCACGCTC GCTGCTANAT ACTITTANCG GTGTGGGTCC ANTANTTGC CATCCGCCAG 300 GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG 360 AATTITTTAA CCTTGGGCAG ATTACGTCTA AGGAGTATGT 400 (2) INFORMATION FOR SEQ ID NO: 845: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDENDESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT 60 ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180 TCCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | 5 | ACAGATGGAT AATTGAGTAC AAATTTAAAA CCCTGAGATT TTCGCTTTAA TTTGAAAACC | 300 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844: 20 AGATGAAGAA AGTGTTTCAT CGATTATCTT AACAGTTGTT GCTTTATATA CTACANTTCT 60 TCCTAGATCT TGTACCGTTG AAAAGAGACC TGGTTGTAAA ATCTTATATG ACATTTTCAA 120 TCACCACCCA GTCATCAACA TTAAAGTTGC CATCTGATAT ATCTCTTTCG ATTTGTATAA 180 ATTTCTGTTC ATCTATTGCA TAAAATTGTA TCCATTCTCC TGCTTCGTAC ATTGACATTG 240 GTTCACGCTC GCTGCTAAAT ACTTTTAACG GTGTGCGTCC AATAAATTGC CATCCGCCAG 300 GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG 360 AATTTTTAA CCTTGGGCNG ATTACGTCTA NGGNGTATGT 400 (2) INFORMATION FOR SEQ ID NO: 845: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 935 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT 120 ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180 TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240 GGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | | TCAGGGnTTA TTTGATTTTT ATATAATGA | 329 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844: (xi) SEQUENCE TRANAGAGACC TEGTTGTAAA ATCTTATATC ACATTTCTAA (xi) SEQUENCE TAAAATGTA TCCATTCTCC TEGTTACTATT ACATTTGTATAA (xi) SEQUENCE TAAAATGTA TCCATTCTCC TEGTTACA ATTGACATTG (2) INFORMATION FOR SEQ ID NO: 845: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: 45 TATTCCTAA CTGATTAATG TTTCCCCAAC TCCCGATC AAACACTTGA ATTGACTTT ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACTATGA TCCAAATATA TCAACGTATT ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTCC CATAACCATT 180 TTCCCAGATAA TGAAAAATCC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT ACCAGACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTCC CATAACCATT 180 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | 10 | (2) INFORMATION FOR SEQ ID NO: 844: | |
| AGATGAAGAA AGTGTTCAT CGATTATCTT AACAGTTGTT GCTTTATATA CTACANTTCT TCCTAGATCT TGTACCGTTG AAAAGAGACC TGGTTGTAAA ATCTTAATTG ACATTTTCAA TCACCACCCA GTCATCAACA TTAAAGTTGC CATCTGATAT ATCTCTTTCG ATTTGTATAA ATTTCTGTTC ATCTATTGCA TAAAATTGTA TCCATTCTCC TGCTTCGTAC ATTGACATTG GTTCACGCTC GCTGCTAAAT ACTTTTAACG GTGTGCGTCC AATAATTTGC CATCCGCCAG GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG AATTTTTAA CCTTGGGCNG ATTACGTCTA NGGNGTATGT (2) INFORMATION FOR SEQ ID NO: 845: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT (A) ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180 TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATGA ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 360 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | 15 | (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| AGATGAAGAA AGTGTTCAT CGATTATCTT AACAGTTGTT GCTTTATATA CTACANTTCT TCCTAGATCT TGTACCGTTG AAAAGAGACC TGGTTGTAAA ATCTTAATTG ACATTTTCAA TCACCACCCA GTCATCAACA TTAAAGTTGC CATCTGATAT ATCTCTTTCG ATTTGTATAA ATTTCTGTTC ATCTATTGCA TAAAATTGTA TCCATTCTCC TGCTTCGTAC ATTGACATTG GTTCACGCTC GCTGCTAAAT ACTTTTAACG GTGTGCGTCC AATAATTTGC CATCCGCCAG GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG AATTTTTAA CCTTGGGCNG ATTACGTCTA NGGNGTATGT (2) INFORMATION FOR SEQ ID NO: 845: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT (A) ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180 TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATGA ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 360 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | - | | |
| TCCTAGATCT TGTACCGTTG AAAAGAGACC TGGTTGTAAA ATCTTAATTG ACATTTTCAA TCACCACCCA GTCATCAACA TTAAAGTTGC CATCTGATAT ATCTCTTTCG ATTTGTATAA ATTTCTGTTC ATCTATTGCA TAAAATTGTA TCCATTCTCC TGCTTCGTAC ATTGACATTG GTTCACGCTC GCTGCTAAAT ACTTTTAACG GTGTGCGTCC AATAAATTTGC CATCCGCCAG 300 GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG (2) INFORMATION FOR SEQ ID NO: 845: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT (A) ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180 TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATGA ATATTAGTCT CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 360 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844: | |
| TCACCACCCA GTCATCAACA TTAAAGTTGC CATCTGATAT ATCTCTTTCG ATTTGTATAA 180 ATTTCTGTTC ATCTATTGCA TAAAATTGTA TCCATTCTCC TGCTTCGTAC ATTGACATTG GTTCACGCTC GCTGCTAAAT ACTTTTAACG GTGTGCGTCC AATAATTTGC CATCCGCCAG 300 GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG 360 AATTTTTAA CCTTGGGCNG ATTACGTCTA NGGNGTATGT (2) INFORMATION FOR SEQ ID NO: 845: (1) SEQUENCE CHARACTERISTICS: | 20 | AGATGAAGAA AGTGTTTCAT CGATTATCTT AACAGTTGTT GCTTTATATA CTACAnTTCT | 60 |
| ATTTCTGTTC ATCTATTGCA TAAAATTGTA TCCATTCTCC TGCTTCGTAC ATTGACATTG GTTCACGCCC GCTGCTAAAT ACTTTTAACG GTGTGCGTCC AATAAATTTGC CATCCGCCAG 300 GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG 360 AATTTTTTAA CCTTGGGCNG ATTACGTCTA NGGNGTATGT 400 (2) INFORMATION FOR SEQ ID NO: 845: (i) SEQUENCE CHARACTERISTICS: | | TCCTAGATCT TGTACCGTTG AAAAGAGACC TGGTTGTAAA ATCTTAATTG ACATTTTCAA | 120 |
| GTTCACGCTC GCTGCTAAAT ACTTTTAACG GTGTGCGTCC AATAATTTGC CATCCGCCAG GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG AATTTTTAA CCTTGGGCNG ATTACGTCTA NGGNGTATGT (2) INFORMATION FOR SEQ ID NO: 845: (i) SEQUENCE CHARACTERISTICS: | | TCACCACCCA GTCATCAACA TTAAAGTTGC CATCTGATAT ATCTCTTTCG ATTTGTATAA | 180 |
| GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG AATTTTTTAA CCTTGGGCNG ATTACGTCTA NGGNGTATGT (2) INFORMATION FOR SEQ ID NO: 845: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT 60 TATTTCTTAA CTGATTAATG TTTCCCCAAC TCTCGGATCC AAACACTTGA ATATGACTAT 120 ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180 TTCCAGGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | 25 | ATTTCTGTTC ATCTATTGCA TAAAATTGTA TCCATTCTCC TGCTTCGTAC ATTGACATTG | 240 |
| AATTTTTAA CCTTGGGCNG ATTACGTCTA NGGNGTATGT (2) INFORMATION FOR SEQ ID NO: 845: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT (A) ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT (B) TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT (CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA (CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA (CGTTTTCACT GATAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA (CGTTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA (CGTTGTTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA (CGTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA (CGTTTTCATGA TGTAGTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA (CGTTTTCATGA TGTAGTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA (CGTTTTCATGA TGTAGTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA | | GTTCACGCTC GCTGCTAAAT ACTTTTAACG GTGTGCGTCC AATAATTTGC CATCCGCCAG | 300 |
| AATTTTTAA CCTTGGGCNG ATTACGTCTA NGGNGTATGT (2) INFORMATION FOR SEQ ID NO: 845: (1) SEQUENCE CHARACTERISTICS: | | GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG | 360 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT 60 TATTTCTTAA CTGATTAATG TTTCCCCAAC TCTCGGATCC AAACACTTGA ATATGACTAT 120 ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180 TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | <i>30</i> , | AATTTTTAA CCTTGGGCnG ATTACGTCTA nGGnGTATGT | 400 |
| (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT 60 TATTTCTTAA CTGATTAATG TTTCCCCAAC TCTCGGATCC AAACACTTGA ATATGACTAT 120 ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180 TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA | | (2) INFORMATION FOR SEQ ID NO: 845: | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT 60 TATTTCTTAA CTGATTAATG TTTCCCCAAC TCTCGGATCC AAACACTTGA ATATGACTAT 120 ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180 TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | 35 | (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT 60 45 TATTTCTTAA CTGATTAATG TTTCCCCAAC TCTCGGATCC AAACACTTGA ATATGACTAT 120 ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180 TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | 40 | | , • |
| TATTTCTTAA CTGATTAATG TTTCCCCAAC TCTCGGATCC AAACACTTGA ATATGACTAT 120 ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180 TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845: | |
| TATTTCTTAA CTGATTAATG TTTCCCCAAC TCTCGGATCC AAACACTTGA ATATGACTAT 120 ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180 TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | | CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT | .60 |
| TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300 GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | 45 | TATTTCTTAA CTGATTAATG TTTCCCCAAC TCTCGGATCC AAACACTTGA ATATGACTAT | 120 |
| CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | | ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT | 180 |
| CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360 | 50 | TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT | 240 |
| | 50 | CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA | 300 |
| 55 | | GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA | 360 |
| | 55 | | |

| | ACCGATTCGG AATTAAATAA AAGCTAAAAC TATGTTAAAT AAACTTAAAC AGTTAGTAGT | 480 |
|-----|---|------|
| | GTTATTTAAG CAAAACTTAT CATTTTTAAG TTGGACAGAA CAGATCAATA AGAGC | 535 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 846: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 509 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ·, |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846: | |
| , - | TCAATCGATC AAATGGTGAT TGACCTTTTA AATTTGTATG ATCAAAATAA TGATTGTTGG | - 60 |
| | CCATATCTTT ACTATGCTTA CGTGCAGTTT CAGAATTCTG TTTAGAATAC TTCAATGTAG | 120 |
| 20 | ATAATTGATG TTGTTTTCTT TCAGCATTAA CTAAATCAAA ATTTTGTAGT TCAAAACTAT | 180 |
| | CTGCAAGCGA TTTCGATGGT GCTCCATATT GTTCTTTTAA TCTATTTTCC ATAGCATCAC | 240 |
| | TTACTTGTAA AACAGCTGTT ACATTATTAC GTCGATGCTT ATCATAAAAT ACCGTCGTAT | 300 |
| 25 | AAATGTGATT TTTATGGAAA ACATCATATT CTTTATTATT TTGTTCGTAA CGCACTCTAC | 360 |
| | CTTTAACAAT CTCTGTTTCT GGTTCGCCTA ATCTTTGCCT TACAACCGAT TTAGGTGTAT | 420 |
| 30 | TGTATTTAAT TTTTGATTTT GAAGTGATTA TATTTTGATT TGTATATAAC GCATTAACTT | 480 |
| 30 | TATCTTCAT GTAACTTATC ATTATAAAA | 509 |
| • | (2) INFORMATION FOR SEQ ID NO: 847: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847: | |
| | CGTATTGATC TATAAATAGT GTTTAGATGC TATAGTCGGA TGCTTAAGTA ATTTAAAGAA | 60 |
| 45 | AGTATCTITA ACATCGATGT GTGTATAATC ATTITTAGAA GTATTATAAT CTTTTTCTTC | 120 |
| | TCCCTTCTAA AATATATACA GGTGCTTCAT CAGCTAGTGG TTCAACTGGA ATGTCAGCAT | 180 |
| 50 | AAACTTCGCA TCATATGTTA AACAAAAACG ATTGTATCTG TACTTCACCT ATAACAGCAC | 240 |
| | TATCCAATTC GTGCTTATCA AATAAACTAA GATTTTTGTC AGTACCTTTT CACAACTAGT | 300 |
| | ACATACGTCT TGAGTTCTGA AGCATCATTT CATAAGGAGA ATACTGGCCA CGTGTGGACT | 360 |

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(2) INFORMATION FOR SEQ ID NO: 848:

| . | (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----------|--|-------|
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848: | |
| | TACCACTTGA ATACATTGCA TATAAAATAC GACGTTGTAC TGGTTTTAAA CCATCACGAA | 60 |
| 15 | CATCTGGCAA TGCACGCTCT TGAATAATAT ATTTACTATA TCTTCCAAAG CGATCACCTA | 120 |
| | AAACATCTTC AAGTGATAAA TCTTGAATTA TTTCACTCAC TAGATTTCCT CCTCATCAAA | 180 |
| | TTGATCATTT TCAAGCACTT GTACTTCAGA ATTATCTAAA ATACTTTGGT CCTCTTGCAT | 240 |
| 20 | ACCAAACTCA ACATGCTTTT CAATCCATTC ACGTCTAGGT TGTACTTTGT GCACCCATTG | 300 |
| | AATGTTGTTA CACGTTTAGA TGGAACGCAC TTGCATCTTG CAACTTGTGA CACGNATTGA | 360. |
| | AAGTTnCGTG TTTGCGGGGG TTnCAGCGTC GTTTGCCCAT | 400. |
| 25 | (2) INFORMATION FOR SEQ ID NO: 849: | |
| : | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid | |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849: | |
| | TTTATATGAT TTATTTGAGG AGTTAAGAGA TTTATTTA | 60 |
| | GACATCATGC GAATTTGATT TTACAAGAGA AGGTGAATTA AAAGTTTCAT TTGATTATAT | 120 |
| 40 | TGATTGGATA AATTCAGAAT TTGGTCAAAT AGGTCGACAA AATTACTATA AGTATAGAAA | 180 |
| | ATTTGGAATT TTACCAGAAA CGGAATATGA AATTAATAAA GTTAAAGAAA TCGAGCAATA | 240 |
| | TATTAAAGAG CTAGAAGAAT AAACTATCTT AATGTAAGAC TAAACAATAA AGCTTTGTTT | 300 |
| 45 | AGTCTTTTTA GCGTTTAAGT AAAAAGCAAT AGATACCGTA AAGTTGATGC TCATCAAATA | 360 |
| | ATAATATAA GATAATTTTA GGTTTTTAAA CTTTTAATCG | . 400 |
| | (2) INFORMATION FOR SEQ ID NO: 850: | |
| 50 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 923 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | * |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850: | |
|-----------------|--|-----|
| 5 | CAGGCCATAC TTACAATTTT GGCCATCGTC CGGATGTATT nGGAATCGTT GGATAATAAG | 6 |
| | CATCAAGGTC GTGACTATTT CGTAAAATTC CAACTGTCCC AGAATTTACA TCATTATGTC | 12 |
| 10 | CAATTACTGG GCAACCAGAT TTTGCCAACT ATCTATATTT CATATATTCC AAATGTTAAA | 18 |
| 10 | ATGGTTGAAT CAAAATCTTT GAAATTATAC TTATTTAGTT TCAGAAATCA CGGTGATTTT | 24 |
| | CACGAAGATT GTATGAATAT TATTATGAAT GATTTGATAG AGCTTATGGA CCCACATTAT | 30 |
| 15 | ATTGAAGTCT GGGGCAAGTT CACACACGTG GTGGAATTTC TATTGATCCT TATACAAACT | 36 |
| | ATGGACGTCC AAATTCTAAA TATGAAAAAA TGGCTGAGCA TCGTTTGATG AATCATGATT | 42 |
| | TATATCCCGA AAAAATAGAT AATCGTTAAA TGTATCATTT AATAAACACA CCAATAAGTT | 48 |
| 20 | GATTTTCCTA ACTTATTGGT GTGTTTTTCA TTTAGCATAC ATAATAGGTT ACATTAAAAT | 54 |
| | AACATTTTAT ACCAAAGTAC ACCAAAAGAA TATTAGTACA CGAATTAAAC AACATTTTTA | 600 |
| | TAGAAACCTA TTGCACTTTA ACGTCAATAA GTATATTTTT ATATTATCTC TAATTAATTG | 660 |
| 25 | TGCGCGCTTA ATAACAGAAT ATTCTCAATA TTTTTATTTT TTTGTGATTT GTTGGAATAT | 720 |
| | TTAGTTGATA AGGCACAATC AAATTTACTT AAACTATTGT ATTAGGGGAA GAAAGGATGG | 780 |
| 30 | GATGTATACA TGACACAACA AAACTCCCAT GGAAATCAAA TTCAAGACAT ACCTCAAACA | 840 |
| ; | GGATTTTTCG GGCATCCTCG AGGACTAGGC GTACTCTTCT TTGLAGAGTT CTGGGrAAGG | 900 |
| | KTTAGTTATT ATGGGCATGC GTG | 923 |
| : 9 5 | (2) INFORMATION FOR SEQ ID NO: 851: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1004 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851: | |
| 15 | TTANTTGCAT CTATTTCAGT TGGTGTAAAG AAAGCGGAAT TTGATTTTAT TGAAAAGTTA | 60 |
| | GCLCAAGAAA AATTAATCCC CGAATATATT ACAATAGATA TTGCGCATGG TCACTCAGAT | 120 |
| | TCAGTGATAA ACATGATTAA ACATATAAAA ACCCATATAC CTGATAGTTT TGTTATTGCT | 180 |
| 50 | GGTAATGTTG GTACGCCAGA AGGTGTTAGA GAATTAGAAA ATGCTGGTGC TGATGCTACC | 240 |
| | AAAGTCGGTA TAGGTCCTGG TAGAGTTTGT ATTACAAAGA TTAAAACAGG TTTTGGTACT | 300 |

| | GCCGATGGTG GTATAAGAAC GCATGGCGAC ATTGCTAAAT CAATTAGATT TGGTGCA | TCA 420 |
|----|---|----------|
| | ATGGTCATGA TTGGTTCATt WTTTGCGGCA CACGAAGAAT CACCTGGTGA AACTGTA | GAA 480 |
| 5 | CTTGATGGTA AACAGTATAA AGAATATTTT GGTAGTGCAT CTGAATTTCA AAAAGGC | GAA 540 |
| | CATAAAAATG TAGAAGGTAA AAAAATGTTT GTAGAACATA AGGGTTCATT AATGGAT | ACC 600 |
| | TTAAAAGAAA TGCAACAAGA TTTACAAAGC TCAATTTCAT ATGCCGGTGG AAAAGAC | TTG 660 |
| 10 | AAATCATTAC GTACTGTAGA TTATGTTATT GTTAGAAACT CTATTTTCAA CGGTGAT | AGA 720 |
| | GATTAATATT TATAGTAGGT GAKGTAAATT AAAAAATTCA TAGTAACTGT TGTTGCG | TTT 780 |
| 15 | TTATCAATTA TTATCATTGC GCCAnTAACA GAATTTAAAC CATTCATTCA TTTACAA | AAT 840 |
| | GAAGTAAGAC AATATATTGA CATTCACATC AATAAAGAAA CAATTTCTGC GGAAAAT | AAA 900 |
| | TTGGATACAC CGAAGAAACA ACAATTTGCC TTTAATAATA TACAAATGAA CATGTCG | AAA 960 |
| 20 | TCAGATGTTG AGAAAACATT AAATAAACCA AAAAGAGTGA CATn | 1004 |
| | (2) INFORMATION FOR SEQ ID NO: 852: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852: | |
| | GTTCGCTCCA ATGTACGCAG TTGTATATGC ATAGACACCA AAATCGAACC ATTCCAT | TGC 60 |
| 35 | ATTACCGATA CCGGTTGCAA CAACGGTTTT TTTAGCTTTC TTTGCATCCA CCATGTT | PAAT 120 |
| | ATTCTCTTTA TTAAAATCCA TGAATTCATA CACTCCCTCT TGTATGTTTC ATAATTA | TAC 180 |
| | GGAGTTAATT AGTTTTGTCA AATTTATAAG AATTTAAACT TTTATATAAA TACCAAA | GTA 240 |
| 40 | TGTTTGTTCA AAAATTTCGC TTTATCGnAT TAAATTCATG GTTTTATACC TCATACA | TTG 300 |
| | · | |

ATTAGACATA ATAATCTAAA CACGACGTTA CTTTGGATAT ACTNAATGGT nnCACACTCA

400

(2) INFORMATION FOR SEQ ID NO: 853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GTAGGAAGCA CGCATTCGCT CGATAATGTA ACCATACTCA

55

45

| | GGTGAAATTG TAACTATATA ATCGATATTA CCTTCAGTGT TCAAAACTGG AAAATAATAA | 60 |
|----|---|-----|
| | TTACCATCAC TCTTTTTGTT GAATTTATAA ATTTTAAAAG GTTCACCAAG TGTATACGAG | 120 |
| 5 | GCTTTCTCTT TATTATAGAT TTTATCAAGT GAAGTAACAT AAGAAAGATA GTCTTTTTGC | 180 |
| | GCTAAATTAC GTACGTCAGT AGGAACACTC TTGTCCTCGA CATTAACTTG CACATGCTTC | 240 |
| 10 | TTATCTTTTG CTTTGATATT TGAATTGCTC TCAGCGTTTG CAATAGGGGT AACACTTAAA | 300 |
| 70 | GABARTATTA AACTTAAAGC TATTAATTTT GGAAAGTTTC TTTTCATATA AAAACTCCTT | 360 |
| | T | 361 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 854: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 605 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 20 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854: | |
| 25 | ACNTTATACT AGANAAAGNT ATTAAAGTAT ATCTGCTTTA CACCATTAAA AAGCGGCAAA | 60 |
| | TGCTATAGAT AATCTAAAGC ATCTGCCGTA TGAGNATTTA TTTATTTTTG ATTGTCATAA | 120 |
| 30 | TCGTGTGGTT TTAAATTAAT TGTTTCTAGC TTTACAAATT TTGTTTTGTG AATGATTTTA | 180 |
| | TGAATAAAGT AAATCAACGC TAGAATGATT AAAGGTAAAA AGTTTTTÄÄA AGCATTTAAC | 240 |
| | CATTGATCTT TTAAAATATA TTCAACTGAG CCACCAAATA GCAAGAATAA TAGTGTAGTG | 300 |
| 35 | ATGACAATGA TTGGTCCTAA TGGATAAAAA GGTGCTTTAT ATGGTAGGAC CTTATTAGGG | 360 |
| | TCTTGACCTT GTTTTTTAAT AGCTTGTCGC AATCGTATTT GTGACCAAAT GCTTGATCCC | 420 |
| | CAAACAACTA TAATCATTGA ACCAATAATT TCAAGTAAAT TAAAAACGGC ATTTGAATTA | 480 |
| 10 | AAGTTTGCAT AAATAATAAC AATAACAACG ACTGCATAAG TAGTTAATAA TGCTCTTAAA | 540 |
| | GGTAACTTAG TTGTCTTGTT TAATTTACTT AAAAATTGGG GTGCTTTTTT GTCTGAACTT | 600 |
| | AAGGA | 605 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 855: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 515 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | TTGAACAAGC ATTTTTAAAT AGTCAACAAC ATCAMGCAAT TAGTGAAGAG GCACAACTTT | 60 |
|------|---|-----|
| | TAAATAATCC AGATGAATTA ATGGCATTTT TAAAGAATAA GCGTAAAAAT ATTTTAGAAA | 120 |
| 5 | ATGCATACAT TATGCCGCAT AATATGAGAG AAATGTTACG AAGTTATTTG GAAAGTATGT | 180 |
| | CTCAAGACTT TAATGTTGGC GGATTTTTTA ATAAAAAGAA GAAAAAACTA CAAATTCAAC | 240 |
| | AACAGCGATT ATTAACAGCG ACAGATGCGT TACAAGAACA TGTTAATCAA CAAATTCGTC | 300 |
| 10 | AACCAATGCG AGAAGATATG TCATTTGTTA CGCGTTTTAT CAATAAAAA GMAGCTTCAG | 360 |
| | aTAMAGTATT AAATCAGCAT TATGACGTTA AGCCAGAAAT GATTGAAGGT TTATATCAAC | 420 |
| 15 | CACAAACATC AATCAGCAAT ACTTATGTAC TTACATTTTC AGACGAAGTG GTTAAAGCCA | 480 |
| ,,, | TTAAGAAATA TGTTGAACAA CAATCAACAC CAATT | 515 |
| | (2) INFORMATION FOR SEQ ID NO: 856: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A)_LENGTH:-1607-base-pairs | |
| | (B) TYPE: nucleic acid | ٠. |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856: | |
| | GTCATTTTTA AAATTTCGCA TTCGCGTTTA ATTTTTTCTC TTTTTTCTTT TTCTTCTAGT | 60 |
| 30 , | GACATACTTT CTTTAGGTGT TTCAACCAAT TCAGATGTAT CTACATCATC AATTTTAGTG | 120 |
| | ATTTTGTCTA CATCTTTCTT TAAATCTTCT GGGACGTTCT CGAAACGCTT ATATTGCTCT | 180 |
| | TTAGAGATAC TAGCAGCTAT TTCATTAGCT CCTAAAATTT CATCTATCAA GCCGAAAGAC | 240 |
| 35 | AAGGCTTCTT CTGCAGTAAG CCAAGTTTCT GCATCTAACA TCTGTTTTAA GTGTTCTTGA | 300 |
| | TCTAAATCTT TTGCTTTATC TAAATAAGCT GAATTACTAA CAGCATCTGT TTTTTCAAGT | 360 |
| 40 - | AAATCCGCTG TCTTTCTTAA TTCTTCTGCA TTACCTACAG TCATAACCCA TGAATTATGA | 420 |
| | ATCATTAAAA AACTATTTTT GTGCATAAAA ATAGTGTCAC CACTCATAGC GATAACACTA | 480 |
| | GCAATTGATG CCGCTAAGGC ATCGACATAG ATATTAATTT TTGCAGGATG CATTTTTAGC | 540 |
| 45 | ATATTGTATA TTGCATGTCC TTCAAATACA CTGCCTCCAG ATGAATTTAT ATGAACATCT | 600 |
| | ATTTCACTGA TGTCTCCTAG TTCATCTAGT TTATTTTTGA AATCTGTAGC AGTTACATCA | 660 |
| | CTTTCAAACC ATTTATCACT TACAATATCA CCATAAATGA ATATTTCACC TTTACTTTTT | 720 |
| 50 | GATTTTCTTT TCATTTGAAA ATACTTAGCT TTCATTGACA TTTTTATCAC CACCTTTCAA | 780 |
| | ስርልተጥጥተርካጥ አልጥጥር አልርጥር ርርርርርርርርስልጥ ጥርርርር የአካል አል ጥርልርርርርር የተካል አጥጥልርርርርርር የ | 940 |

| | AACCACTACG AACTGCTTTA AAGTACACTT CTGCTTGTGT TGCACTATCA GCCCTTAAAT | 960 |
|----------|--|------|
| | AAGATTTAAC GTTAAATTTA AAATACCTAT TTTTTTCTCT GTCTGTTTTA GTAAGTAGTT | 1020 |
| 5 | TCCGATTAAn TTCTTCTTCA TACTGTTTGA CGATTGGCAA TAAGGTATGC TGCAAGTAAA | 1080 |
| | ATCTGTTTAA CTCTTCATTT TTCGCGAAAT TTGTATTTGA TCTTGCATTT AAGAATATTG | 1140 |
| 10 | AGGGCAATTG AAAAACGTTA GCTACTCTTT CTCTTGTTAA ATTCTCGCTT GCCACTATAT | 1200 |
| | CTTCAGAGAC ATATTTTTTA GGTAAAGGTT CGATTTCAAC ACCAGGCTCT TGGAATAATA | 1260 |
| | TTCCACCGTT TTCTTCATAG TACTGTTTGA AATCTTCTAA CACTTGTTGC CTTTTTTCTG | 1320 |
| 15 | TACTTACATT GGAACCATAT TTAAGCATAA AAGAATCTGG TTTTTGCATT TCTGTAAGAT | 1380 |
| | TAAAGGTTCT TACTGCATTG TCAAAATCAG TTGTATTCTT CAACACATCA ATCGGACTAA | 1440 |
| | TACCTTGAAC CATATTAGAT GCCACGATGT GTTTAAAATG CAACATGTCC ATATTATGAA | 1500 |
| 20 | CAATCAATTT ATTTCCAGTT GCAGCATGAA TGGAATAATA AAGTTCACCG TGATTGGTTT | 1560 |
| | TCAATTAACA TTTCAACAAC ATCTGGATTT AATAAGAAAA GCTTTGA | 1607 |
| | (2) INFORMATION FOR SEQ ID NO: 857: | |
| 25 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 346 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| , | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857: | |
| 35 | ATGCGCATTT AACCGCATTT AGAGATGCTG AAGATCAGTA TAAAGCTTTG TTAGAAATTA | 60 |
| | CAACATTACC AGAAGGTAGA ATTTATGTTG CTCGCCAAGA TCAACTCATT GTGGGTTATG | 120 |
| | TCACTTTCCA CTATCCTGAT GAAATTGAGC GCTGGTCTAC AGGTAAGCTT CCATATTTAA | 180 |
| 40 | TCGAATTGGG GGCAATTGAA GTCAGCATCA ATTTTAGGCA ATTACAACTT GCAGAAAAGC | 240 |
| | TGATACAACT TAGCCTTCTA CACCAGAATT CGAGAATTAT ATCGGNATAA CTACAGGATA | 300 |
| | TTACCGGCAT TGGGGGTTTA AAAAATTCCC AGTHAGAGGT ATTHCC | 346 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 858: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1176 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

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| , | AATTTMAATT TACAATAAAT AGTTCTATGA TTAAATGTCA GTTTTATGAC ATTTATTTAT | .20 |
| 5 | TGAAAATACG AACGAATGAG CGATATGATA ATATAGATAA GAATGATTTT AATTTAGGAG | .80 |
| | GCCTTTATGG TGCATAATAA AAACAATACA ATTTTAAAAA TGATCAAAGG TGAAGAAACA | 40 |
| 10 | TCACATACAC CTGTTTGGTT TATGCGACAA GCTGGCCGTT CGCAACCAGA ATATCGAAAA | 00 |
| | TTGAAAGAAA AATATTCACT ATTCGATATT ACACATCAGC CGGAGTTGTG CGCTTATGTA | 60 |
| • | ACACATTTAC CAGTTGATAA TTATCATACA GATGCAGCAA TTTTATACAA AGATATTATG | 20 |
| 15 | ACACCATTAA AGCCAATTGG TGTCGATGTA GAAATTAAAT CGGGTATTGG TCCAGTGATT | 80 |
| | CATAATCCAA TCAAAACAAT TCAAGATGTT GAGAAACTTT CTCAAATAGA CCCCGAACGA | 540 |
| | GATGTACCAT ATGTATTAGA TACAATTAAA CTTTTAACAG AAGAAAAGTT AAATGTGCCG | 500 |
| 20 | CTAATAGGAT TTACTGGGGC ACCATITACA TTAGCGTCAT ATATGATTGA aGGCGGACCA | 60 |
| | TCGAAAAATT ACAATTTTAC AAAAGCGATG ATGTATAGAG ATGAAGCAAC ATGGTTTGCT | 720 |
| | TTAATGAATC ATTTAGTTGA TGTATCTGTT AAATATGTAA CAGCTCAAGT CGAAGCAGGT | 780 |
| 25 | GCCGAATTGA TTCAAATTTT CGATTCATGG GTAGGTGCAT TAAATGTCGA GGATTACAGA | 340 |
| | CGTTACATTA AACCACATAT GATTCGATTA ATCAGTGAGG TTAAAGAAAA ACATGATGTG | 900 |
| 30 | CCGGTAATTT TATTCGGTGT AGGTGCCAGT CATTTAATCA ATGAATGGAA TGATTTACCG | 960 |
| | ATTGATGTAT TAGGCCTAGA TTGGAGAACG TCTATTAATC AGGCTCAACA ATTAGGCGTT 10 | 20 |
| | ACTAAAACAT TACAAGGGAA TTTAGATCCA: TCAATTTTAT TAGCACCATG GAATGTCATT | 080 |
| 35 | GAAGAGAGAT TGAAACCAAT ATTAGATCAA GGTATGGAGA ACGGTAAACA CATCTTTAAT | L40 |
| | TTAGGACACG GTGTATTCCC AGAAGTGCAC CAGAGA 11 | 176 |
| | (2) INFORMATION FOR SEQ ID NO: 859: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 621 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859: | |
| 50 | ATTTGGTGCA TTGGTANAAT TGACCTGAAA GNAAAAAGTG GTTTAGTTGC ACATTGAGTG | 60 |
| - | NAAGTGCGCA GATGAATTAT GTTGAAAACG TGAGGAAGAG CACCTTTGCT GTTGGTGATG | 120 |
| | AAGTAGACGT AAAAGTATTA TCTATTGCTG ATGATGGAAA AATTAGTCTT TCAATTAAGA | 180 |

| | AAAAAGCCGA AGATTTTGAA AAGAAATTAA GCAATTTCTT AAAAGATAGT GAAGATAAAT | 300 |
|----|--|-----|
| | TAACTTCAAT CAAACGTCAA ACAGAATCTA GACGCGGTGG CAAAGGTTCA AGACGTTAAT | 360 |
| 5 | TAAAATAAAT AAAGACTGTT TCGATAAGGA ATATATTTAG AATGATGCGT ATCGAATAAT | 420 |
| | CGATTGCAGC GTTAGACAAT CTAAGACTGT TTCTTAAATA AGGAGCAGTC TCTTTTATTT | 480 |
| 10 | GTAATGATAT AACTAAGACT TATACCATTT TTGAAAATTG TAAAAGTGAG GTGATGTTAT | 540 |
| | GCAGTTAAAT AGTAATGGTT GGCATGTTGA TGACCATATT GTTGTCGCTG TTTCTACAGG | 600 |
| | TATTGATAGT ATGTGTTTnn T | 621 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 860: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 544 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . • |
| | (wi) GEOVERNOR DESCRIPTION GEO. ID NO. 050 | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860: TATATTAGGT ACTTGTGTG GTATTGTGCC AGCTTTGCTG TCTACTATAA TTTCTAAAAG | 60 |
| | | 60 |
| | GTTTGAACAT ATAAAAGGGA AAGTGCTAGG TGTATTTAAT TTTGTGAGAT ATATTGGAAT | 120 |
| 30 | GACTGTCGGT GCATTATTAA TTGGTATCAT TTCTCAGCCG TTGGTAGCCT TTTACTTCAC | 180 |
| | AACTATAACT ATCATGTTAA TAGTAATATT TCTTTATATA AAGATAGTTG ACTTTCAGCT | 240 |
| | AAAGTATGCC AAATAAACTT AAAAAAGCAG TGAATCATTT CAATAGATGG AATGATTCAC | 300 |
| 35 | TGCTTTTTGT TTATAGAAAT TTAAAATTCA TGCCTTTATG CTAACAACAA TATTATTTTA | 360 |
| | CTCTCTTACG TTTGCCAATG TAACCGTATA GCAAAGTAAA TGACTGCGAT AATGATGACA | 420 |
| 10 | ACATACATAL ACGTGAATAG GAAGGAAGAC CAGTCATCAA CATACCAAAG CTATCGCTCA | 480 |
| | AAGTGCGnCT GGTAAATTAA ACCGAATTCC ANGATTGTAG GAACCCNATT AATGGAAATA | 540 |
| | ACGG | 544 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 861: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 651 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861:

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| | AATTTAAAAT ACATTTATGC TTTACCCATT CGAAAATACC TTAATCATTT TCATTTATAG | 120 |
|-----------|--|------|
| | CATTGTTTGA TTGAAGGATA AAAAGTTGTT GTTTACAATA AAAATAATGA GTATCTGAAA | 180 |
| <i>5</i> | TGAGGGATTC ANTATGACAC ATGTGGAAGT AGTAGCGACT ATCGCGCCAC AATTATCTAT | 240 |
| | CGAAGAAACT TTAATTCANA ANATTAATCA TCGTATTGAT GCAATAGACG TATTAGAATT | 300 |
| | ACGAATTGAT CAAATTGAAA ATGTCACAGT TGATCAAGTG GCAGAAmTGA TTACAAAGCT | 360 |
| 10 | GAAGGTTATG CAAGATTCAT TCAAATTATT AGTTACGTAT CGTACAAAGT TACAAGGTGG | 420 |
| in . | CTATGGGCAA TTTACAAATG ACTCGTATCT TAATTTAATA TCAGACTTAG CAAATATCAA | 480 |
| 15 | TGGCATAGAT ATGATTGATA TAGAATGGCA AGCAGATATT GACATTGAAA AACATCAACG | 540 |
| | AATCATTACA CATTTGCAAC AGTATAATAA AGAGGTGGTT ATATCACATC ATAATLTCGA | 600 |
| | AAGTACGCCT CCATTAGATG AATTGCAATT TATATTTTTN NAAATGCAAA A | 651 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 862: | - |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 401 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862: | |
| 30 | TGTGAGTGGT AATGACACAC AAGCAGATTT AATAGGTTAT AGTTTTAAGT TTGACGGTGC | - 60 |
| | GATTTCAAGG CAAGAGGCTT CTAAAGATGT ACATGCAGTT ATATTATCGA ATAAAACACT | 120 |
| 35 | ATATTTATTA GATGTATTAC AAAAATTACC GATAGATAAA ATGAATTCAT TGAATATCCA | 180 |
| | TCAAGAAATT ATTGATGAAA TGTCAGATAT CATTTTAATG TTATATCGTG AATATGCAGG | 240 |
| | TATGTTTTTT AAAAGTCAGA AACTAATCAA CCAATTAAAA AGATTGGAmC AATAACATAA | 300 |
| 10 | AATAATAAAa GGTATTCAAG TAGCCACATA GATGTGTTTA TTTGAATACC TTTTKGAATA | 360 |
| *. | GaaAAGaGAT ACTGGCAATT TTACTAACCA GLATCTCTTT T | 401 |
| | (2) INFORMATION FOR SEQ ID NO: 863: | |
| 15 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 308 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863:

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| | ACAAAGTAAT CAATATGTAA TATAAAATAC ACTGGTACTC AATATATAAT GATGATAAAA | 120 |
|-------------|--|------|
| | TTAATTTTAA TTAGATAGAG TTGCTTTGTG TTTTTAACGC NGATGCTACT ACTTATCTTA | 180 |
| 5 | ACAGTTGATT AAGTAAATCA TTTAACAGCG AGATTATnCA ACCAGGGGGA TGACTTAATG | 240 |
| | AATTTATTCA GACACCAAAA TTTAGTATCA GAAATTTAAT GTCGGTATTT TTTCAGCTTT | 300 |
| 10 | AATGCCAC | 308 |
| ,,, | (2) INFORMATION FOR SEQ ID NO: 864: | * . |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1827 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 864: | |
| | TTCTACATCT TAAACGATGA CCTAACTATG ACGTTAATCT GGAAAGATGG GGAGTTGCTA | 60 |
| | GTATGATGTT GAAATTTAAA GCTTGGGATA AAGATAAAAA AGTTATGAGT ATTATTGACG | 120 |
| 25 | AAATCGATTT TAATAGTGGG TACATTTTGA TTTCAACAGG TTATAAAAGT TTCAATGAAG | 180 |
| | TAAAACTATT ACAATACACA GGATTTAAAG ATGTGCACGG TGTGGAGATT TATGAAGGGG | 240 |
| 30 | ATATTGTTCA AGATTGTTAT TCGAGAGAG TAAGTTTTAT CGAGTTTAAA GAAGGAGCCT | 300 |
| | TTTATATAAC TTTTAGCAAT GTAACTGAAT TACTAAGTGA AAATGACGAT ATTATTGAAA | 360 |
| ** <u>*</u> | TTGTTGGAAA TATTTTTGAA AATGAGATGC TATTGGAGGT TATGAGATGA CGTTCACCTT | 420 |
| 35 | ATCAGATGAA CAATATAAAA ATCTTTGTAC TAACTCTAAC AAGTTATTAG ATAAACTTCA | 480 |
| | CAAAGCATTA AAAGATCGTG AAGAGTACAA GAAGCAACGA GATGAGCTTA TTGGGGATAT | 540 |
| • | AGCGAAGTTA CGAGATTGTA ACAAAGAACT GGAGAAGAAA GCAAGCGCAT GGGATAGGTA | 600 |
| 10 | TTGCAAGAGC GTTGAAAAAG ATTTAATAAA CGAATTCGGT AACGATGATG AAAGAGTTAA | 660 |
| | ATTCGGAATG GAATTAAACA ATAAAATTTT TATGGAGGAT GACACAAATG AATAATCGCG | 720 |
| 15 | AAAAAATCGA ACAGTCCGTT ATTAGTGCTA GTGCGTATAA CGGTAATGAC ACAGAGGGGT | 780 |
| .5 | TGCTAAAAGA GATTGAGGAC GTGTATAAGA AAGCGCAAGC GTTTGATGAA ATACTTGAGG | 840 |
| | GAATGACAAA TGCTATTCAA CATTCAGTTA AAGAAGGTAT TGAACTTGAT GAAGCAGTAG | 900 |
| io | GGATTATGGC AGGTCAAGTT GTCTATAAAT ATGAGGAGGA ATAGGAAAAT GACTAACACA | 960 |
| | TTACAAGTAA AACTATTATC AAAAAATGCT AGAATGCCCG AACGAAATCA TAAGACGGAT | 1020 |
| | GCAGGTTATG ACATATTCTC AGCTGAAACT GTCGTACTCG AACCACAAGA AAAAGCAGTG | 1080 |

| | AGTGGTGTAA | GTAGTAAAAC | GTATTTAGTG | ATTGAAACAG | GCAAGATAGA | CGCGGGATAT | 1200 |
|----------|------------|------------|------------|------------|------------|------------|-------|
| 5 | CATGGCAATT | TAGGGATTAA | TATCAAGAAT | GATGAAGAAC | GTGATGGAAT | ACCCTTTTTA | 1260 |
| 3 | TATGATGATA | TAGACGCTGA | ATTAGAAGAT | GGATTAATAA | GCATTTTAGA | TATAAAAGGT | 1320 |
| | AACTATGTAC | AAGATGGAAG | AGGCATAAGA | AGAGTTTACC | AAATCAACAA | AGGCGATAAA | 1380 |
| 10 | CTAGCTCAAT | TGGTTATCGT | GCCTATATGG | ACACCGGAAC | TAAAGCAAGT | GGAGGAATTC | 1440 |
| | GAAAGTGTTT | CAGAACGTGG | AGCAAAAGGC | TTCGGAAGTA | GCGGAGTGTA | AAGACATCTT | 1500 |
| | AGATCGAGTT | AAGGAGGTTT | TGGGGAAGTG | ACGCAATACT | TAGTCACAAC | ATTCAAAGAT | 1560 |
| 15 | TCAACAGGAC | GACCACATGA | ACATATTACT | GTGGCTAGAG | ATAATCAGAC | GTTTACAGTT | 1620 |
| | ATTGAGGCAG | AGAGTAAAGA | AGAAGCTGAG | CGCAAATACG | AGGCACAAGT | TAAGATAAGG | 1680 |
| | AGAGATGGAG | ATGCCAAAGA | AAACGGTAAC | GATTGATGTA | GATGAAAACT | TATTAGTAGT | 1740 |
| 20 | AGCTAGTAAT | GAAATATCAG | AACTATTATA | TGAATATGAC | AGTGAGTTAA | TGTCAGCTGG | 1800_ |
| | ATGGAAGATG | GCGATAATAG | GGATATC | | | | 1827 |

(2) INFORMATION FOR SEQ ID NO: 865:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1379 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double

 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865:

| TCAATTGCAT | CATCATATGA | AATTCTaGGG | AATGGTGTCG | CAACTTTTTC | AAGTTTTGAT | 60 |
|------------|------------|------------|------------|------------|------------|-----|
| GTATCACGCT | CTAAAATTTT | CAACTCTAGT | TTACAATTTT | CTAAAACTGA | TTTTACAACA | 120 |
| TGTGTTACAT | ATTGTTCTTG | AATTTCTAAA | CTTTCAGCAT | GATTTGTGAA | AGCCATTTCT | 180 |
| CCTTCAATCA | TCCAGAACTC | GATCAAGTGT | CTACGTGTTT | yTGATTTTTC | AGCTCTGAAA | 240 |
| GTTGGACCAA | ATGAAAATAC | TTTTCCGTGT | GCCATTGCTG | CAGCTTCTAA | GTATAACTGA | 300 |
| CCACTTTGAG | ATAAAAACGC | ATCTTGATCA | AAGTATTTAG | TATGGAATAA | TTCACTTGTA | 360 |
| CCTTCTGGCG | CACTTGCTGT | CAAAATTGGT | GGATCAACCT | TTGTAAATCC | ATCTTTGTTG | 420 |
| AAAAATTCAT | ACGTTGCACG | AATAACTTCA | TTTCTAATTT | TCATTACAGC | ATGTTGTTTT | 480 |
| TTAGAACGTA | ACCATAAATG | ACGGTGATCC | ATTAAGAATT | CTGTACCATG | ATTTTTAGGT | 540 |
| GTAATCGGAT | AGTCATGCGC | TTCTGAAATA | ACTTCAATTG | ATTTCACTTG | CATTTCGTAT | 600 |
| CCTAAGTCAG | AACGATTATC | TTCTGTAATT | GTGCCTGTAA | CGTATAGAGA | TGATTCTTGA | 660 |

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| | TGCATAAAGC CTGTTCCATC ACGTAATTGT AAAAAGGCGA TTTTACCACT TGAACGTTTA | 780 |
|------------|---|------|
| • | TTTGTTAACC AAGCACCAAT TGTAACGTCT TGGTTTAAAT GATCTTTCGC TTGTTTAATC | 840 |
| 5 | GTTGTTTTCA TAACCATTCT CCTATTTATT TTTTCGKTAT ACAATACTCA TTCATTTTAA | 900 |
| | CAAAATCCGC TITCAAGTTC TAGAACTAGA CTAAAAGATA ACGLGTAAAT GGTAATGATT | 960 |
| 1Ò | TACGCACAGA TTTGAACATT AATTTATATT AAGACAATAC AATCATCAGT TTCAGACAAA | 1020 |
| | ATATATAATA AAGCCTCAAT ATTATTAGTA TGAAGGTCGT TTTTTGTnCT AACATTCAAG | 1080 |
| | TTTAATTATA AAACTCAAAT TTTGACGACC AAACAAAAAT TCTTGTAACA GAACATAGCA | 1140 |
| 15 | CATGTCATGT CACAAGAATT TTACTTTGTA TTTCACTTTT TCTTTTTTTG AATTTGTCTT | 1200 |
| | AATAATTTTC CAAACTGTTG AATGTCGCCT TTTTTCTGAC GATAATTTTC AAGTGTTTGT | 1260 |
| | TCAAAAAAGT TTTTATAATT ACTGTTTATG AGTCGATCAT CAAATGAAAC TATTATGCCG | 1320 |
| 20 | CGATCATTTT CATTTCTAAT TAATCTTCCA AGTCCTTnGT CTANAACGTG TAACTGCAT | 1379 |
| | (2) INFORMATION FOR SEQ ID NO: 866: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 450 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 3 0 | * | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866: | |
| | TTACAACGAA TAGTTCACCG TTCGAGTCTA ATCTATGTAA TGCTTGCTCG AATATACGAT | 60 |
| 35 | GCACGGTTTC TTTCCCTGCT CTTATTGGTG GATTGGTTAA AATAAAATCA AAACTTTTGT | 120 |
| | CTTCCACAGC AGACAAAGCA TCACTTTCCT TTACGATCAC ATTATCAATA CCATTTAATT | 180 |
| | TTTTGTTTTT TTCAACTAAG GCTAGCGCTC TGTGATTAAC ATCTAGCATT GTAATTGAAT | 240 |
| 40 | GATGTGGTGA TACTTTAGCA ATCATCAAAC CAATTGGTCC GTAACCACAA CCAACATCGG | 300 |
| | CAATTCGCTT ACTTGGACCA GGTGGATGCG CTTTTAAAAA AGTTTGAACA AGAACATCTG | 360 |
| 45 | AACCATAATC TACTTTAECE TTCGAAAACA CTCCETATCA GTTATTAAAT CAATTTTATG | 420 |
| •• | ANGGTTNTAA TTGGATATTG AGTACGTTGT | 450 |
| | (2) INFORMATION FOR SEQ ID NO: 867: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| - | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867: | (1) |
|-------|---|-----|
| | AATGTTAACA ATATAGCACC AATTAACCCC GACATGATAA TAACGTGTAA TGTTTTATTT | 60 |
| 5 | CCTATTAATT GTCTCGCAAT ATGAGGTGCA ATTAATCCTA AAAAGCTAAT ACCACCGACA | 120 |
| | ACTGAAATTG CGGATCCTGC TAATATTACT GCTAAAATTA ACAATAGCAT TTTAATAGTT | 180 |
| 10 | TTAACTTTTA AACCGAGTGC GGTTGCAACA GCATCACCTA GATTCAATAC ATCTAATTGA | 240 |
| | TAACTCCATA AAATGATGAT GGATCGTTAT TAAAACCAGG GAATATAGAT AATATCCGCA | 300 |
| | TATCAGGCCA TATAGCTACC TGTCACCAAC AGGTTTnTGC TCCAnGGTTC TnTAATAAGA | 360 |
| 15 | CGCACACGCG ACAATGCGCT TGCTACCATT AGGCAGCTTG | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 868: | |
| | (i) SEQUENCE CHARACTERISTICS: | • |
| 20 | (A) LENGTH: 1132 base pairs | |
| · · · | (B) TYPE: nucleic_acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868: | |
| | AATCCHTHAA GTGCCATAAC ATCATCTCCT AACATCTTTA TTATACATCA ACATTTTATA | 60 |
| 30 | AAAATAACnT CTTATGATAA AAATGAAAAT ACTAATTTTA ATGAGAGCGT CTTAAGCCGC | 120 |
| • | AATTGATAAA ACATATGCTA CAATATTTTT AAACACTATA CAGGAGGTAC TCTATGACAA | 180 |
| | AATATACATT TAAACCTAAA GATTTCAAAG CGTTCAACGT AGAAGGCTTA GACGCACGAA | 240 |
| 35 | TGGAAGCTTT AAACGAATAC ATACGACCAC AACTCCGTGA ATTAGGAGAA TATTTTAGTG | 300 |
| | ACTICITIAC AAGTCAAACT GGTGAAACAT TITATCCTCA CGTAGCAAAG CATGCTAGAA | 360 |
| | GAAGTGTGAA TCCTCCTAAA GATACATGGG TTGCTTTTGC AACAAACAAA AGAGGCTATA | 420 |
| 40 | AAATGTTACC TCATTTCCAA ATTGGTATGT TTGAAGATCA ACTGTTTGTT ATGTTTGGAA | 480 |
| | TCATGCATGA AGCAAAAGAT AAAGCAACaC GTGCAAAAGT TTTTGAAAGA AAATTTAAAG | 540 |
| 45 | CTATTCAACA ATTACCTGAT GATTATCGTG TTTGCTTAGA TCATATGAAA CCTGATAAAC | 600 |
| | CATTTATTAA AGATTTAACG GATGATGATT TAATAGAAGC GATACAAAGA GCCATCAATG | 660 |
| | TGAAAAAAGG TGAATTCTTT ATAGCGCGTG CAATCACACC ACAAGATAAA AGATTAAAAA | 720 |
| 50 | GTGACAAAGC ATTTATTGCA TTTTTAGAAG AAACCTTCGA TCAGTTCTTA CCATTTTATT | 780 |

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900

CTGCATAAAT AACTTTGTTT AAATAATAGA GCACTTAATC ACATCCATGA TTTCGTGCCC

TTETTTCTTA ATATTAAATC GAACGTECAA CATAATAATT CATACTTTTA AAAAAATTAA

| | GGTGAGTCAA AATGAATAAT AAACGACATT CAACAAATGA ACAATTAAGT TTAGACGAAA | 1020 |
|----|---|-------|
| | TAAACAATAC AATTAAATTC GATCATCGCA GTTCAAATAA ACAGAAATTT TTATCATTTC | 1080 |
| 5 | TTGGACCTGG GTTATTAGTC GCTGTTGGTT ACATGGATCC CGGAAACTGG AT | 1132 |
| | (2) INFORMATION FOR SEQ ID NO: 869: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 418 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869: | • |
| | CTCAATGTAT TGACTGTGAT TTGGAGTGTA TAATGCTACT GTTTTGTCTA TAGCCATCGC | - 60 |
| 20 | ATCAAATATT ATATTTGAGT AATCAGTGAT AACGACATCA GACATTAGAA TTAAGTCTTG | 120 |
| | AGCACTAAGA TACTTTGGTG CAACAAGCGC CTCTTCTGGT AAGATCGCTT CATCAACACC | 180 |
| | CTGAACCACA ACATGATAGG CTTTGAATAA AGCATCTGAT AGTGGTAATT GTTGCGCACT | 240 |
| 25 | CACTAATCCA ATAGGTGCGT ATAATAAAAC TGGTTTTTGA TCATTTATTT TAAACGATTT | 300 |
| | CTTATACTGT TGTTGAGTAG TACTTTCGTT ACTCTTTTGT AGTAAATATT GGTGTTTAGG | 360 |
| 30 | ATTACCATAA GCCAATACAT TGCTTGGTGA CTAGGAAAAG nCGTTTGATA AAAGGGCT | 418 |
| | (2) INFORMATION FOR SEQ ID NO: 870: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 587 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| ю | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870: | • |
| | GAGTNTGTTA CAGTAATTGA TTTTATTGGT AATTNTAAGA CAAATTATTT AATTCCGATT | 60 |
| | GCGCTTTCTG GGGATCAATC GCAANATAAA GATAATTATA AGAAGTTTTT AACGAATAAC | 120 |
| 5 | GATTCGATTA ATGGAGTATC TACAATTAAT TTTGAAGAAG TTGCTAAAAA ACAGATTTAC | 180 |
| | AATTCATTGG ATGCAGTATC ATTAAATCAA AATAAATTAA TATTAAAAGC TTATGAAGAA | 240 |
| :0 | GTTGAAAATA GATTGGGACA CATGCCGTTA CTAATGGATT TCATACAACA ACATTCTATA | 300 |
| _ | GATCCAAGCG TTATATTTTC TAAATTTAGT AATTATTACG AGTTCTTAGT GAGATATAAA | - 360 |
| | AAAATAGATA CATTATTGAC GGAAAATGAA TCTAAAAATC TGGTTTTCTT TTCAAGGCAA | 420 |

| | TTAACATATG ATGAATTAAA AAATAAAATG TTGAACGAAG TTAAGGATAT AACAGAAGAT | 540 |
|---------------|---|------|
| | GATATAGATA CTTCATTAAG AATTTTAGAT TTTTCATTTT ACAACGC | 587 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 871: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 971 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEO ID NO: 871: | • |
| 15 | CTACTAAACC AGGTAATCGG TAGAATCCAA GCAGGAATAA ATAAATTAAT GCNACACCAA | 60 . |
| | TARACGATGC ARACACAGTM TTATCTARTG CATCTTGACC ARATTGGGCA CCTACTGAGT | 120 |
| 20 | TTGAATAAAT TTCTTTCAAG TCAACTGGTA AAGAACCTGC ATTTAACAAT kCGGCGATTT | 180 |
| | GTTTTGCTTT TTTAACGCCT TCTTGTCCTT TAAATCCACC CGAGATTTCT ACGCTATCAG | 240 |
| | AATTGATTGG TTGATCAACA CTTGCTGCAG AAATAAATTT AGGGTTTTTC TTTTGTGCTT | 300 |
| 25 | CTTTTTTATA GCTGTCACCT TTTTTGAAAT CTAACCAAAC AACCATGACA TTATCACGTT | 360 |
| | TCTTAGAGAT TTCTTCCGTT ACTTTTTAA ATTTGTTTTT GTCTTTTACT TTAAAAGTAA | 420 |
| | CTGTAGGCTG GTTTGTTTCC tGtTTAAATT CTTGtTTGGC AGATCCCTGT TTaATATCAG | 480 |
| 30 | AACCGCTTAA TITLACTTTA TCTTCTGCAT CGCGAATTGT TAAATTAGCT TGAGAAGATA | 540 |
| | AAATTTTACG TGCTTCATTC TGGTCTGTTA CACCAGCAAG TTGTACTCTA ATTCTATTAG | 600 |
| | GTTCTTCAAC TTGAATTTTA GGTTCCGAAA CACCTAAAAC GTTAACACGA TTTTCTAATG | 660 |
| 35 | TTTGCGCTGT TGATTGTAAG GCTTTTTTAT CTATTTTGTC GCCTTTATTT AAAGGATCGA | 720 |
| | CTTGATAAAG CACCTCAAAT CCACCTTGCA AATCAAGTCC TAAATTGmCA TTCTTTATAA | 780 |
| 40 | CACTITTATA AGTIGCAGCC ATTCCGGCAA ACAACAATAC GACTAAAAGC AAGAACGCAA | 840 |
| | TTATTCTACT ACTTTTCTTC ACATGAACAC CTCATTATTT ACGTATGTAT TTAGAATACT | 900 |
| | TGAATACTAT TTTATAACGC AAGTGAAATC TTTCTTACAA AATTTATTAG CCTTATACAT | 960 |
| 45 | ATTAACATAC T | 971 |
| | (2) INFORMATION FOR SEQ ID NO: 872: | |
| 50 · . | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 636 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (b) 1010000 | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872: | | | | | | |
|-----|---|-----|--|--|--|--|--|
| | CTGGTTAACA ACATCTGGTT CGGCATCTCC TTAGCTTCCA CTAAATCTTG GATGTCTTGG | 60 | | | | | |
| 5 | nnATCTTGCG CAAGTnGTGC TTTGGCTTGT TCAATTECTY CTTTAGTCAT CGCATTGTTA | 120 | | | | | |
| | ATGCCGTTAT GACCTTGTTG AAGTATTTGA TTAATACGAT CTTTAAGTGC TTGTTTTTCC | 180 | | | | | |
| 10 | TTATCTGTTA GATTTGGATT TCGATCAATT TCGTCAATTA ATGCTTGAAC TTGCTTATCA | 240 | | | | | |
| ,,, | ACGTCTTTAT TGGCATCAAT TTTTGCTTTT GGTATTTCAT TGGCATGCAC TTGTTCAATC | 300 | | | | | |
| | GCGTGGTTGC CTGCTGTTTG AACTTGAGAT ACAGCCTGAT TACTTGTTGC TTTATTAATG | 360 | | | | | |
| 15 | TTGTTGATGA TGCTGTTTGC CAATTCTTCT GCTTTATTTT TCGCAATAAG CTTGTCTTGA | 420 | | | | | |
| | TCCGTCGCAT TTGAAGCTTC GATTTCTTTT AGCTTATTAG CTAAAGCTTG ATTAATAGAT | 480 | | | | | |
| ٠ | TGAATTGCCT TGTCTTTAGC ATCTTGTAGT CGTTGATCAC CATTAAGATT ATGGATTGCA | 540 | | | | | |
| 20 | TCATTGACLG CTTGGATTGC GCCATTGATA TCATTCACAT tTGTGTATCA CTATTTAGCA | 600 | | | | | |
| | ATGTATTTGC TAGACGTTgG CATCATCGAA GTTTGT | 636 | | | | | |
| | (2) INFORMATION FOR SEQ ID NO: 873: | | | | | | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 659 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | | | | |
| | | | | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873: | | | | | | |
| 35 | CTCTGAATGC ATTCATTAAA CGCTGGGTCT CTTTATATGA AACGTATTTG TCATTTTTAG | 60 | | | | | |
| | AACTCAATCC GTAAAAATTG TCAACTTTCT TTTTAATATT ATCGTAATCA ATGGTTACAT | 120 | | | | | |
| | TACTTAAATC AATATCTAAA TCTATATTTT CTGCATCTTC TTTAAAGCCC GCTATACTGA | 180 | | | | | |
| 40 | AAAAGCCTTC AATCGGCTGA TCAATCATTT CAATATATTT TAAAGCTGTG ATTGAACCTA | 240 | | | | | |
| | AACCATGTGT TACAAAATAT GTATCCTTTT TGCGTACATT AATTTGTTTC GTCATAGCTT | 300 | | | | | |
| 45 | CAATCCACTG ATCCACTGTC TTCGCTECAG GGGATTCAAA ATTAAATAAT GTTACGTCAT | 360 | | | | | |
| | ATCCTTCTAA AGTTAAGTTA TGCTCCAACC ACTGATACCA ATGATTTCTA CTATTTCCAT | 420 | | | | | |
| | GCATAGAATG TACAATALTA CATCTGTCAT CTCATTCTCT CCTTTCAACT TACTACTTCT | 480 | | | | | |

TTTCTATTTT TAAAAAAATG ACTGATTACC TATAATTGTA AAATAAAAAC ACCTTAATTA

GAAATGTTAT ATCGCAAAGT GACATTTCTA ATTAAAGTGT ATTGTCATCA TTTCAATATC

ATTCAAAAAC AGCTAAACCT TTGTCTCTGC TTCAATTTCA CAAAAATAAT TCCCGCTGA

540

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| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-------|
| - | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874: | |
| 10 | AAAATAAAAT CCATTTTAGT ATTCGTAGAA AATGAGAGCC CCCTTTACCA CAATATGTAA | . 60, |
| | ATGTATATTG TGAAAAGGGG GCTTTTATTT ATGACATAGT TGTTCAACTC ATACATTCAG | 120 |
| 15 | TTGATAATGC AGTGCGTTAT GCAGCTATCC ACTTCATATG TATGGCGCAT ACTTGATATA | 180 |
| | TGAATATCAT CAAGATTTTA AAAGTATCGC TAATTTTAAA GTCTTAAAAC GCAGATTAAT | 240 |
| | GGTCATGATG TGTTANTGCG TTTTGGTTTT TAGAGCCACG TAATTCCCAN GGACATATAG | 300 |
| 20 | GAGGAACCAT TCCAC | 315 |
| | (2) INFORMATION FOR SEQ ID NO: 875: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 482 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ٠. |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875: | |
| | TACACGACCT TGTAACTCAG CTGCTTTATA AGCTAGGGCG ATGTTATCAA AGTTGGATGT | 60 |
| 35 | ACTITGAGCT TGGCATTTCG TTAATACTTT TAACGAAGGA TTTAATATAT GTCTGATACG | 120 |
| 33 | TATATATTGA TTATATTCAA TTCTTaATTL GGATAAGATT GCTGATAATT TGAAGCAATC | 180 |
| | GGAGCTAAAT GGATCGAAAA ATGAATAAAT TTCGATTTTA CTTACAGGTG ATAGATTGAT | 240 |
| 40 | ATCTTCACGA CTCTTATTTT CCATTAWTCG TAATTCTCCA GCCATGTTTA TTCACCTACA | 300 |
| | ATTAATTTTA GGAATTCACC ATATGATTAG CAGTTAATCT TAAGCGCTCA AATAAATAAT | 3,60 |
| | CTCCAACACC TTGTGGAAAC CAGCGCGATT AATTGCTGTC TGCATATTTT CTAGCCATGC | 420 |
| 45 | ATCTCTTCA AATTCAGTGA TTGTAAAATC TATATGTCTT TTTCTTAGCA TAGGATGTCC | 480 |
| | GT | 482 |
| | (2) INFORMATION FOR SEQ ID NO: 876: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 670 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876: | |
|----|---|-----|
| 5 | ATGCAATTGA ATTCTTAAAA GCAGAAGGCT TTGATGATAT TGAATGGGGC GAAGATTTTG | 60 |
| | GTGCGCCACA TGAAACAGCC ATTGCTAATC ATTATGATTT ACCGGTGTTT ATTACTAATT | 120 |
| 10 | ATCCAACTAA AATTAAGCCT TTCTATATGC AACCAAATCC TGAAAATGAA GAAACTGTAT | 180 |
| | TATGTGCAGA CTTAATTGCA CCTGAAGGAT ACGGTGAAAT TATTGGTGGA TCTGAACGTG | 240 |
| | TGGATGACTT AGAATTGTTA GAACAACGCG TTAAAGAACA TGGATTAGAC GAAGAAGCAT | 300 |
| 15 | ATAGTTACTA CTTAGACTTA CGTCGTTATG GTAGTGTGCC ACACTGTGGA TTTGGTTTAG | 360 |
| | GTTTAGAGCG TACAGTAGCA TGGATTTCTG GTGTTGAACA CGTTCGTGAA ACAGCGCCAT | 420 |
| | TCCCAAGATT ATTAAACCGT TTATATCCAT AAGTTTTAGG GTCGTTACTT AAAATATATA | 480 |
| 20 | TTATGATAAT AAAAAGAATC GTCCAGCCTA TATTAATAGC TGGGCGATTT ATTCTTGGAA | 540 |
| | AATGAAGATT GATAACGGCT TATATTAATC ATGAACAAAC TTTTGTTTAG TAACTATATT | 600 |
| 25 | TGGAAAATAA ATAGTTCATC TGATTATCCA TAAAGTTCAT TGTTAAAATC TAGTGTTAAA | 660 |
| 25 | AAATACTGTT | 670 |
| | (2) INFORMATION FOR SEQ ID NO: 877: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1258 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| , | (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877: | |
| | TGCAAAGTAA ACTGGATGGC TnTCTTGCCG CCAAGGATCT GATGGCGCAG GGGATCAAGA | 60 |
| 40 | TCTGATCAAG AGACAGATCC TAACCTCTCA TTTCCGATAA GTTTAGTATG TATTATAGGT | 120 |
| | GATGATTNTC TTGTTTTCAA CCTTATACAC AATATTTTTG ANATTTATAT TATATTCATA | 180 |
| 45 | TAAGGAAGGC GATTAATTAC GATTCATCAT TATATCTCTA CGTGTTAATT TATTAACCLA | 240 |
| | TACTATATT ATCAACACAA CAGTTTTCC TTTCATTTTC AAACATAACA GAAAAAGCCT | 300 |
| | GAGACATACT TAGTCCCAGA CTGTTCTATA ATTAATTAAA GATATAACAA GGTTAATCAT | 360 |
| 50 | TCAAAGCTAA CATCACATTT ATTCACTGTA ATTTTTCATA AAGAATAATA ATGACTGTAA | 420 |
| | TTCTATACCT AAGTCAATTT GATGTACTTG CACATCTGAA GGCGTATTAA TTCTACCAGG | 480 |

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AGTGAAGTTT AAAATACCTT TCACACCAGC TTGGACGAGT TCATCTGCAA CTTTCTGTGC

| 20 | AATGTAATAA | TTACGCTTGT | TTCATAAGTT | AATAAAATTT | GAGAAGACGA | AGGTGAAG | <u> </u> | 1258 |
|-----|------------|------------|------------|------------|------------|------------|----------|-------------|
| = = | | | | | | AATGGTTATT | | 1200 |
| | GTTAGATTAT | TAAAArACAA | ATAATTGaTT | ACAATGAATA | CCTAAATATT | ATACATTAWT | | 1140 |
| 15 | TTTCCTCCTT | CGTGTTTGAA | TGAATTATAT | CTATGTATTC | AAACGAGTTA | GAGCGTAATT | . : | 1080 |
| | ATATAACGGC | AAACGTTTTA | AAGTTGCTCG | AGGAATTTTA | ACTTGGTCAC | TCATTCGCTA | : | 1020 |
| 10 | AATCGCTTTT | GAATTTACAC | GATCTATACC | TTTAGATTTT | AATGAACTGA | CAAATCTATA | | 960 |
| | TTCGCCAAAA | TATGAAAAGT | CACGACGAAT | TGTtGCCGAG | TCAATTTGTa | ACGCATCGCT | | 900 |
| | TTCAGATTTA | AAGAAATCCA | ATAAACTATC | TATATTATAT | CCGTaCCCTT | TTTTACCTAA | | 840 |
| 5 | AGCTTTCCCT | AGGTTCCCAA | CTCCGACAAT | TGCGATTTTG | ATCATGTCAC | TCTCGCTTAG | | 780 |
| | TACGTCAAAC | GCTTCTGTAA | TCGTCATATC | GTCATGTATT | GAAAAGTTAT | ATGTGAGCAA | | 72 0 |
| | TAATTCATCG | TTATCTTTAA | CAATAACGTT | CCCTATTTTC | TGGCCAATAA | CATCTTCTTT | | 660 |

(2) INFORMATION FOR SEQ ID NO: 878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 546 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878:

| AAACAATCCC CnC | CAAAGTA ATTCCACCAC | TAATTGTAAA | TAACTTTGGA | AAGGATGTTG | 60 |
|----------------|--------------------|------------|------------|------------|-----|
| TTTGTnATTC CCA | TGGACAC ATGCCATCTn | ATTTAAGTTT | TATACTCTAT | TTTTCTGATG | 120 |
| TCTTGATTAA TTG | CAAGCGG TCTTGCGAGC | CTTGTTCAAG | CTCATATTCT | TTATCTACTT | 180 |
| GCTTACCGTT TTC | TYTTATT AATCTTACGG | TTGCGGTAAT | CTTATCACCA | TGTTTTTCAG | 240 |
| CATCTATAAT TTG | TGGTGAA CTAATCATCA | TTAAACTTCC | TTTAGATACA | CGCTTCTTTA | 300 |
| CATCATCATA AAA | AGATGAT CCTTTTTTA | TATATGATGA | TACAAAATCA | AAATCCGACT | 360 |
| GATTAAACGC AGC | ATTATTC GCTAAAGAAT | ATCCAGCAAA | GAATTCTATC | AATTIGTTCT | 420 |
| TCAAGCTGTT TTC | TTCTTTT TCTTTCTTT | CAACATAGTC | TTCGATATCT | TCACTGTCAA | 480 |
| AATTCAAAGT TAT | CTCTGTA TTGTATTTT | AATCGCTAAG | CTTTAATCGT | CTTCGTCTGT | 540 |
| GATGTA | | | | | 546 |

(2) INFORMATION FOR SEQ ID NO: 879:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 870 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

| 5 | \cdot , \cdot | |
|----|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879: | |
| | TTTATGAATT TTTTATGTAA CATTAAATAT TCTTCTGGCA ATCTTCCLAC TATKTCTKTT | 6 |
| 10 | ATATATCCTT CTTCTCCTTC TTTAAATACT AAACCTGTGG GAGTTAGTGT GTTATACCTA | 120 |
| | ATTTCTATCT CATTCAAATG ATCATTCAAA AGGTCAAAAA ATTCTCTATT AAAATAACCC | 186 |
| | CATTTCCCAT TTTGTAATAA ATATTTCTTT CCATCTTCCA TTTCAACTTC TGCATGTAGT | 24 |
| 15 | ATCGTTTTTA GTAGCATATT ATTTGAATGC CCCAAATTAT CKATCACKTC AATTCTGACA | 300 |
| | TCATTTATAG AATTAACGTC ATATTTTAAT AAGTAATCTC CTATTTCAGT GATGTAATCA | 36 |
| | ACTTCAGGAT CAGTCGCATC AAATGTCTCT AATGTATTAT TTTTAAAAGA ATTTATATAT | 42 |
| 20 | ATATTGACGT CGAGCATATC ATCTAACAAG AGTATCATAT TACTTAGTTC TAAAAATCTT | 48 |
| | GATATATCTA TAGATATATT TTCTGTAGTT GAAGAATTCG ATAGTTTTTT TAGCAATAAA | 54 |
| 05 | GTATCTAATA CTTCTATTTT ATTCAAGTCT TTTAAAGTTA CTATTCTAGG AAATTCACTA | 60 |
| 25 | ATTTTTGAG GAAGATTAAT AATAGCGTTT ATTTCTTTGA TTATCACACT AATTTTATCT | 66 |
| | ATGAATTGCT GCTTTCTATT CGGLACACGC AATGAAATAC TTGTACCACA AGTCCATTGL | 72 |
| 30 | TTTTCCaAAA ATTTGAGGAT TCTGTGGATG tCCTTGGACT GGATATATAA GATTCTGAAG | 78 |
| | GTCTAACGTA ATCTACACTA TTCCTTCTAT AATTAACAAT CTCTTTAAGC CTGTTTTGTT | 84 |
| | GAAAAAATT AACATTTTA nTAACTAnGG | 87 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 880: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid | |
| 40 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880: | |
| 45 | GGTTTACATC TTTATCAACT GTAATTTCAT TGACATCTTC ATTCATATTT AAAACACCAT | 6 |
| | TARATGTCCC TGARTATTCA CTTGTTTGTT TARCTGTGGC AGTGACTTGT CGTTACCATA | 12 |
| 50 | TGTCATCATA TATTGTGCAA ATGTTAAAGT CCCCATTGAG TTGACCGACA AAGTTGAATT | 18 |
| -• | TATCGAATTG TATTCAGATT GTAAACTTAG CAGACATTTT TAACCACGAG CATTCTTATC | 24 |
| | CAAATAGNCC TTGTCTGTTA TTTTCAAGTC AATTTTCACA ATAGGATCAC TGCATCTTTT | 30 |
| | | |

| | ACCCTCTTTT TCTGCTnCTC ACATAACTTT CAGATGGACT | 400 |
|-----------|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 881: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881: | |
| . 15 | AAGATATTGC GAAAAGAAGT GACAGTAACA GAGGAATTTC AAAATTTATT CAACCATATA | 60 |
| | TTGAAAATTG ATGAAATGGT GCATGCAAAT GAAGCGCGTA TTGCGTATGA AGCAGACATG | 120 |
| | CGAAAACCTT TATATAGTAA ACGCATTTAT CAAAATTTAA CATTAGACTC TATTGTTTTT | 180 |
| 20 | AGAAATACAT TGAGATATAC AGCGATTATG ATGATAGCGG ATATTTATTG CGTTAATGTT | 240 |
| | TGATTTTGAA AAAGCATCCT GGATCCCGTT ATCTGCACAT CCANTATTCC TAGGGCCATC | 300 |
| | Ancetatace atgreaters agagagetat egn | 333 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 882: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 617 base pairs (B) TYPE: nucleic acid | |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882: | |
| | ATTGAAAGAA AAACTGACGT ACTTATCCGA TGATAAAATG AAAGAAGTAG ATAATGCACT | 60 |
| | AATGATTAGT TTAGGGCTGA ATGCAGTAGC TCACCAGAAA AATTAGGCGT CTATTATATG | 120 |
| 40 | TATTTTTCAG AGATAAATAA AATATTGATA TAAAAGACAA TAACTTTATA ATAATTATAA | 180 |
| | CTATTTCTAA ATTCTGTACG AAGAATTTTC TTATAAACAA AGATTTTAGC AAATACCAGT | 240 |
| | TATGATATTC ATATTTTTA TTATAAAAGG ATGTCTTAAG TTTTTTAGGC TTTAGGTATT | 300 |
| 45 | CCATCCTAAA GTTTTTTTAG CTTAAAAGTA TCATCTACAG CAAAATTGCA AACGACAAAA | 360 |
| | TTGATAAGTG CAATTAAATA AATGTTAGTA AGTGAATCAT AATTATCCTT GCTTAAGCAT | 420 |
| | TTGCTTTGTA AGGGAAGTGA GGAGGCAACT AATCGTGGAA GAATTTAAGC AACATTATAA | 480 |
| 50 | GGGTTTAATT GATGAAAGTT TAACGTGCCA AGATAAAGTA GAATTGATAA AAAAGTGTGA | 540 |
| | GAAATACACT GACGAAGTGA TTCGTAAGGA CGTCTTGCCT GAAGACATTG TCGATATTCA | 600 |

(2) INFORMATION FOR SEQ ID NO: 883:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 583 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|------------|---|----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883: | |
| | GTTGTATTAA AATTTTTCAA TTTAACAACG AAACAATACG AAGAAAAACA TATTACTGAG | 6 |
| 15 | CCACTGGAAT TGACGAGCTT ATTAGGTANT ATTTCTCGTC TAGACAATGG TCATTTTGCA | 12 |
| | CATTTGCATG CTACTTTCGG TACTCAATCA TATGAAACTT TTAGCGGACA TCTCGCTAAA | 18 |
| | GCAATTGTTT CTGCAACTGC TGAAATCATT CTTACTGTAA CTGATTTGGA CATTCAACGT | 24 |
| 20 | TCATTCAAAG ATGCAGTCGG TTTAAATTTA CTTGATCCTC AATAGCACTT TACTTTTTAG | 30 |
| | TTGAATCAAA TITTATTACA AGTTATCATA AGTGCTTAAT CATAAATGCA TTCTCGTTTA | 36 |
| • | TTAATATACT TCAACGAGTT AAATTAAATT TTTAATTAGG AATTGAATGC GTTTATAACT | 42 |
| 25 | ATCACATTTG AATGAATAAC TTTTTCATTA GAAAGTAGTG TKTATTATTG ATGCAATCTC | 48 |
| | GaTACATCGC TAGAATTTAC TTTtaATTTT ATTTATCGTC TCCCTTnTTG AGACTAAAAT | 54 |
| 3 0 | TTTTCAATTT ATGACTTTAA ATTTGTTTTT AGCATATATA CCT | 58 |
| | (2) INFORMATION FOR SEQ ID NO: 884: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 524 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884: | |
| | GCAGAGGGCT TACGATAAAA AGAAAAATCT CGCTCGCCCG CTTCAGTCAA ACTCACAAAA | 6 |
| 45 | GCTAACGCAt GWYTGCTYCA TTCGTGCGAT ACACTTTTGA TACATCTACA CCAATACTTG | 12 |
| | ATATCGTTTC AATAATGCTA TCTCCAAATG CATCATTACC TAATTGTGTA ATCATALACG | 18 |
| | CTTGTTGTCC LAACTTTTGA ACTGTACAAG CTACATTGCA TGGCGCGCCA CCAATTTGCT | 24 |
| 50 | TCGTAAATGT TTGAACATCT TTTAAATTCG CATTTGTAAC ATTTGGAATA AAATCAATTA | 30 |
| | ACGCTTCTCC TATTGAAAAT AGACGTCTCA TTTATGTTCA TCCTTTAAAT CATATTTAGT | 36 |
| | AAATTGTAAA TATACTTGCC CTGATTCTGT TGATGTTTTA ATACCTAGTG CGTCTTCTGT | 42 |
| 55 | · | |

| | TGTATCAACA AAAATTTGTA ATTGCTTTAA TGGCGTGTCT A | ATA | | 524 |
|------|--|------------|------------|-------|
| | (2) INFORMATION FOR SEQ ID NO: 885: | | 0. | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs | | * | 100 |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 10 | • | |
| 10 | (D) TOPOLOGY: linear | | | |
| ···· | - X - S - W | * | * * | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88 | 5: | | ** |
| 15 | TTAATGATTT CTTCGTATGA TTCACCAACA ATTTGCGCTA A | AATATCATG | CGCAAGTACT | 60 |
| .* | TCACCTTCAA CCATAAATTC TATTTGCTCT ACTAAAAATT T | TACGTCATT | CATGCTATTC | 120 |
| | ATTTTTGGAA TTAACAAAGC ATATAAGTTT GTAAATTCTT T | TAAATACGC | AGCATCAGCT | 180 |
| 20 | TTTAAGTAAT GGCGTAATGC GTCACTCCTA TATCTCCGGA T | TAACATCTTC | TGAATAAAGT | 240 |
| | CATCCTCATA AATATCATAA TGATGGCTTG CAGCTGGGTA C | CAATTTTGTG | AAATTCCATG | 300 |
| • | TAAAAATCCT CCCTAAATAA AAAACTACTT CCAACATGAA G | AGTTGAGGC | ATGTGCAAAC | 360 |
| 25 | TAGCCCATCA CTCATAACAC TTCCACGTGG GACTACCAAC | | | (400) |
| | (2) INFORMATION FOR SEQ ID NO: 886: | | | ** |
| 30 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 857 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | | | • • • |
| | (D) TOPOLOGY: linear | | i | |
| 35 | * | | 0.0 | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88 | 86: | | |
| | AAGAATTTAA ACAAAATGAT ATTTGGAAAC ATTTTAAAGC | igtgaaaaat | AATCATGTTT | 60 |
| 40 | ATGACTTAGA GGAAGTGCCA TTCGGTATTA CAGCAAATGT | TGATGCTGAT | AAGGCAATGA | 120 |
| | CTCAATTATA TGATTTATTT TATAAGGATA AAAAATAGTG | agttgatatg | ATGATAAAAA | 180 |
| · X | ATAAAAAGAA ACTACTATTT TTATGTTTGT TAGTCATTTT | AATCGCAACT | GCTTATATTT | 240 |
| 45 | CGTTTGTAAC CGGTACAATT AAATTGTCAT TTAATGACCT | ATTTACAAAA | TTTACAACTG | 300 |
| | GTAGCAATGA AGCAGTGGAT TCAATCATTG ATTTGCGATT | GCCACGTATA | TTAATTGCAT | 360 |
| 50 | TGATGGTTGG CGCAATGTTA GCAGTTTCTG GAGCATTATT | ACAAGCAGCA | CTACAAAATC | 420 |
| | CTTTGGCAGG GCGAATATCA TTGGCGTTTC CTCAGGTGCA | CTTATAATGA | GAGCCTTTGt | 480 |
| • | ATGTTGTTLA TTCCACAATT GTACTTTTAC TTACCATTAT | TAAGTTTTAT | TGGAGGTTTA | 540 |

| | ATATTAGTAG GTGTTGCGTT ATTCGTATTA TTAAATGGTG TTTTAGAAAT TTTAACTCAA | 660 |
|----|---|-----|
| | AACCCTTTAA TGAAAATTCC TCAAGGCTTA ACAATGAAAA TATGGAGCGA CGTATACATA | 720 |
| 5 | TTAGCAGTAT CAGCATTATT GGGATTAATA TTAACATTAC TATTGTCCCC TAAATTGAAT | 780 |
| | TTACTAAATT TAGACGACAT ACAAGCGCGA ALATCGGTTT TAATATTGAT CGTTACAGAT | 840 |
| | GGTTAACAGG GTTATTA | 857 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 887: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 675 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887: | |
| | GATTTATTTT AATATTATTG TTAGAAGGAA TTTTTACAAA TTCAGCGAGT GCAATCGAAT | 60 |
| | ATTCAGACTT ACATCATAAA AGTAAGTTTG ATTCAAAGCG TCTAAGTAAT GCTAAGATGT | 120 |
| 25 | CATTCATCAA TCCAACTCAG CTTGAAAATA AAAACACAAA CGATAGACTG TTGAAGCATG | 180 |
| | ATTTGTTATT TCATGACATG TTCGTAAATG ATGATTGGAA AAAGGATTTT AAAGTTGAAT | 240 |
| 30 | TTGAAAATGA GGCACTTTCA AAGAAATTTA TAAATAAGGA TATCGATATA TTTGCTGGAA | 300 |
| | ATTATGGATA CGGATGTCAT GGGGGAGCAA CCAATAAAAC GCAATGTAGT TATGGTGGTG | 360 |
| | TTACTTTAAG TGACAATAAT AAATACGATG ATTATAAGAA TATACCTTGT AATTTATGGA | 420 |
| 35 | TTGACGGACA TCAAACAGAA ATAGAACTAA CTGCAGTAAA AACGAAAAAG AAAATTGTTA | 480 |
| | CTATTCAAGA ATTAGAGGTT CAATTAAGAA ATTATTTGAA TGAGAAGTAT AAGTTGTACG | 540 |
| | AACAAGGTGG CGACATTGTT AAAGGGTATG TTAAATATTA TAATGATGAT GAACAAAATG | 600 |
| 40 | TAGAATATGA TTTTTATAAT TTAAATGGTG AGTATGGTCG TGAGGTATTA AAAATGTATG | 660 |
| | Cngataatna aacna | 675 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 888: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 851 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888:

| | AATTCCTAAT | TAACAATGCC | TTCATTTAAA | AACCTTCTTC | CATCAATTTG | ATGTTTTCAT | 120 |
|-------------|---|---|--|---|--|---|---|
| | GATATTTAGG | TTTTCTCTTT | TCAAGATAAA | CCATTAAGTY | CTCAATAGAA | GGTGTAGTGA | 180 |
| , 5 | TATTCACTTT | AKGACCTAAA | ATTTCTTTAA | ATACTTGCGC | ATGTTCTGTT | AATCCTATAA | 240 |
| : | ATCCCGTACG | CTTATGTTCT | тсаталатал | GTAGAGATGC | TAATTCATCA | TCAAGGTCCT | 300 |
| | CAATAGCACC | ACTCACAACT | TGATATCTTT | GTAACAGTTG | TTCTTTTGAA | CCATTTAAGA | 360 |
| 10 | TAACTTCACC | GTCACTTAAG | TGAATGATAT | AATCAGCTAT | TTTTTCTAAA | TCTGAGATAA | 420 |
| | - TGTGTGTCGA | CATGAATATT | GTTTTATTTT | CATCAATTAA | TTCTTGCTGA | ATTATCTCCA | 480 |
| .÷ 15 | ATAGCTCATT | TCTAGCTAAG | GGATCGAGAC | CTGAAGTAGG | CTCATCAAAA | ATATACAATT | 540 |
| | CAGCATGATG | TGAAAATGCA | ACTGCTAGTG | ATAATTTCAT | TTTCATCCCA | GTCGAAAATG | 600 |
| * | TTTTTTTTGA | TTTATTGATT | GGTAAATCGA | ACTTTTCAAG | ATAAAATTCA | AATACTTGAT | .660 |
| 20 | GGTCCCATTT | ACGATAAAAA | GGGGCAATCA | TTTTTTCAAG | TTGCTTCGTA | GTCCATCTCT | 720 |
| , | CATTAAAATA | ATTTTCAGAG | таааспаасс | CAATTCTATT | CTTTAACTCT | ATCGGATTGA | 780 |
| -)(- | GAGCCATATC | CTCTTCTAAT | ACTCTAATAA | CACCAGTTTG | TGGGTGATAC | AAATCCATAA | 840 |
| 25 | TTAACCTAAT | n | | | | | 851 |
| | | | | | | | |
| | | ATION FOR S | EQ ID NO: 8 | 89: | | | |
| - | (2) INFORM | ATION FOR SI | - | | - () | | 1 () () () () () () () () () (|
| <i>30</i> . | (2) INFORM | EQUENCE CHAI (A) LENGTH: | RACTERISTIC 362 base p | S: airs | | | |
| 30 . | (2) INFORM | EQUENCE CHAI (A) LENGTH: (B) TYPE: no | RACTERISTIC 362 base p ucleic acid | S: airs | | | (X) (4) |
| <i>30</i> . | (2) INFORM | EQUENCE CHAI (A) LENGTH: | RACTERISTIC 362 base p ucleic acid DNESS: doub | S: airs | | | |
| | (2) INFORM | EQUENCE CHAI (A) LENGTH: (B) TYPE: no (C) STRANDE | RACTERISTIC 362 base p ucleic acid DNESS: doub | S: airs | | | 7 7 |
| <i>30</i> . | (2) INFORM | EQUENCE CHAI (A) LENGTH: (B) TYPE: no (C) STRANDE | RACTERISTIC 362 base p ucleic acid DNESS: doub | S: airs | | | |
| | (2) INFORM | EQUENCE CHAI (A) LENGTH: (B) TYPE: no (C) STRANDE | RACTERISTIC 362 base p ucleic acid DNESS: doub Y: linear | S: airs le | 889: | | |
| | (2) INFORM (i) S (xi) | EQUENCE CHAI (A) LENGTH: (B) TYPE: IN (C) STRANDEI (D) TOPOLOGI SEQUENCE DE | RACTERISTIC 362 base p ucleic acid DNESS: doub Y: linear SCRIPTION: | S: airs le SEQ ID NO: | | TCATGATACT | 60 |
| | (2) INFORM (i) S (xi) AATCACCTTC | EQUENCE CHAI (A) LENGTH: (B) TYPE: no (C) STRANDEI (D) TOPOLOG SEQUENCE DE | RACTERISTIC 362 base p ucleic acid DNESS: doub Y: linear SCRIPTION: | S: airs le SEQ ID NO: GCGTAAATAC | TTGTGCCGTT | TCATGATACT GCTGCATGAC | 60 120 |
| 35 | (2) INFORM (i) S (xi) AATCACCTTC | EQUENCE CHAI (A) LENGTH: (B) TYPE: no (C) STRANDEI (D) TOPOLOG SEQUENCE DE: ACGCCAATAT TGCGTGTTGC | RACTERISTIC 362 base p ucleic acid DNESS: doub Y: linear SCRIPTION: TGATTTTCAT | S: airs le SEQ ID NO: GCGTAAATAC | TTGTGCCGTT | | |
| <i>35</i> | (2) INFORM (i) S (xi) AATCACCTTC TTGTCAATCG | EQUENCE CHAI (A) LENGTH: (B) TYPE: no (C) STRANDED (D) TOPOLOGY SEQUENCE DES ACGCCAATAT TGCGTGTTGC | RACTERISTIC 362 base p ucleic acid DNESS: doub Y: linear SCRIPTION: TGATTTTCAT TGGGGGGGAAT GCAGGATTAA | S: airs le SEQ ID NO: GCGTAAATAC ATTTTCAGT | TTGTGCCGTT AGCCCAATTG | GCTGCATGAC | 120 |
| 35 | (2) INFORM (i) S (xi) AATCACCTTC TTGTCAATCG CTTCAATGGC GCTTGTGAAT | EQUENCE CHAI (A) LENGTH: (B) TYPE: no (C) STRANDE: (D) TOPOLOG SEQUENCE DE: ACGCCAATAT TGCGTGTTGC TAGTTCAATT ATAATCAAAC | RACTERISTIC 362 base p ucleic acid DNESS: doub Y: linear SCRIPTION: TGATTTTCAT TGGGGGGAAT GCAGGATTAA AGCTTTGGAA | S: airs le SEQ ID NO: GCGTAAATAC ATTTTCAGT TTAAATCTTC | TTGTGCCGTT AGCCCAATTG CAATGACAAT ACGACAGTTT | GCTGCATGAC | 120 |
| <i>35</i> | (2) INFORM (xi) AATCACCTTC TTGTCAATCG CTTCAATGGC GCTTGTGAAT AGTCATATCA | EQUENCE CHAIN (A) LENGTH: (B) TYPE: no (C) STRANDES (D) TOPOLOGY SEQUENCE DE: ACGCCAATAT TGCGTGTTGC TAGTTCAATT ATAATCAAAC AAAAATGATT | RACTERISTIC 362 base p ucleic acid DNESS: doub Y: linear SCRIPTION: TGATTTTCAT TGGGGGGAAT GCAGGATTAA AGCTTTGGAA TATATTCGCC | S: airs le SEQ ID NO: GCGTAAATAC ATTITTCAGT TTAAATCTTC TTGCTGGCAC | TTGTGCCGTT AGCCCAATTG CAATGACAAT ACGACAGTTT AGATAAAATT | GCTGCATGAC TTAGCATAAC TACCATGTGT | 120 180 240 |
| <i>35</i> | (2) INFORM (xi) AATCACCTTC TTGTCAATCG CTTCAATGGC GCTTGTGAAT AGTCATATCA | EQUENCE CHAIN (A) LENGTH: (B) TYPE: no (C) STRANDES (D) TOPOLOGY SEQUENCE DE: ACGCCAATAT TGCGTGTTGC TAGTTCAATT ATAATCAAAC AAAAATGATT | RACTERISTIC 362 base p ucleic acid DNESS: doub Y: linear SCRIPTION: TGATTTTCAT TGGGGGGAAT GCAGGATTAA AGCTTTGGAA TATATTCGCC | S: airs le SEQ ID NO: GCGTAAATAC ATTITTCAGT TTAAATCTTC TTGCTGGCAC | TTGTGCCGTT AGCCCAATTG CAATGACAAT ACGACAGTTT AGATAAAATT | GCTGCATGAC TTAGCATAAC TACCATGTGT GGTTGGCTAC | 120 180 240 300 |

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-------|
| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890: | |
| | TTGGTTTATT CCCAAAAGT ACGCGAAAAT TAGTAGAGAA GAATTTGAAA GTTTAAATAT | 60 |
| | TGTCAAACCC GCTAAAAATA ATACTTTCTG GCCTGTTGCA GGATTTGCAG TGTTATTAAC | |
| 10 | | 120 |
| | AACCITAACA AGAAAATATA TCTATTTGCT TAACATCCAT TTAGAAAAAG AAATAGTTAT | 180 |
| | ATTAACATGC TGTATGATAC TTCTAGGTGT TTTCGCATTG TTTATATATA TAAATACAAA | 240 |
| 15 | ATTGAAGTTA CATATTTTTG ATAAAAATAA AAGTAATAAC GAAAAGATCA TATTAATACC | 300 |
| | TACATTTAAA AATATTTGTT TATCCTTATT TGCTTATATA TTATTTGGTG GATTGTCAAC | 360 |
| 20 | AATGGCTCTG AGTATGTTAG TAACTTCATC CCCTCAAAAT ATAATAGAAT TTCTTGCTTT | 420 |
| 20 | AATTGGCATG ACTGCATGCT TCTTTCTACT GAATATGTCA TCGGTTCTAG ATAAAAAAAT | 480 |
| | TCATGTTATT TTAAAAACAA ATAAGTAGTA AAATTGATTA ACTTAGGTAG TATCGGATAC | 540 |
| 25 | TTAAATGTTG GTTCATAAAA AGCAATGATT TTAAATCGAG GAGCTATCTT AGAACAGGGA | 600 |
| | AATAAAACAG CCAAAGTTAT AAAAAGTGAA TTAATAACTA ATTATATTAT | 660 |
| | CTTCAAATAA AANATAATTA GAATAAGGTG GGATTGATAA TCAANGCTAN GCGAATCTAA | 720 |
| 30 | AATCATCAAT AAAAACCCCA AATATAG | 747 |
| | (2) INFORMATION FOR SEQ ID NO: 891: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 526 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891: | |
| | ATTTTGAAAT TTTAGCAGAT ACTGATAATG GTCTCGATGC AATGAAACTT ATTGAAGAAT | 60 |
| 46 | ATAATCCTAA CGTTGTTATT TTAGATATAG AAATGCCAGG CATGACTGGA CTTGAAGTTT | 120 |
| 45 | TAGCGGAAAT TAGAAAAAAG CATTTGAATA TTAAAGTGAT TATTGTAACA ACTTTTAAAA | 180 |
| | GACCGGGATA CTTTGAAAAA GCAGTTGTGA ATGALGTGGA TGCATATGTT TTAAAAGAAC | 240 |
| 50 | GTTCTATAGA AGAATTGGTG GAAACCATTA ATAAAGTAAA TAACGGAGAG AAAGAATATA | |
| | GCGCCACATT GATGACTTCA TTTTTTGTAG ATAAAAACCC ATTAACGCCC AAAGAACAAA | |
| | TTGTATTAAG GGAAATTGGC AATGGTTTAA GTAGTAAAGA AATAAGTGAA AAATTATTTT | 420 |
| 55 | 1101ATIANG GUNNATIOGC NATUGITIAN GINGIANNAN ANIANGIGAN AMAINTITI | , 420 |

| | ATCCTTTTGA TGCTTGGGAA AAGGCAAATG AAAAAGGCTG GACCTA | 526 |
|----|--|-----|
| | (2) INFORMATION FOR SEQ ID NO: 892: | |
| 5 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 751 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892: | |
| 15 | TATTGATGT AAAAGCGAAN GAACCATACA ATGTAACAAT TACTAGTGAT AAATACATCC | 60 |
| | CTAATACTGA TTTGAAACGT GGGCAAGCTG ATTTATTTGT AGCGGAAGGT TCTATCAAAG | 120 |
| | ATTTAGTGAA ACATAAGAAG CATGGTAAGG CAATTATAGG AACGAAAAAA CATCATGTTA | 180 |
| 20 | ATATTAAGTT ACGTAAAGAT ATTAATAAAA TCTATTTTAT GACAGATGTT GATTTAGGTG | 240 |
| | GACCAACGTT TGTCTTAAAT GACAAAGACT ATCAAGAAAT AAGAAAGTAT ACAAAGGCAA | 300 |
| | AGCATATCGT CTCTCAATTT GGATTCGATT TGAAACATAA AAAAGATGCT TTAGCATTAG | 360 |
| 25 | AAAAAGCGAA AAATAAAGTT GATAAATCTA TTGAAACAAG AAGTGAAGCG ATAAGCTCAA | 420 |
| | TATCAAGTTT AACCGGAATA TTATTATTTG TAACATCATT TTTAGGTATT ACATTCTTGA | 480 |
| 30 | TTGCTGTATG TTGCATTATA TACATAAAGC AAATAGATGA AACCGAAGAT GAGTTAGAGA | 540 |
| 00 | ATTATAGTAT TTTGAGAAAG CTTGGATTTA CACAAAAAGA TATGGCAAGG GGACTAAAGT | 600 |
| | TTAAAATTAT GTTTAATTTT GGGTTACCTT TAGTTATTGC ACTATCACAT GCATATTTTA | 660 |
| 35 | CATCATTAGC ATATATGAAA TTAATGGGTA CAACGAATCA AATACCGGTT TTCATAGTAA | 720 |
| | TGGGATTATA CATTTGTATG TATGCTGTTT T | 751 |
| | (2) INFORMATION FOR SEQ ID NO: 893: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 357 base pairs (B) TYPE: nucleic acid (C) STRANDENESS: double | |
| 45 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893: | |
| | | 60 |
| 50 | GGATGTTGTA CATTATTCAG ATTACTTTGA AGGGGCACAA AAATATTTGA GCTATTTAAA | |
| | ATCAACAGTA GATGTTAACT TTGAAGGTTT GAAAATTGCT TTAGATGGTG CAAATGGTTC | 120 |
| | AACATCATCA CTAGCGCCAT TCTTATTTGG TGACTTAGAA GCAGATACTG AAACAATTGG | 180 |

| | TAGCTGAAAA AGTAGTTGAA ACTGAAATGA TTTTGGGGTT AGCATTTGGA | CGGCGATGGG | 300 |
|----------|---|------------|-----|
| | AGACAGANCC ATAGCAGTAA GATGGAGANG GNCCAATCCG TTGACGGTGG | ACCCAAT | 357 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 894: | | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 464 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894: | | |
| | GCTAACCTGC AAAATTCGAT AAGCGATTCA ATACTGACGC CTGCATTTCG | CAAATTTTTC | 60 |
| • | ACTAAATAAA TCCAATTTAA ATCACTATCA TTATATATTC TATATCCATT | TTCATCTCGA | 120 |
| 20 | TTAACTGGTG GAATCACACC AACCTTTTCA TAATATCTTA AAGTGTCTTG | AGATATATTC | 180 |
| | ATGAGCGCTA CGACTTCTTT AGTTTTCATT GCGACTATCC TTTCAGTTAT | GTTTGGTCGT | 240 |
| | CTAAAGTAAT GTTGCTTTAT ATATTGTCAT CTTCGTTTGA ATACTTCTTA | TTTTATTACT | 300 |
| 25 | CAAATTTAAA TTTGTCTCTT TTTTAACATT TTACATTTCA TCGTTTTTAA | TTACTTTAAA | 360 |
| | AATTGTATAA CTKAAATATT TAAAATGATA TAAWCACTAA GATTGATAAT | Atttaattnt | 420 |
| 30 | TTGGAAAATT ATnTTAAGTT GCCAATTTTG GGGGGATGCG GAAA | | 464 |
| | (2) INFORMATION FOR SEQ ID NO: 895: | 1 | |
| 35 | (A) LENGTH: 599 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895: | | |
| | ANAATGAAAG AGTTACAGGA CTTTATTGCT CGTTTCTCAG TAACGCTTCT | AAATCTAAAC | 60 |
| | AAGCAACAAG TCGTAAAAAA CAACTCGAGA AAATTGAATT AGATGATATT | CAACCATCAT | 120 |
| 45 | CAAGAAGATA TCCTTTCGTT AAATTCACAC CTGAGCGCGA AATCGGTAAT | GACTTACTAA | 180 |
| | TCGTTCAAAA TCTATCTAAA ACGATTGACG GTGAAAAAGT ATTAGATAAT | ATTTCATTCA | 240 |
| 50 | CAATGAATCC AAATGATAAA GCAATTTTAA TTGGGGATAG TGAAATTGCG | AAAACCACAT | 300 |
| | TGCTTAAAAT ATTAGCCGGT GAAATGGAAC CAGACGAAGG TTCATATAAA | TGGGGTGTAA | 360 |
| | CAACGTCATT AAGTTACTTC CCTAAAGATA ACTCAGAATT CTTTGAGGGC | GTTAATATGA | 420 |
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960

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| | | GCGGCTTCTT AGGCCGTATG CTATTTAGTG GAGAAGAAGT TAAGAAAAAA GCTAGTGTAC | 540 |
|----|-------|--|-----|
| | | TTTCAGGTGG AGAAAAAGTA CGTTGTATGC TAAGTAAAAT GATGTTATCA AGTGCAAAC | 599 |
| 5 | | (2) INFORMATION FOR SEQ ID NO: 896: | |
| 10 | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1057 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | 0 + 4 | (D) TOPOLOGY: linear | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896: | |
| 15 | | TCATTAGTAG AAATCGTTAA AGATGCATCT TGCAATTTAA AATCCGAATC TTTGTATTGT | 60 |
| | - | TTGTTCACAC TATCTACGTT TAACAATGTT GTCATATCCA TGCTCCTCTT TGTTTAATTT | 120 |
| 20 | | TAATAAAAC GTCTTCTCTT CAATAAATAA CTAAAGGCGT TATATATGAA AATAGCAATG | 180 |
| | | ATAAGTAGCA AACTAAAGCT TTGATTAATT CCAGTAGTAA TTGAATAAAG CCCAATTACT | 240 |
| | | ACAATGGCTA GTATCAATAT TGATAAGTTG ATCGCATATG TTTTAAATAA TGCAATTAAT | 300 |
| 25 | | TCTATATGGC GTTCACCTTC ATCCAATATT TCCAATCGCT TTTCAGTGTA ATTCTTATCT | 360 |
| | | GCAATTTTTG GTATTCTGTC ATCAAACCTT CTATTAAACA GTGTAAATTG TGTATTGAAA | 420 |

ATAGCACTAG CAAAAAATGG TATTAAAAAG AATAGTATTG CATTTGCTGC AGCGTGCCCT

ACCACAAAAA TAAGCAATAC TAAAAAAGCA ATAACTGTCT GCAGAATACT TAATATACTT

CCATTTAAAA CATAACGATT CGCAAGCAAC TCATATTGAT CTGTTGCATC GATATCTACC

TCTTTATCTA CAAGTTGCTT ATACTTCAAT GCACGTCTTT GATTCATCAA AACAATGGCT

TCTACCAATA TGATAATAAT CGTCGCAACA ATCGATATTA CAACGACATT GTTATATGTC

GCAAACGTCA AGTTCTCAAT ACCAAATCCA TCAAAATTAC CTAAAATTCC ACCTATGATA

CCCCCTACAA GTCCACCCAG TAAAAGATAT CCGATATATC TTAGTATTTT CATGCCTCAT

CCTCCTCAAT AATAAAAACA GTTYCCACCG TTTCATTGAA AATGCGAGCA ATTTTTATTG

CCGTTAATAC TGATGGCATA AAATTGTTTC GCTCAATTAG CGATATGGTT TGTCTTGAAA

CGCCCGCTTG TTTAGCAAGT TGCGTTTGGT TTAAGCCATC TCGTGCTCGT AATTCTTTCA

(2) INFORMATION FOR SEQ ID NO: 897:

(i) SEQUENCE CHARACTERISTICS:

ATCGATTACG CACATCGCAT CAACTCCNTA ATTACAC

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897: | |
|----|---|------|
| 5 | AAATTATTGA GTTAACAAAT CATTACGGAG CACATAATTA TTTACCATTG nCAATTGTCA | - 60 |
| | TTTCAGAAGC CGANGGGGTA TGGGTTAAAG ATCCTGAAGG CAATAAATAT ATGGATATGT | 120 |
| | GANCTGCATA TTCCGCTGTT AACCAAGGTC ATAGACATCC GAAAGGTATT CAAGCATTAA | 180 |
| 10 | AAGATCAAGC TGATAAAGTG ACTTTACTCT CACGTGCTTT TCATAGTGAT AACTTAGGTG | 240 |
| | AATGGTACGA AAAAATTTGT AAACTGGCAG GTAAAGATAA AGCTTTACCA ATGTAAŢACA | 300 |
| | GGTGCTGTAA GCAGTAGAAA CAGCTTTGAA AGCAGC | 336 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 898: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 302 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898: | |
| | TGNTGNTTTC TTATTGTTGA CCAATTATTT TGCATACCAA ATCCAAATCA TGTATTTATC | 60 |
| | AATCACATCC TAATGCTAAA TCCAATGTAT TACATTGTTT AATGGTATAG CACAATCTAT | 120 |
| 30 | CATATTTGGT ATATCAAGTA TGGAAAACAT TCCATATCAT TTTTACTTTA TTTTATTCTT | 1.80 |
| | ATGTTTÄATA GCTGCÄGTAA ATTTCGTATT AĞCAGGTATA CGACACACGG CAATTTATAA | 240 |
| | TAAAACATCT AAAGTGACAC AAACTGATAA TCAACAGGGA GTTTCAAAGA TAGTCAGACG | 300 |
| 35 | GG | 302 |
| | (2) INFORMATION FOR SEQ ID NO: 899: | •. • |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 469 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899: | |
| | CCACTAGCTG ATACAGTAGG TATACCAAGA TTCGTCATCG TTACGACATA TCAATTTGGT | 60 |
| 50 | CAATATGCGA TGTTATTCTT AGCGCCGACT GGACTTGTTA TGGCCACACT ACAAATGTTA | 120 |
| | AACATGCGAT ATTCACATTG GTTCCGATTT GTATGGCCGG TAGTTGCTTT TGTATTGATT | 180 |

| | TATAAAAAAT ACTAATGGGG TTTTATGCAT CTCGTAGGTT TGTAGAAATA CTAAACTAAG | 300 |
|-----------|---|------|
| | CGAGGTGCAT TATTATTTT GATTAAGAAA ATAATGACGG TAATGATAAC ACTAGTAAGT | ∵360 |
| 5 | AATTGATACA ATGCTCTATT TAATAATGAT ATTTTTAAAA TTTGTTTTTA ATGTAATGTT | 420 |
| | AGATCTATGG TATATTATAT TTAACGTGGT AAATATGTAT TTGCTGTAA | 469 |
| | (2) INFORMATION FOR SEQ ID NO: 900: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 821 base pairs | |
| 15 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900: | |
| 20 | CTTTATTGGT AACTCTCTAT AATATLTTAA CATTTTTACG CTATCGTGCA AACGCAACCA | 60 |
| | CTTTGAATTY TCTGATATTT TTAGCATATA ATTTACACCC TGCACGATGA ATTGTTAATC | 120 |
| | CAGTTGTATA AATATCGTCA ACGAGTAATA TTTCCTTACC ATTTAAATCT AATTCCGTAT | 180 |
| 25 | CAATAATAAA TGGATTTTCA TCTGCCAGAC GCTCTTTCTT AGTTAAATGA GACTGTTTTG | 240 |
| | GTCTATTTGA CATCTTTAAA ATCTTATCAA AGCGAATCCC TTTAGCTTTT AGTACTGCTT | 300 |
| | CTACCGGGTT AAATGTTCTA GATAAATCAT GTGCCGGCGA AGAAGGAATT GGCACAATAT | 360 |
| 30 | AGTCATAAGA TGTTTGTGGT ATTTCAATCA AATGTGCCAA TAATTCACAT AAATAATAGT | 420 |
| | CTTTCAAAAA TTTATACTGA TGTATCATCT CTTTCATTAA ACCGTCATAT TGAAATTGAC | 480 |
| 35 | AATATAATTG TTCCATTAAA TTAAAGTGTG CCGATAGAAA CTTGCAGTCT AAACAATACG | 540 |
| 35 | CTTCATCTTG ATTTAAGTGT TTTAAGCACC TTGAACATCG CCTTGCTTTA ATATCAAGTT | 600 |
| | TAATATTGTC CCAATTCTCT TTGCATCTGT CACATAATCT ATTAGGTTTC TTGAACAAAT | 660 |
| 40 | TATAAATGGT TATATTTTCA TATAACTTAG CACCACAACT CAAACAATTA TTCATCAATC | 720 |
| | CAACCTCTTT TTAATGCTAA TTTGTTCATC CTTTGAATCT CTTTTTTAGC TTGAATCATA | 780 |
| | TTCATACTTA CCCCTTnCAT GAAAAAACAA TACTTTTTCC A | 821 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 901: | |
| <i>50</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 349 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | TGATGCTATT AAAAAGTTAA TTGTGCGGTC TGTTTTGATA ATTTTAATAA TAACTTCAGG | 60 |
|----|---|-----|
| | TAACTAAAAA TCCTAATATT GAAAAAACAA AGCCATTTAA AACATAACCT AGTATATTCC | 120 |
| 5 | ATGTATGATT GTAACTCATT TGCCAGTTnT GTACTGACTT GCATAATTCT GTCACGTnCG | 180 |
| | AACCATGTAC AAGCCTGCAA CTACTGCTGA ATGATTCCTG ATGCGTGAAC AATTCAGCAA | 240 |
| | TTAAATACGT AACAAATGGT GTTACAATTG AATAATTGAA ACATATTAAT GTTTCATATC | 300 |
| 10 | CTCGACGNCA TCAATGTTAA TCCGGACCTT ACTAATGCAT ACCTATAAG | 349 |
| | (2) INFORMATION FOR SEQ ID NO: 902: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 390 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902: | |
| | CAAGTGGTAT AAATTTACCT GGTGAAATGT AGGTCGTGGT GGCGATGATA CATTATTCGC | 60 |
| 25 | TAAAATCGAC GGCGTTGTTA AATTCGAACG TAAAGGTCGC GACAAAAAAC AAGTTTCTGT | 120 |
| | ATATGCAGTT AGCTGAATAA TTTTGTCTAG TTAACACCAG AAAGTGAATC TTCTGGTGTT | 180 |
| | TTTTACTTT TATAAAATGT TTTTCATTAT TATTTTCATT ATGnTATTTA AAAATGGGGA | 240 |
| 30 | TTTTAGACGT TATACTAAAT GTGCACTGTA TAGGGGCCCT AATCACTAAC TATAGGGGGA | 300 |
| | CAAGGATACA GTGCAGCGTT AAGGATAACT GnCCACATTG GTCTGGGAAT ATAGGATTTA | 360 |
| 35 | AGCAAGGTTA TAAAGTACTC nTAGGCCCTA | 390 |
| | (2) INFORMATION FOR SEQ ID NO: 903: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903: | |
| | GGAATAGACG TATATGCGCG TTGAATTTAA TCCTAATAAG CTTTCGCATG ATGAAGTGCT | 60 |
| | TTGGTTAAAA CAAAATATCA TCAGTTATTT GGACGATGTT AGTTTTACGA GATTAGATTT | 120 |
| 50 | GGCTTTGAT TTTGAATTTG ATTTAAAATG ACTATTATGC ATTGTCAGAT AAGnCGGTAA | 180 |
| | AAGAAACTAT ATTTTATGGC CGAATGTAAA ACCAGAACAA AATATTTTGG TGTnCGAATA | 240 |

| | GATTCACATT CTATGCGGTG GAATTGATTA AACG | 334 |
|----------|---|----------|
| , | (2) INFORMATION FOR SEQ ID NO: 904: | (1) |
| 5 | (i) SEQUENCE CHARACTERISTICS: | * |
| | (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904: | |
| 15 | CAAGTTGGGG ACACTGTTTC AAATGAAACA ACAGTGTGTA TTTTAGAGGC AATGAAACTA | 60 |
| * 10 | TITAATGAAA TICAAGCAGA AATTICAGGI GAAATTGIIG AAATCITAGI AGAAGACGGA | 120 |
| | CAAATGGTAG AGTATGGCCA ACCGTTATTT AAGGTGAAAT AATGAAAAAG GTTTAATTGC | 180 |
| 20 | AAACCGCGGT GANTCGCAGT TAGGATTATT CGCGCTTGTC GTGATTTAGG CATCCAAACT | 240 |
| | GTTGCATCTT TCTGAGGGGA TAAAGATCGC TACATCTCAA ATGCTGATGA GGCATATnCG | 300 |
| | TGGGCCnCTT GTCTAAGGTC ATATTTAATA TCCG | 334 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 905: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| Е, | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905: | |
| 35 | TTCACCCTGT AATTCTTAAC CGTCAATTGA CCTTTATGCA GATTTAATAT TCCTAAAACG | 60 |
| | TATAACTCTT CTAATGATAA TTGACACATA TTTAAATAAC ACTTTAGATT CCGCAATAAT | 120 |
| 40 | TCTTGTGACG ACAATAAATA CGATACATAG TCACAACTAA AATCAAATGT ATATTGACCA | 180 |
| | AAATAACGTT CAATATAGTC ACTAAGCTCA TTATTCATAT ATTCTATTTN ATCTATATGC | 240 |
| , | ATTTTATTAA TCGAAATAGT CAATTTACGT TGATCCCTTT GATCTCTTCC TTTCAATAGC | 300 |
| 45 | CATTGATGAT TGTnTAAATA ACTTAACATT TGAAGAAGGG CCATCTTAGA TTGGATTTCT | 360 |
| | TTCATTnTTA ATAAACTATC TATTGAAGCG CTATTGGAA | 399 |
| | (2) INFORMATION FOR SEQ ID NO: 906: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1478 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906:

| 5 | TACATTITTC | AATTTATGGC | AAAATnCACA | ATTTTCATCG | AAATATTTŢG | TANANAATCA | 60 |
|-----------|------------|------------|------------|------------|------------|------------|------|
| | TTGCTAGGTG | ATGAGTTATC | TCGGTTAATT | ACAAAACGAT | ATCTAAGTTT | AAATATTAGA | 120 |
| | TCATAAAAA | ACTATCTACT | GAATATCCCT | CCATAGCATC | ATTTTTCTAA | GCAAAAGTTA | 180 |
| 10 | AACTTAGTTA | GATAAAATGC | AAATGAGATT | ATTGTAGATA | GTCTCTTTTT | AATGTTTAAA | 240 |
| | AATGATTAAT | GCCaTAAACA | TAAATAATTC | Caaagaatgc | CGCGCCACTA | AGCACTGTTA | 300 |
| | ATATAAGACT | TAGTAACAAT | GTGCGTTTAT | AATGTTTaAC | AAATGCtATG | AACAAAATGA | 360 |
| 15 | CTACATTATA | CGCAAAGAAA | AGTCCGAATA | ATGTCATTGT | TATTTTCAAA | TCAGAATAGA | 420 |
| | AAATATTTAA | TAGTAATACA | ATGACTGCAT | AAATTAAATA | CGGAATAACT | ATAAATTTGC | 480 |
| - | GTTCAAATCT | TAATTGTTCG | AAaCGtTTAT | CTTCGTTTGT | CATGATATGC | TCCTTTATGA | 540 |
| 20 | TTTAAAAGTA | AATAAGTTTA | CGGAALATCT | TGTCCGaTAA | TAGCGGTGTA | AAtGTCAAAC | 600 |
| | CACGACTGAT | CATCLAAATT | AAGTKGTAGC | CCtTCGATTG | CTTGATCAAT | ACGCTTTAAC | 660 |
| 25 | TGACTTGTTC | CAAGTATCCG | GCATGATACG | ATGCGGTATT | TTTACTAACC | ACGCTATCAT | 720 |
| | CACAGCTGTG | TCACTYACAC | mATATTTGTC | AGCTATTGAT | TGAACAACTT | TCATAATACG | 780 |
| | TTGCGCTTTA | ATATCTTCCT | TGTCGAAAAT | TTTACCGCCT | GCAAAAGGAC | TCCAAGCCAT | 840 |
| <i>30</i> | GATTTGAACA | TGGTTTTGAT | ACATTGAATC | CATTGTTCCA | TCTTGTAAAC | TATCAACGTG | 900 |
| | ATATGGCGAT | AATTCTAATT | GATTGATGCT | AATATGTAGT | CTTTCTTTCA | TAATATATTG | 960 |
| | ATTTAACAAT | TGGTATTGTG | AATGATTAAA | ATTCGACACC | CCGAATGACT | TCAACTTACC | 1020 |
| 35 | TTGTTTAACA | AGTTTAGTTA | ATGCATCAGC | AACTTGTTCT | GGaTCCATCA | ATGGTGaAgG | 1080 |
| | ACGATGAATG | AGTAGACTAT | CTAAATAATC | TACATTCAAA | TTGATTAATG | ACTGTTCAAC | 1140 |
| | AGATTTCACG | ATGTGCTTAC | TACTCAAATC | ATAACGATGT | CCATTTGTAA | AATCAAATTG | 1200 |
| 40 | CTTAGAAGGC | AAAATGATAC | CACATTTCGT | AACAATTTGA | ATTTTATTTC | TTAATTCGGG | 1260 |
| | TGATAAATCC | AAAGCATTAC | CAAACAGTGA | TTCACATTGA | TAATCTCCAT | AAATATCAGC | 1320 |
| 45 | ATGATCCATC | GTTGTAATTC | CACGTTCAAC | TAATTCATTT | TAAAAATAAT | TTAACTCTTT | 1380 |
| | CGCAGTCATC | TTCCATTCAT | TTGCACGCCA | AAAACCTTGT | ACAAGCCTAG | AAAAATGAAC | 1440 |
| | ATAGTGATTA | ATCATTATTT | GTTCCATATn | TCATCCAC | | | 1478 |

(2) INFORMATION FOR SEQ ID NO: 907:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 543 base pairs

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| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----------|--|--------------------------------|
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907: | |
| | TTCTATGAGA ATAGATATTG TTAAATTAAG AAAGTAGTCA ATTTTATTAT GACAAAAGAA | 60 |
| 10 | AGAAGAACAT TTAGTTCAGA GTTTAAGTTA CAAATGGTTA GATTATATAA AAATGGTAAG | 120 |
| | CTTAAGAATG ABATTATACG ABAGTATGAT TTABAACCCT CAATTATCTC ABATTCGATA | 180 |
| | AAACAACACC AAAATACTGG ACCCTTCAAT CATCAAGATA ATTTAAAAAG TGATGAAAAA | 240 |
| 15 | GAGTTAATAA AATTACGCAA AGAAGTTCAA CATTTAAAAA TGGAACATGA TGTTTTAAAG | 300 |
| | CAAATTTTAA AGTTGATTTA GAAACTGAAC TTTTTAAAGA TACATTACTT GAAGATTCTA | 360 |
| | ATTTATCTGA TTATATAAG AACCAACTTC CAACGATATG GAGAGACTAA GAAATAGTTT | 420 |
| 20 | AAATTTATTT AATTTCAATA AAAACTCATA ATAATATTTA AGTAAGTTAG ATTGCTTTTA | 480 |
| | GCATTAGGAA TTCGCTTATA ATTAGATGTT CAATATAGAC TTTTTTACAC ATACATGAAC | 540 |
| | TAT | 543 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 908: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid | |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| * | | |
| | The second secon | |
| 35 | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 908: | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908: | 61 |
| | TTTnCGGTng AACATGATTn CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGAA | 60 |
| | TTTMCGGTMG AACATGATTM CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGAA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATTA | 120 |
| 40 | TTTnCGGTng AACATGATTn CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGAA | |
| 40 | TTTMCGGTMG AACATGATTM CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGAA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATTA | 120 |
| 40 | TTTMCGGTMG AACATGATTM CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGAA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATTA GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACTT | 12 |
| 40 45 | TTTMCGGTMG AACATGATTM CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGAA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATTA GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACTT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTTG | 120 180 240 |
| | TTTMCGGTMG AACATGATTM CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGAA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATTA GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACTT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTTG AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTTC | 120 180 240 30 |
| | TTTMCGGTMG AACATGATTM CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGAA AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATTA GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACTT GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTTG AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTTC TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGAA | 120 180 240 300 36 |

AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAA

GAAATTGGTA ATGCGGCATC TCATGGTGTT GCAGCTTTGT TAACATTATT AGTGTTACCC

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| | TATGITATIT CTATCITTAT GATGITTATI TCATCIACTA TITATCATIC TATGCAAAAT | . 720 |
|----|---|-------|
| | GAAACACCTC ATAAATATAT TTTAAGGATT A | 751 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 909: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 394 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| • | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909: | |
| 13 | AAATTGTCAC AATTCAGTCT AATTTAAAAG GAAGTTAATT ACAAAATTAA AAAATCATGC | 60 |
| | ATCGTGTCAT TTAGATATTG AAAAAGATGA GTCAAATTTG TTTCATATAT TTTCCAATAA | 120 |
| 20 | CAAATTATTA TATCTAAATA TACAATCAGA AATATATGAA TAGAAATATC AATAAGAAAA | 180 |
| | ATAATATGAT TAAAAATGAT GAATGGCATA CTTATAAAGT GTCTAAATAT TGGCGGTCAA | 240 |
| | TATTACTTAC AAACACGAAT GTTAAGTAAT GTAGACAATG CTGAAAAAAC AATAAGTAGA | 300 |
| 25 | AACTCTATAT AGAATGTTCG TTTTTATTTT TAATAATTGA ATAATCATTA TTGGGTGGAT | 360 |
| | TTTAATATGG NATTCCGGTC GGCACACGGA TTAC | 394 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 910: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1022 base pairs (B) TYPE: nucleic acid | |
| 35 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910: | • |
| 40 | TAAAGCTAAG AAAAAAGAAA AACGTAAAGC TTATAACCAA CGAATGAAAG AACGTAGGAA | 60 |
| | AAATCAACCT AGCGCAGTTA GTCAACGTCG AATGAATTTT GAAGAGCGAC GTCAAATTTA | 120 |
| | CAACAATGAT ATTTCTGAAG AACGCAATTC AAGTGAAGTT AAGGACAAAA AAGAGCAAGA | 180 |
| 45 | ATAAATATTG ATGATACCCA GATTAGTAAG CAGAGGTCTT TTGCTTATTA ATCTGGGTTT | 240 |
| | TTATATGAGG TTAATTATCG ATAACGTTTA ATTAAAGTGT TTAGGTGTCA TAATTTTAAA | 300 |
| | TGACGATTTC CCCATTACKA TACACCTAAA TEATCATCAA TCTGAATTCA GATGTTTATK | 360 |
| 50 | ATAAAAATTA GATGAAAAAT ATGTTAATAT ACAAGKAATT TAATGTGCGK ATATCTATAG | 420 |
| | GCTCGTAGTA TACTTATTAA AATATTAAAC AAAGAAAGGA TTTTAAGATG AATAGAAAAC | 480 |

| • | GGCTATCCTA TTTTTCTTTA AAAAGTGGTA ATGCATCACA ACGTGAAGAA TTAGCGAAGC | 600 |
|------------|---|-------|
| | AATTATCTCA GAACGGTGGC AAGGTTTCTT TAGATATGCT TCAGACAACA ATGGGTGCAT | 660 |
| 5 | TAGCAATTAT TTTATTAATT TCAACACTTT ATGGTATATT TGCGACAATT TGTATTAAAG | 720 |
| | GACGTAGAAA ATTATCGATT ATACTTTTTG TTATCGCGAT AATTGTAAGT TTGATGGCTC | 780 |
| | TTAATTTAAT TGCAATTGTC TTATGGGTTA TCGTGATGAT TATGTTGATT TCTAAAAAAG | 840 |
| 10 | AATCAAAAGA AACAACACAT AAGGACGATG AGTATATTTA TCATTAATAT GTTCATAGCA | 900 |
| | AAAGAAAAC CATTAAAATG TTAAGTTGTT AATTATTAGA TACAACCAAC ATTTTAATGG | 960 |
| 15 | TTTTATTTTT AACTTTGTAG TTCTTGGAAT GTTTGAACGA TTAAATAGAC ATTTAAAATA | 1020 |
| * | CT * | 1022 |
| | (2) INFORMATION FOR SEQ ID NO: 911: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 274 base pairs | · 1 . |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911: | |
| 30 | GGTACTITAT TTTTATTTT GGTCTTAGTG ATTTTTACAT TATTTACATA TAAAGCGCCT | 60 |
| | AATGGTATGC GTGCCATGGG TAGCATTAGC TAATGCAGCA ATCGCAACAT TTTTAGTGGA | 120 |
| | AGCATTTAAT AAATATGTnG GTGGCGAGTA TTCGGTATTA AATTTTTAGA AGAGCTAGGA | 180 |
| 3 5 | GACGCTGCGG AGGTCTAGGT GGTGTCGCTG CCGCTGGATT AACAGCATTA GCTATCGGTG | 240 |
| · , | TGTCACCAGT ATATGCATTA GTTATAGCAG CCGC | 274 |
| | (2) INFORMATION FOR SEQ ID NO: 912: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: | • |
| | (A) LENGTH: 679 base pairs | |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| 45 | (D) TOPOLOGY: linear | |
| 45 | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912: | |
| 50 | CTTTAATTGT TCACTTTATC ATTATTATCA ATCAACTCTA TGATATGAAA TTGTGTTAGA | 60 |
| | GATAAATCTA GTTCCTCATT TTCCTTTTTA TACTGTCTTC TTTTATCGGC ATTTTCTCTT | .120 |
| | TCTATAATAA ATTGTTGTAA TTTTAAAATA ACTTCTCTCT TCATATCCAC TATTATTCCT | 180 |

| | TTGTTGTAAT TAACATATAT TTACTTAGTT ATGCACCATT TATTCCGCAT TTCACAAATC | 300 |
|------------|---|-----|
| | CACCTATAAT ACAAACTATC ATTTTAAATA AGCAGAATTT ACCCTGTCTT CCACACAAAT | 360 |
| 5 | TGTTTTCGAC ACTTTAATGT GCCTACTATC CAAAAAAGTT ACTCATAACA AATTGCGCAT | 420 |
| | TTTAATAAAT GTAGCAATGC CATTTGCATG CTGCAAAAAT ACTCGTATTC ATATTTATGT | 480 |
| 10 | TTTATATTAT TAAAGTTTTT TAAATCCATA TTTTTATAAC ACTTGCTATG TGATAAAATT | 540 |
| | AATmTTATAT ATAAAATCTT AAGATTCAGA TTATTTAATA GCAAAGGAGA TAGTGATATG | 600 |
| | GATGTTTTAA CAATAGAACA TTTAACAAAG AAGATAGGCA ACAAAACGAT TCTCGAAGAT | 660 |
| 15 | GTATCATTTA AGCTGAAAC | 679 |
| | (2) INFORMATION FOR SEQ ID NO: 913: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 564 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913: | |
| | GCCATCCTTC AGTGCTAATT TTTTCAAATT CTAATGCAGA TGCACCACTA ACCATACCAT | 60 |
| 30 | ATATAAGAA AAAGACCACG AAAGNAATAA GTAGTAGTAT AGATGCACAT ATCATAATGA | 120 |
| | CATTGGAGTT TTCAGCGCCA AATTTAAATG TCAATGBGAA AATGATAGAG TATGCCCCTA | 180 |
| | TGATACCAAA ACTCATTAAA CCTGACATAA TACCAATCAT CACACTTTGG GTCACAATCG | 240 |
| 35 | TAGTCACAAC TAATCCAATC ATTAAACTTG CACCGAATAA GATTAAATAA AAGGCAAAGT | 300 |
| | ATGACTTAAT ATAATCACTA CGTTTAACCG GTAAAGTAGA TACATAATAC ATCCATCTTG | 360 |
| 40 | AGTCTTTTTC aTGTTTAATA TTATCAGTAA TAGGTGTGAT TAACATAACC CCAGCCATKG | 420 |
| | CCGAACTCAT CAACGGATTA AATACTGCAA AGTATCCTGC AGCTATAATA GCGACTATAA | 480 |
| | AATAAATATA TGTTTGCnTT CTCGTTGCAT AAAAACTACT TAGGAACATA CCTTTCATTA | 540 |
| 45 | TACTTCACCT CGCATTATGA TTTT | 564 |
| | (2) INFORMATION FOR SEQ ID NO: 914: | |
| 5 <i>0</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 643 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | AAAGAAGAAG CAAGTGCAAA TAATTTAAGT GATATATCAC AAGAGGCACA AGAGGTTCAA | 60 |
|----|---|-----|
| | GAAGCTAAAA AAGAAGCACA AGCAGAGAAA GACAGTGACA CATTAACTAA AGATGCAAGT | 120 |
| 5 | GCAGCAAAGG TAGAAGTATC AAAACCAGAG TCACAAGCTG AAAGATTAGC AAACGCTGCA | 180 |
| - | AAACAGAAGC AAGCTAAATT AACACCAGGT TCAAAAGAGA GTCAATTAAC TGAAGCGTTA | 240 |
| | TTTGCAGAAA AACCAGTTGC TAAAAATGAC TTGAAAGAAA TTCCTCAATT AGTTACTAAA | 300 |
| 10 | AAGAATGATG TATCAGAGAC AGAGACGGTT AATATAGATA ATAAAGACAC TGTTAAACAA | 360 |
| | AAAGAAGCTA AATTTGAAAA TGGTGTTATT ACACGTAAAG CTGATGAAAA AACAACTAAT | 420 |
| 15 | AATACAGCTG TTGACAAGAA ATCAGGTAAA CAATCTAAAA AAACAACACC TTCAAATAAA | 480 |
| | CGAAATGCAT CAAAAGCATC TACAAATAAA ACTTCAGGTC AGAAAAAGCA ACATAATAAG | 540 |
| | AGATCATCAC MAGGTGCAAA GAAACAAAGT AGTTCMAGta AGTCAACTCA AAAGAATAAT | 600 |
| 20 | CAAACTAGTA ATTAAGANTT CAAAAACAAC AAATGCTAAN TCC | 643 |
| | (2) INFORMATION FOR SEQ ID NO: 915: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915: | |
| | AGGTTTAAGG GAAAAATCCT ACCTGGAGAG ATTCAAAAAC TAAATGGACT ATTTCCAAAA | 60 |
| | ATAAAGGGCA ATCACATGGT GGTTCTTATT GGAAGTTAAT AAATAACAAA GGAAAAAGAA | 120 |
| 35 | TAGCTTCTTT AACTAAAGAA GGAAAAATCT TAAGGGAATA AGGTGTTGTA AATTATGTGC | 180 |
| | TTTGATATAA ATAATTTGGA TATAAAAAAG TTGAATTTTA GAAAGGTAAA AAACGCAATT | 240 |
| 40 | CATTTAAGTT TAAGTGGCGA TAAATACCAG TTTTTGGAGG ACGGTAAAAC TATCAATAAT | 300 |
| 40 | ACTTATTTT TAGCTGTATA TGATAATGCA ATAAACATTT TTGAAGATTT GTTTLCGCCT | 360 |
| | | 400 |
| 45 | tCTGATTCTA TAAATTTGGN TCATGTAGTA TATGTTTATA | * |
| ¥ | (2) INFORMATION FOR SEQ ID NO: 916: | • |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | CCCAAAGTTC GATAGTGTAT TAGTATTATC TTAATAAAAT GTTAGGTACA ATAAAGATGA | 60 |
|----------|--|-----|
| _ | TTATATATCG GAGGTTAGTA TAAAAATGTA TGTAGATCGA AAACCATCAC TATATTTAGA | 120 |
| 5 | GGATTIGCGA CATGATTITA AAAATAGTTI AAGTAAATTI GAAAATGGTG ATGAAGCATT | 180 |
| | TGATACGTTA TTAGGTTTCG TAGAGTTAGA TCATATTTAT TCGTCAGCAC TAAAGGAAAT | 240 |
| 10 | AAGCACTAAA CTGAGTATTT TAGATGACAA TTTCAATCAC ATTTATAWAC ACAATCCTAT | 300 |
| | ACATCATATG GAGCGACGTG TGAAAGAAAT GCGTAGTTTA ATAGAAAAGC TTAATCGTAA | 360 |
| | AGGATTACAG ATTAGCGCAG AAACTGCCAA AGAACATATA | 400 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 917: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917: | |
| | GAAAATTACT ATGAAGATTG CATTAGGATG CGACCATATT GTTACAGATA CAAAAATGCG | 60 |
| | TGTATCTGAA TTTTTAAAAT CAAAAGGACA TGATGTCATT GACGTAGGAA CATACGATTT | 120 |
| 30 | CACAAGAACA CATTATCCAA TTTTTGGTAA AAAAGTTGGC GAACAAGTTG TTAGCGGTAA | 180 |
| | TGCAGACTTA GGTGTTTGTA TTTGTGGAAC AGGTGTTGGT ATTAACAATG CTGTAAATAA | 240 |
| | AGTACCGGCG TTCGTTCAGC ACTAGTACGT GATATGACAT CAGCGTTATA CGTAAAAGAG | 300 |
| 35 | GAATTAAATG CGAACGTTAT TGGCTTCGGT GGACGTATTA TAGGTGAGTT ATTAATGTGC | 360 |
| | GATATTATCG ATGCCATTAT TAATGCTGGA TTATAAACCC | 400 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 918: | |
| 40 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1220 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918: | |
| 50 | GTCTCCAGCC ATTWCACCAC ACATACCTGT CCATTTACCT TCTTTATGTG ACGCTTCAAT | 60 |
| | AACTTGTTTA ACTAAACGTA AGATTGAAGG GTTATATGGT TGGTATAGAT ATGATACACG | 120 |
| | CTCTGACATA CGGTCAGCAG CTAATGTGTA TTGAATTAAA TCATTTGTAC CGATACTGAA | 180 |

| | GATTCCTAAT TCTATATCAT CCGAAATGTC ATGACCTTCA TTTTTAAGGT TTTCTTTTTC | 300 |
|----|---|------|
| | TTCTAATAAT ATAGCTTTAG CTTCTCTAAA TTCGTTAATT GTTGCAACCA TTGGGAACAT | 360 |
| 5 | GATATTTAAC TTACCATAAA CTGATGCACG TAATAATGCA CGTAGCTGTG GTCTGAAAAT | 420 |
| | ATCTTGTTGC GCAAGGCATA AACGAATCGC ACGGTAACCT AAGAATGGAT TCATTTCTTC | 480 |
| 10 | AGGCAAGTTT AAGTATGATA ATTCTTTATC TCCACCTATA TCTAAAGTAC GTACAACAAC | 540 |
| | ACGITTACCG CCCATTGCTT CTAATACTTC TTTATAAGCT TCAAATTGTT CTTCTTCTGT | 600 |
| | AGGCATTIGG TCACGACCCA TATATAAAAA CTCAGTTCTA TATAAGCCGA TACCTTGTGC | 660 |
| 15 | ACCATTITCA ATAACACCIG GCAAATCATT AGGTGTACCA ATATTIGCAG CAAGCTCIGC | 720 |
| | GTGAACACCA TCAACTGTAA CAGTATCAGC ATCACGTAGW TTTTGTAATT CTTTCTTGTC | 780 |
| • | AGCAAAATAA CGCTCACGTT TATCTTGATA AGCGATTAAC TCATCTTCAG TTGGATTAAC | 840 |
| 20 | GATTACATCA_CCATTTAATC_CATCTACGAT_AATCATGTCG_CCTTGTTTAA_CTTCTTGAGT | 900 |
| | AATTGATTTT GTACCAACAA TTGCTGGAAT TTCTAAAGAA CGACTCATAA TTGCAGAGTG | 960 |
| | aCTTGTTCTT CCGCCAATGT TTGTAGCAAA ACCTTGTACG AATTCTTTAT TTAATTGAGC | 1020 |
| 25 | AGTATCAGAT GGCGTTAAGT CATTCCCTAC AATAACAACG CTTTCATCAA TCATACTCGG | 1080 |
| | ATTCGGTAAT TCTACACCTA AAATATGTGA TAACACACGT TTAGAAACGT CGCGAATATC | 1140 |
| 30 | AGCCGCACGT TCTTTCATGT ATTCGTTATC CATAGATTCA AAAATTGTAA CAAATTGTGT | 1200 |
| | TGTnACATCC GCTTAATGTG | 1220 |
| | (2) INFORMATION FOR SEQ ID NO: 919: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | • |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919: | |
| * | TTAGATTGAC TGCAAATGCC GACTCAAAAG AACAAGCACA ATCATTGATT CAACCTGTTA | 60 |
| 45 | AACAAGAAAT TCTTGATCGT ATTGGAGAAT ATTATTATGG TTCAGATGAC ACATTAATTG | 120 |
| | AGCAAGCTGT AATAAAGAAA ATTCATGAAC CTTTTGTAAT ATATGATGGT ATTACTAATG | 180 |
| 50 | GTGCTTTATA TCATCGATTG AAAGAAGTGG ATTTAAACGA TGTTCTAAAG GGTATGATTA | 240 |
| | ANGER AND COUNTY GATATTANTS ANCOTATION GCAGCANTIA ANAGATGCAG | 300 |

1746

TGCAATTTGT TAATA

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| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 433 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920: | |
| | ACTITGIAAA CCTACAAAIG TAAIGAAIAA TCCTAIACCI GCIGAAACAG CCAICITCAI | 60 |
| | TTGATAAGGA ATTGCATTAA TAATAACTTC CCTAAACCCT GTGACGGTTA ATATCGCAAA | 120 |
| 15 | GAATATACCT GAGAATAAAA CGCCTGTTAA ACCAACTTGC CAAGGAATAC CCATGGTTAA | 180 |
| | CACAACAGTA AATGCAAAGA ATGCATTTAA TCCCATACCT GGTGCTAACG CAATTGGATA | 240 |
| | TTTAGCTATT AGCCCCATGA ATAGCGAGCC TACAAATGCT GCTAATGCAG TCGCTACAAA | 300 |
| 20 | AATGGCACCT TGGTCCATTT TCATATCTTC TGATACGCCT TTAACACCTG CTAAACTTAA | 360 |
| | AACTTGCGGG TTAACTGCTA AAATATAGGC CATAGATAAG AAAGTTGTGA TACCGCCTAA | 420 |
| 25 | GATTTCTCTT TTA | 433 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 921: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 439 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921: | |
| | CTATTTATT TGTATAGCGC TTGATGTAAA GTTATTTTAG CTGTCATACT ATGTGCTAAA | 60 |
| | CCAAATTCAG TTGTGTCATA TCTTCGCTTT TTTGTCACTG TTATAATAGG TATAATCGGA | 120 |
| 40 | TATAATGAAA AGGKGAGGGA GGATTCAAAA TGCGTAGGTT ATTATATTCA TTTCTTTTT | 180 |
| | ATATGATCAT AGGTTTATTT AGTGGCTTTT TCTATAGAGA GCTAACAAAA GCATATGATT | 240 |
| 45 | TTACTGGTAC AACACAATTA TCACTTGTAC ACACACATAC ACTTATTTTA GGTATGTTTA | 300 |
| | TGKKTTTAAT ATTATTACCA TTGGAGAMGT TATTTAAATT ATCAAGTTAC TACTTATTTA | 360 |
| | ACTGGECTTC TATGTATATA ACATAGGTGT TATCGTTACT ATAGGTATGA TGGTGACAAA | 420 |
| 50 | AGGATTCTTC CAAGTCACT | 439 |
| | (2) INFORMATION FOR SEQ ID NO: 922: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 474 base pairs | |
| 55 | | |

(C) STRANDEDNESS: double(D) TOPOLOGY: linear

| | • | |
|------------|---|-------|
| 5 · | () CROVENUE DECERTIFICAL CEO ID NO. 022. | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922: | |
| | GTAATATCTA TATACGTATA TTTAAATGAT ATATCTGGGT ATTTTCTTTT TAATAGCGGC | 60 |
| 10 | TGTAGCCAGT CATAAATATC TETCGATGTT GGCGCATTAA CGCAACTTGC ACATATAACA | 120 |
| | TCTGCCCCAT AAACTACCAC ACTCACGTGC TCCATATATT TATCCCCCAT TGGTTTGATA | 180 |
| ٠ | GATTTTTATT ACACTATCTA TTATAATATA STMATAAAGA TTATCAAATT CATCTCTCGA | 240 |
| 15 | AAGGAGACTT GCCTGATGCC TACTGAAGAT ACAACGATGT TTGATCAAGT AGCAGAAGTT | 300 |
| | ATTGAACGTC TTCGTCCATT TTTATTACGT GATGGTGGCG ACTGmTCATT GATTGACGTG | 360 |
| | GAAGACGGTA TTGTAAATTA CAATTACATG GTGCATGGTG GNACATGCCC CAAGTTCTAC | 420 |
| | AATCACTCTT-AAAAGCTGGG-TATTGAGCCG-TGCATTACAC-GAAGAAGTGG-CTGG- | 474- |
| | (2) INFORMATION FOR SEQ ID NO: 923: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 25 | (A) LENGTH: 554 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923: | |
| | TCAACTTGTG AAGAAAATTT ATTAACTTTA GTAACTCTTC CAACAAAACC TTGTGATGTC | 60 |
| 35 | ATCACAGCCA TATTTGAAGT TATACCTGAT TTAGATCCCT TATCAATTAC AATTGTATTC | 120 |
| | ATCCACTGAT CCGGATTTCT TGCCAAAACC GTAGTAGAAA TAGGATCAAA TTTTGAAATA | 180 |
| | TCTTTTAAAT CAAGCTCTTT TTTTAATTTT TCATTTTCCG CTTCTAATTG TTGGTTCTTA | . 240 |
| 40 | GATTCTAACT GGCTAATCTT ATTTTTAGAT TCTTTAGAAT CTCCTTTTTT AAAAAAGTCC | 300 |
| | CCAATCGTAC CAGCAACAAA ATTAACTGGA TAACTCACAA CTCGTTGTCC AAAAGACACA | 360 |
| 45 | GAATCACCTA TATATTGTTC AGGAGGTGAT TGAGATTGTG AACGTATGGA CAGCCCAATT | 420 |
| | AATGCAATAA AAACGATAAT TGCACATAAA ACAACAATTA ATTTGGTATT TTTAAAAAAC | 480 |
| | TTAAGCACCC AGAACACCTC TATTATGTCA NAATATTGTA TATCCTTTTC TAATTNATAT | 540 |
| 50 | TACTCCCATT ATGA | 554 |
| | (2) INFORMATION FOR SEQ ID NO: 924: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 55 | (A) LENGTH: 575 base pairs | |

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

| 5 | | |
|----|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924: | |
| | ATCTTTAGGC ATTAAGCAAG TTTATGTAGA AGACTTTGAA CATAAATCCT TTAGCAAAGC | 60 |
| 10 | TAAAAAAGCC TTAGAAGAAA AAGGGTTTAA AGTTGAAAGT AAGGAAGAGT ATAGTGACAA | 120 |
| | TATTGATGAG GGTGATGTGA TTTCTCAATC TCCTAAAGGA AAATCAGTAG ATGAGGGGTC | 180 |
| | AACGATTTCA TITGTTGTTT CTAAAGGTAA AAAAAGTGAC TCATCAGATG TCAAAACGAC | 240 |
| 15 | AACTGAATCG GTAGATGTAC CATACACTGG TAAAAATGAT AAGTCACAAA AAGTTAAAGT | 300 |
| | TTATATTAAA GATAAAGATA ATGACGGTTC AACTGAAAAA GGTAGTTTCG ATATTACTAG | 360 |
| 20 | TGATCAACGT ATAGACATTC CTTTAAGAAT TGAAAAAGGA AAAACAGCAA GTTATATTGT | 420 |
| | TAAAGTTGAC GGTAAAACTG TAGCTGAAAA AGAAGTCAGC TATGATGATG TATAAATATA | 480 |
| | ATTGAAGTAA ATGTACCGAG GTTTCTATTT GGAAGTCTCG GTATTTTAT GTTGGAGATT | 540 |
| 25 | GCGGTAGTTT TAAAATGCNT CNTGTCNTCA TATAC | 575 |
| | (2) INFORMATION FOR SEQ ID NO: 925: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 307 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| , | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925: | |
| | AAAAACGCTG CTGAGTTTAA AAAGCAACAA TTAAATGAAC AAGGTATTTT CAAGAAACCA | 60 |
| 40 | GTGATTACAC CTATTAAACC ATATAAAAAT TTCTATCCAG CTGAAGACTA CCATCAAGAT | 120 |
| 40 | TATHACAAAA AGAACCCCGG TACATTATTA CCAATATCAC CGTGGGTCAG GTAGAAAAHC | 180 |
| | GTTTATAGAT CHCATTGGGG GGATCCAAAG CTTAAAAAGA TAAAAGTGAC TACCAGATAT | 240 |
| 45 | AGATATATTG TTACACAAGA AACGGCACTG GACCACCATT TATGAATGAT ATTGGACCAT | 300 |
| | TTGCTAA | 307 |
| | (2) INFORMATION FOR SEQ ID NO: 926: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 55 | | |

| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926: | |
|----|-----|---|-------|
| , | • | CTCTACGCAC TCATTCAGAT ACACACATTG CGCATTGCTC ATAGAATCAG GTGTACACAT | 60 |
| 5 | *** | TAAAGAAATA CAAGAACGAT TACGGCATAA AGATATCAAT ACCACTATGA ATATCTATGC | 120 |
| | | TAAAATCACA AATTCATACA AAAAAGACGC CTCCCATAAG TTTAGTCACC AAATGGAAGA | 180 |
| o | ٠. | CGTCTCGTAA TTAAAATATA TTTGCGTGCA TTCTAATTTA TACTTAGAAT GAATCATACT | 24.0 |
| | ٠. | CGTGCATAAT GTAATTTTCT AGTTAGTCAA AACTATAAAC AGTTTTACAT CATTCCTGGC | 300 . |
| | | ATGCCACCCA TGTTAGGTTG GTCATTATTT TTTTCTGGAA TTGATGCTAC AACCGCTTCA | 360 |
| 5 | | GTCGTTAAGG ACATTGCTGC AACACTTGCA GCAGTTGNAA | 400 |
| | | (2) INFORMATION FOR SEQ ID NO: 927: | |
| 20 | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 809 base pairs | |
| _ | | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | : | (D) TOPOLOGY: linear | |
| | | | |
| 25 | | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927: | |
| | : | TTTAGGTGGT TTTAATnGTT ATGGTCATTC TGGACACCTA CTTATAATAA AATTTCAAAT | 60 |
| 30 | * | CAAACTGAAC nTTTTGTACC GTTTGATTAA ACTCAAATTT ATTAGCTCCG TATTTAAATT | 120 |
| | è | TTGGTTGGGC TATATTCGTT TCGGTACTTA TTTCAACACC GTTTTTATAA ACTCGGAAGC | 180 |
| | | TATCATAAAC AATTCTGTCT CCAGCTTTTA GTTTGATCCC TTCGATTTTC ATTATTTCAG | 240 |
| 35 | | CATGCGTTAA ATTCCATACA AACGATTCTG TATCTTCGCC TAAAATAATT GTTATCTTTT | 300 |
| • | | TATACATGTT GAATTGGTCG TTAGGAGCAC TACCATGATA GTAAACTGTA CCTTTGCTCA | 360 |
| | | AATTTTCAAA TGTATACTTT CTTTTGTCTC CGCCTGCATG CCAATCAATA TTAAAATCAA | 420 |
| 40 | | ACGACCACAA TCCAACCTTT TTGTTTTCTT CTAACTCTAG GCTTGTTCCA ATACTTTCAC | 480 |
| | | CGTATGGTAA TTCTGTAGTT TCGAATTTTA GTTCAAAAGA AACTTTATTA CCTTTTTGTT | 540 |
| | | TAGGGTTTAT AACTCCGTTA AAAATAACTT TATACTGTTT ACCATTTACA TAAATTTGTT | 600 |
| 45 | | GATCGTGTCT TGAATATTCG TAATCCGGGA AGTTGTTTTT ATCTAATTTC ACGTAATCAT | 660 |
| | | CAGAAGTTGG TTGAGTAAAC CTGTAATTCA ACTCTTCTTT TCTTCTGATn TCTCGCAAAT | 720 |
| 50 | | ACATAGGTTC TATGTCTGTC GTTAACGAAT ACAACATATC TCGCATATAA GCAATGTCTG | 780 |
| | | AACGATTTT AACTTTACAA AAACAAGGA | 809 |

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(2) INFORMATION FOR SEQ ID NO: 928:

| 5 | (A) LENGTH: 1016 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|----|--|------|
| | (xi) SEQUENCE DESCRIPTION: SEO ID NO: 928: | |
| 10 | naaaactatt atcgcatcta cagtaatcgc tgcaggtctt ttaactcaaa ctaatgatgc | 60 |
| | TAAAGCTTTC TITAGTTATG AATGGAAAGG TTTAGAAATC GCAAAAAATT TAGCAGATCA | 120 |
| | AGCTAAAAAG GACGATGAAC GTATTGATAA GTTAATGAAA GAGTCTGATA AAAATCTAAC | 180 |
| 15 | TCCTTACAAA GCTGAAACTG TTAATGATCT GTACCTTATT GTTAAAAAAT TAAGCCAAGG | 240 |
| | TGATGTGAAG AAAGCAGTTG TCAGAATTAA AGATGGTGGT CCTAGAGATT ACTATACTTT | 300 |
| | TGACTTAACT CGTCCTTTAG AAGAGAACAG AAAAAATATT AAAGTTGTTA AAAACGGTGA | 360 |
| 20 | ., | |
| | AATCGACTCG ATTACTTGGT ATTAAAAAAC ATACTGAATT AAATAGTTGT ACGCCAAACG | 420 |
| | TTAGAAAACA ATGCTAACGT ATTGGCGTGC TTTTTTATTT TAAGTAACTT CCAATTTATT | 480 |
| 25 | TAGCATCTTT ACGACTGTTT AATAAAGCAC GTATGATTAA CACGGTTGCC ACTATATCCG | 540 |
| | TTACAATTTT TATGATTGTT AATACATTCG ATTTCCTTTT CACAATAGCC ACCTCGCTTG | 600 |
| | TTCAAAACAT AAACAACTAT TGCATTCACT TTTAAGTAAT TATTTATATT ATTTATCCCA | 660 |
| 30 | ATAAGCTCAC CATTCAAATA AACACAATAT TATAAAATAA TTATACCTTT GGATATAGCA | 720 |
| | AAAAGCCACA CTCTATAGCA TGGCTTCTAT CAATTATTTT AAAGTATTAT ATTTTAAAAC | 780 |
| | TAGATCGATT TGTCTTTGTA ATTTTTCTT TTCATAACTG TGTTGGAAAT GAATTAAATT | 840 |
| 35 | AACAGCTCTT TGTGCTTTAC GGTGTGTTGC AACAGTTCTT GTACGTTTGA AAAAGTTTAC | 900 |
| | AGCTTTTTGT GCATCCACAA CTTTTLLATT TACTTGWTTT KTAAAGTTTG TTGATACTGA | 960 |
| | TCATATTTTT TAGCAGCTTC ACCGTTNTTA GTTGTGCATG AGATCACCGG CAACCG | 1016 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 929: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929:

AAATGAAATC ATACCTAAAA GAGATATTAT TACAGAATCA ATGATTTGTG ACTGTATTCA

AAATGCAGGT ATTGATTTAG AAGTATTTAA AGACGACTTA CAAAAAGTA AACTAACCGA

50

| | CGTTTTCTTT AGTGAAGATG TTCATGAAGA AGGTTTAAAA GTCGAAGGAT TATACCCATA | 240 |
|----------|---|-----|
| | TCACATCTAT ACTTATATAA TTAATGAATT GATGGGTAAA CCTATCGAAA AGAATCTTCC | 300 |
| 5 | TCCTAAATTA GAAACTTATA TACAGCAACA ACAACTTGTA ACGATGGAAG AATTACTTAC | 360 |
| | TATTTATGAA TGGCCAGAAA AACTTTTAAA CAAAGAGTTA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 930: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 15 | (D) TOPOLOGY: linear | • |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930: | |
| 20 | TATTTCTGAC ATGTATCATG CTCCTTCGTG CTTTATTCTA ATGTAATATA CACAATTATA | 60 |
| • 1 | CATTGAAATT CAAATTTGTG AACACATTGT GAACTGACAT AAATTATACA CAATTTCATA | 120 |
| | GCGCATAATG TTTTAAAAAT ACACATTATA GCAATTATAA TTAAGTTCAT TGTGTTGTCA | 180 |
| 25 | TCAAAAAAG AAAAAGGTGA TGTTTTAAAT GGATACAGTT GAATCAGTCG GTTTTTGACA | 240 |
| | GCATGACTTA GCAGTTCATA TCATTTTGCA ACGATGGTGT GGTATGCTTA ATGTCGCAAT | 300 |
| | TCAGATTTTA GGATCGCAAA ATGACTCATA TATAGCATGC CAAGTGGCAA GTATCATACG | 360 |
| 30 | ACATGGRGTG TCAGGCATAN GGCTCATACT GTGCAATATG | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 931: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931: | • |
| | CCAATCAATG TTGCCAATGG ATCACCTAAT GACAACCAAG TAATTGCTAC CATAGTAACT | 60 |
| 45 | GCTGTTTTAA TTTTACCTAA TTGACCAGCT GCACTTACGA ATCCTTGTTC AATTTGTAGT | 120 |
| | AAACGTAAAC CAGTTACGGC AAATTCTCTG GCAATAATAA TGATTGCTAC TACAGAATTT | 180 |
| | GTTAGTCCTA GTTGCACAAG TACAATTAAA GCACTTGCAA CTAATAATTT ATCCGCTAAT | 240 |
| 50 | GGATCCAAAA ATTTCCCCAT ATTTGTAACT AAATTCCATT TTCTAGCTAA ATAACCATCA | 300 |
| | ACAAAATCGC TAAGGGAAGC CAATATAAAA ATAAAACCAC TGATTAATAA CTCAATTCTT | 360 |

| | ATAMAMACIG GTATTAACAC TACTCTAAAA ACCGTAATCT GGTTCGGAAT ATTCATTATA | 480 |
|----|---|-----|
| | CATCCTCATT TCTCACTAAT TTATTTCTGT TAAAAATATT AAAACTAACC ATGATCCATA | 540 |
| 5 | ACC | 543 |
| | (2) INFORMATION FOR SEQ ID NO: 932: | • |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932: | |
| , | GATTGCGAAT GAGATTAGTG GGATGATACC GGTAGAATGG GAGCAAGTAT TTACAATAGC | 60 |
| 20 | TTATGTAACT GATCAAGCTG GAGAAGTCAT CTTTAATTAT ACTAAACCAG ATAGTGATGA | 120 |
| | ATTAAATTAT TATTCAGMCA TACCTAAAGA TTGCAATGTC TCAAAAGATA TTTTTAAGAA | 180 |
| | TTCATGGTTT AAAGTTTATC GAATGTTTGA TGAGTTAAGA GAAACTTTTA AAGAAGAAGG | 240 |
| 25 | GCTTGAACCA TGGACATCAT GCGAATTTGA CTTTACAAGA GATGGCAAAT TGAATGTATC | 300 |
| | TTTTGATTAT ATAGATTGGA TAAATACAGA GTTTGATCAA TTGGGCCGTC AAAATTATTA | 360 |
| | TATGTACAAA AAATTTGGGG TTATACCAGA AATGGAATAT | 400 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 933: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 759 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933: | |
| | ATTTTACAA AGAAATAGTA GTCTTATATA TCTTAACATT TAATAACTAA ATCAAACATA | 60 |
| | TTTTGAGCCT TTTTTTGAAA ATTAACATTT TAACCTTTTT GATTTTACAA CAAATTATAG | 120 |
| 45 | CTACGTATTG AAAATTAAAG CMTTGGLTTA AGTGTTGTGT TAAAAGYTTT TATGTTTAGA | 180 |
| | TTGTTATATT ACTATGTATT CTTAAATTTG TTTAAAAAAT TAATGCTTTA AATTGATGTA | 240 |
| | TAATGGGAAT AAGAAATAAA TAAAAACGAC CCGCACGATT AACGTACGGG TCCACTACTA | 300 |
| 50 | AAGGGAGTCA AATTTTTACC TCGTTTGTAT CATGCAGCGT TTTACACATA CTTTTAAGAG | 360 |
| | ATGITTATTC GTTATCGAAG GTACACCTTT ATTATAACTT ATATCATTTT TATTAAAATA | 420 |

27.

| | ATAATGATTA TTAAATAGTA ACTAAATACA AAATTACATG GGGTGAATGA TAATGAAACA | 340 |
|-----|---|-------|
| | ATACTTAATT ACTGGTGGGA CTGGTATGGT TGGATCTCAA TTAGTTAATG AAATTAAAAA | 600 |
| 5 | ATCAGATTCA CATATCACGA TATTAACGCG ACACGACCAA ATTTCAAATG ATAAGAAAAT | 660 |
| | TTCATATGTC AACTGGGCTA AATCTGGGTG GGAACACAAA GTTCCTCAAA ATATCGATGT | 720 |
| | GGTCATCAAC TTAGCAGGTG CTACATTGAA TAAACGATG | 759 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 934: | ÷ |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs | |
| 15 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (C) STRANDEDNESS: GOODIE (D) TOPOLOGY: linear | |
| | | |
| . , | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934: | |
| | GATCAAGCTG GGGAAGTCAT TTTTAATTAT ACTAAACCAG GTAGTGATGA ATTAAATTAT | 60 |
| | TATTCAGACA TACCTAAAGA TIGCAATGTC TCAAAAGATA TTTTTAAGAA TTCATGGTTT | 120 |
| 25 | AAAGTTTATC GAATGTTTGA TGAGTTAAGA GAAACTTTTA AAGAAGAAGA GCTTGAACCA | 180 |
| | TGGACATCAT GCGAATTTGA CTTTACAAGA GATGGCAAAT TGAATGTATC TTTTGATTAT | 240 |
| 30 | ATTGATTGGG TGAATTCAGA ATTTGGACCA ATGGGAAGAG ACCATTATTA TATGTATAAA | . 300 |
| 00 | AAATTTGGnA TTTGGCCTGA AAAAGAATAT GCCATAAATT GGGTTGnAAA AATAAAGnTT | 360 |
| | ATGTTAAGAG CAAGNTTGAG CTGAACTATA GGGGAGATAA | 400 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 935: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 345 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | |
| | | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935: | į· |
| 45 | CTGAATATAA TTTTTnCAAC TACATCTCGT TTATTAGACA CCGTGCACTG ACTAAGAAAA | 60 |
| | TTTCTCTTGA CTCCATTAGT CCTGACGAAT ACTAACATTT AACTACCTTG CTCATCGATA | 120 |
| | GAAACAACTT GTAATGTTAA TTTCCCTTAT TTTCTTAGTT TTAATCTATC AGCGATTAAT | 180 |
| 50 | TCGATTGCAT CTTTTTCATA AGCAATTGGA TAAACTTGAC CGCGGTACAC CTAACGCTCG | 240 |
| | AAATATGATT TINTATCGTC ATAATCTAAA ATATTATNGG CAAAATCACA GCAGTTTTCA | 300 |

(2) INFORMATION FOR SEQ ID NO: 936:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 619 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|--|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936: | |
| | GTTATCATCA TCTTCTGAAG TATCATCTTG CCCATCGACT TGACTTGCAT CAGTTCTCTT | 60 |
| 15 | TAAATCATCA AACTCTGGAC TAGCTAATGT ATTATATAGT GTTTTAGGTA AGTAATAATA | 120 |
| 15 | TTCGTTTAGC ATATCTTCTT TTAAAATATC ATCTACTTGA TACATAATTC TTTGAGCCAG | 180 |
| | ATACATATTA TCTTCAGAAT TTTGATTTTG GAAAAAATTA GGTAAATATA AGAACATATT | 240 |
| 20 | TACTAAAATA TCATCTAAAT CTGAATGTAT AGATGGTATA TCAAAGAAAT CTTGGCTTAA | 300 |
| | AAATGCATGT TCTAAATACA AAAATAATAA ATCTGTATAT TGTGTTTTAG TACGATACAC | 360 |
| | TTTAATTTGA GATTCCGTAT ATGATATACG TGTATCTAAG CGAAGATCAA TTAATTTAGC | 420 |
| 25 | AGTACTTGGG CGCTCAACTT TAATAGAATT TAATACGCGC ATATCTTCTA ATAATTTAAA | 480 |
| | AAGTTGTTGG ATAAAATTTA GGGLGTTTAA AAGTTTTATC TTGLACTACT TCATTTACAA | 540 |
| | TTTGtACATC CaTCATATGA TAACCGTAAG CAGCTAACAT AACATCTGTT TTTAAACCAG | 600 |
| 30 | CCATTTCGAT ATGGCTTGG | 619 |
| | (2) INFORMATION FOR SEQ ID NO: 937: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 615 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937: | |
| | TAATCCCTTT CATAATGGGC ATCAATATCA TATTAATCAA TCTAAAAAAC TTACAAATGC | 60 |
| 45 | TGACGTTACT ATTGCAATAA TGAGTGGTAA CTTTGTCATG CGTGGCGAAC CAGCAATCTA | 120 |
| | TAATAAGTTT ACTCGTGCAA AAATGGCATT ATCAACAGCT GATTTAGTTA TCGAACTACC | 180 |
| | AGCAACTGCC AGTTTATCAT CTGGGGATCA TTTTGCCGAA CTAGCAGTTA AAGTCGCNGA | 240 |
| 50 | TTATATGAGT GTCGATACAA TTGCATTTGG TAGTGAAAAT AATGALATCA AAACATTAAA | 300 |
| | אליים אל איני און אינים אליים ליים אינים און אינים אליים אינים אליים אינים אליים אינים אליים אינים אליים אינים אליים אל אינים אליים | 260 |

| | AAGTCCTAAC AACATACTTG GTATTAGTTA CCTGAAAGCA ATTGCTAAAA ATGCTAAAAA | .480 |
|----|---|------|
| | CATCAATGCA ATTTCTATCA AACGAGAAAA TGCTCAACAT CATGATTCAT TAATTCAACA | 540 |
| 5 | CCATCAGTTT GCAAGTGGTA CATCTATTAG AACATCAATC ATTAGTCAAG ATGATCATTG | 600 |
| | GCATCATGTG GTACC | 615 |
| | (2) INFORMATION FOR SEQ ID NO: 938: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 15 | (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 938: | |
| 20 | AGAATTGAAG ATGGTAAAGT TTCAAAATAT CATTCGGTTA TCATAAAAGA CGCACAAGCA | 60 |
| | ACTTCACCAT ATTCAATTTT TATCAGAGGT GCTATTTATC GCTTTGAACC ATTAGTATAA | 120 |
| | ATATACGTAA GTGCTATGAG CGAGAATGCC CATATGAATA ATGACAAGCA CAATGGAAAG | 180 |
| 25 | AATCGTAATA TATTATTTAA TCGTGATGCT TAATTAAAAT GAAAAAGATT GATAATATAA | 240 |
| | ATGTGAAAAA GTAAGTATAC CCGTAAACTA AAGTATTCAC GGTGAGAGGT GCTCATGTCA | 300 |
| 90 | TAATGATGCA CGTGTCATAA TTATAATAGC TTANATATGT CCATACAACA CCATGTAGAT | 360 |
| 30 | ATGCATATAC AGGGTATGAT AGACATAGNG TCTGNGAAAT | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 939: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 466 base pairs | |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 939: | |
| | GTACAGGTAT GATTGGTGAT CCCATCAGGT AAATCAGAAG AACGTGTGCT ACAAACAGAA | . 60 |
| 45 | GAACAAGTAG ATAAAAATAT CGAAGGTATT AGTAAGCAAA TGCACAATAT TTTTGAATTT | 120 |
| | GGAACAGACC ATGGTGCAGT GCTTGTTAAT AATAGAGACT GGTTAGGACA AATCTCATTA | 180 |
| | ATTAGTTTTI TACGTGACTA TGGTAAACAC GTCGGCGTTA ATTACATGTT AGGTAAAGAT | 240 |
| 50 | TCAATCCAAA GTCGTTTAGA ACATGGTATT TCATATACAG AATTCACATA CACGATTTTA | 300 |
| | CAAGCTATTG ATCTCGGTCA TTTGAATAGA GAATTGAATT | 360 |

| | GTAGATAAGC AAATGATTAA TAGTTGAGGG GTATGTCGAT GAAGCG | 466 |
|-----------|---|-------|
| | (2) INFORMATION FOR SEQ ID NO: 940: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940: | |
| 15 | ATGAATCACC CATTGATACC AATCATTTAC ATCACTGTCA TACGAACATA TATTTAAATA | 60 |
| | GAAAAAAATT ATTTTAAAGA TTATAACTAC TCTTAATCAT TTTAGTGAAT TAAAAAAAGT | . 120 |
| | AGTGCAAAAA GCAAAATATA CTTTATACAC TACAAATCAT TTATTTAT | 180 |
| 20 | CCAAAAAATG TTCCAACTAA TGAAACCGCT TGTTCAGCAG TATGATTATH ACTGTCAATC | 240 |
| | AATGGATTTA CTTCAACTAA ATCCATTGAG GAAATTAAAT GTGATTGATG CAGTAATTCC | 300 |
| | AATGCNAAAT GGCTTTCTCT ATNACTAAG | 329 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 941: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 941: | |
| <i>35</i> | CGATATAGTA CCAATTTATT TGAAGAAAAA TCCGAACTTC AAATTTCCGA TGAAGCAAGA | 60 |
| | TATACCEGTT ATTATEATTE GACCAGGTAC TEGAATTECT CCTTTTAGAG CATATTTACA | 120 |
| | AGAACGTGAA GAACTTGGTA TGACTGGAAA AACATGGTTG TTCTTTGGTG ATCAACACCG | 180 |
| 40 | TAGTTCTGAC TTTTTATATG AAGAAGAAAT AGAAGAATGG CNTGAAAATG GAAACTAACA | 240 |
| | CGCGTAGATT AGCATTTCCA AGAGNCCAGA CACAAGATAT GACAGCCNCG ATATGGAGAA | 300 |
| 45 | | |
| 43 | GTAACGTTCC ATGAT | 315 |
| | (2) INFORMATION FOR SEQ ID NO: 942: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 699 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | y. |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 942: | |
|----|---|-------|
| | TACCAATAAT CAACTTGTTT TACATCATCG TGTGTTTCAA TCACTTTCCT TTTTATACCT | 60 |
| 5 | TTCTTACCTT TAAAGAATGC ATCAACATCT TTTATTGAAG ATCCTTTTGA ATCTTTAGTA | 120 |
| | AATCTATAAT CTGCAAGTTC CACTTTACCC ATTAATTCTT TGTAATCTTT CCATCCTTGA | 180 |
| | ATCCCTTAC TATTCGTAAA CGACTTTCT GTCATTAATG GATCCAACTT ATCAAGAGAT | 240 |
| 10 | GGCGCATCTT TAATTCCTTT CATTTTCTTC TCTATTTCTT CATATTTCTC TAAATCTGGA | 300 |
| | TCTTTCTCTT CTTCCGATTC TTTTTTTACA GTTTCTTGTT TTGATTCTTC TGATTTCTTT | 360 |
| 15 | GATGATAATT TATGATTCCC ACCAAAAGAA CAACCTGCTA CGACTAAAAG CATAATTAAA | 420 |
| 15 | AGTAAACATC CCAGTGTCTT TTTCATAAAC TTTCTCCTCT TAAGTTATTT TGTTTGAATC | 480 |
| | AAATAAACAT ACATAAATTT AAAAAACTTA TTTATATTGA TATTTTACAT TAACCATCAA | 540 |
| 20 | TATTTTAAA TACTTTAAWT GATAATTTAA GAAAATTGTT TTGTCTAATA ATTTAAGTAG | 600 |
| | TTAAAACATA GATAGATATA AAATAGTTTA TAGCCATTAA TTTATAAGTT TAAAATTCGC | . 660 |
| | ACTATTTCAA TTTGCCATTT AAAAATAGTT TGTTTAATC | 699 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 943: | • |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 943: | |
| 35 | CGCTCCATAA ATCAACAATG TTCGAGTCTG TAATCTAGAT GATAAAACGC CAAGAATGAT | 60 |
| | CATAAATGGC ACTTCTAAAG CAGCACATAA ACTAGCTAAA TAACCGACAT GTTGTTCATT | 120 |
| 40 | TTCTTTTAAA TAATCAGTAA CAAATAAAGG CATATTCATC GTATACATCC ATTGTCCAAT | 180 |
| 40 | GTGTAATAAA ATAAATGCAA TAAATGGTAA TAAAAGCGTT TTGTCTTTAA ACATATTAGG | 240 |
| | AGCAATTTTT TCAACATGTT GTTGCGTACT AATAGGGTGT TTAATGTTTA AATCCTTATA | 300 |
| 45 | GAMAAACACT TGAAGTACTA AAGTAAATAA AATGATACTT ATTGGGCCAC CAAACAATCC | 360 |
| | AGCATAGCCT TTTAATCCGA TTAATTGGGC ACCAATAAAT | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 944: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 570 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 944: | | | |
|----|--|-----|--|--|
| 5 | AAGATGACAA TACTTTGTTT CAAGAATTGA AAAAAGAATT AGAACAATGG GATTTTAATG | 6 | | |
| | TTGCTGGTAT TGAAGATTTC GGCAAAGTAA TGGATACATT TGAAAGTTTT AATCCTGAAA | 12 | | |
| | TTGTTATATT GGATGTTCAA TTACCTAMAT ATGATGGGTT TTATTGGTGC AGAAAAATGA | 18 | | |
| 10 | GAGAAGTTTC CAACGTACCA ATATTATTTT TATCATCTCG TGATAATCCA ATGGATCAAG | 24 | | |
| | TGATGAGTAT GGAACTTGGC GCAGATGATT ATATGCAAAA ACCGTTCTAT, ACCAATGTAT | 30 | | |
| 15 | TAATTGCTAA ATTACAAGCG ATTTATCGTC GTGTCTATGA GTTTACAGCT GAAGAAAAAC | 36 | | |
| 15 | GTACATTGAC TTGGCAAGAT GCTGTCGTTG ATCTATCAAA AGATAGTATA CAAAAAGGTG | .42 | | |
| | ATCAGACGAT TTTCCTGTCC AAAACAGAAA TGATTATATT AGAAATTCTT ATTACCAAAA | 48 | | |
| 20 | AAAATCAAAT CGTTTCGAGA GATACAATTA TCACTGCATT ATGGGATGAT GAAGCATTTG | 54 | | |
| | TTAGTGATAA TACGTTAACA GTAAATGTGA | 57 | | |
| | (2) INFORMATION FOR SEQ ID NO: 945: | | | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1241 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | |
| 30 | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 945: | | | |
| 35 | CCGAGnCCAC CGTTCCAAAG TCCATTTTTA TCCCCATCCC TCTCTGAATT GAACTATAAT | 6 | | |
| | TTTTGAATTT ATTAATAATG CTATTTTTNT TATTTTATCA AAAACTGATT ACAAATACAC | 12 | | |
| | ATAGAAAATG AAATATATTT TTCTTTGACT ATACATAACT GTTATTTCTT TGGATATTTA | 18 | | |
| 40 | TATTAAATGC ATTGGTAGTA GTTGTAGCGC ATTAATGTTT GACGGTGTAT AGTATTAATT | 24 | | |
| | ATATTGAAAG TTAGTTGGAA GTTGATAGTA GGAGTGGGAG CATTGAAGCG ATTTGTGGCG | 30 | | |
| ٠ | ACGGTATTAT TATTACTAGT CTTTATATCA GGATGEGGTA ATGTTAAATA TGTGAAAGAA | 36 | | |
| 45 | ATAGATGAAG CAGTTAAAAT TCAAAATCAA AAACAAGAAC ACTTGCCCAA AAAAGGCAAC | 42 | | |
| | GGTGATCGTG TTGATCATTT TGAACGCAAA GATGCTAATA TTTATGTCTA TGATAAGGAT | 48 | | |
| | AAAATTATCA TTTTAGCTTA TAAACCTTTG AGTAATGATG ATGAAGTGCA TTATTATGCA | 54 | | |
| 50 | | | | |

TATGATTTTA GTGATAAACG TGTATCATAT AAGCAAGATT TTGATTCGAG ACGATATTAT

CAACAACATG ATGCGGATTA TCATGAAGAA AATATGACGA ACTAGATATG AATAGGAGTT

55

600

| | GGTAAAAAAG | AATCAGCAAC | GACATCTTCG | AAAAACGGCA | AACCATTAGT | TGTCGTATAT | 780 |
|-----|------------|-------------|-------------|------------|------------|------------|------|
| | GGCGACTATA | AATGTCCTTA | TTGTAAAGAA | TTAGATGAAA | AAGTCATGCC | AAAGTTGCGT | 840 |
| | AAAAATTATA | TAGATAATCA | CAAAGTGGAA | TACCAATTTG | TCAATTTAGC | TTTCTTAGGT | 900 |
| | AAAGACTCAA | TTGTTGGTTC | GCGTGCGAGT | CATGCAGTAT | TGATGTATGC | ACCTAAATCA | 960 |
| | TTTTTAGATT | TTCAAAAGCA | ATTATTTGCT | GCCCAGCAAG | ATGAAAATAA | AGAATGGTTA | 1020 |
| | ACAAAAGAAC | TATTAGATAA | ACATATTAAA | CAACTGCATT | TAGATAAAGA | GACGGAAAAT | 1080 |
| · . | AAAATTATAA | AAGATTACAA | GACAAAAGAT | AGCAAGTCTT | GGAAAGCTGC | AGAGAAAGAT | 1140 |
| | AAAAAAATAG | CGAAAGATAA | тсататааа | aCGACACCAA | CTGCATTTAT | TAATGGCGAG | 1200 |
| | AAAGTTGAGA | TCCATATGAT | TATGAAAGTT | ATGAGAAGTT | A | | 1241 |
| | (2) INFORM | ATION FOR S | EQ ID NO: 9 | 46: | | | . , |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 base pairs

 (B) TYPE: nucleic acid

 (C) STRANDEDNESS: double

 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 946:

| 120 |
|-----|
| 180 |
| 240 |
| 300 |
| 360 |
| 420 |
| 480 |
| 540 |
| 600 |
| 660 |
| 720 |
| 780 |
| 840 |
| |

| | CAATCTACCA TTAATAAAAT CTTATGTTTT TTTCCTAAAA CTTCTGGCTA CTTCATTTAT | 960 |
|----|---|------|
| | TTGATGTATG GGTAGATAAT TCCGGTTTGG GATACCTCCA TATCAAACCT TTTTTCCTAA | 1020 |
| 5 | TCAATATCCT GGAAAAnCCC TTTTTTTGGG CAGGGCG | 1057 |
| | (2) INFORMATION FOR SEQ ID NO: 947: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 649 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (b) TOPOLOGI: Timear | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 947: | |
| | GATATCCGCT CGATGAATAT ACCTTTAAAG GTGTTGGTGC AAATTCTGAA CAATTAAGTG | 60 |
| 20 | CTATGAATCA TGATTCTTTA AAAAAGGAGT ACATTTCAAA TGACTGTTAA ATATAATCAA | 120 |
| | AATGGCGAAT TAACAATGGA TGGTATTAGT TTAAAAACGA TTGCACAAAG CTTTGGTACA | 180 |
| • | CCTACCATTG TTTATGATGA ACTACAAATT aGAGAACAGA TGCGCCGTTA CCATCGCGCA | 240 |
| 25 | TTTAAAGATA GTGGATTAAA ATACAATATT TCATACGCCT CAAAGGCATT TACTTGCATT | 300 |
| | CAAATGGTCA AACTTGTAGC TGAGGAAGAT TTACAGTTAG ATGTTGTTTC TGAAGGTGAA | 360 |
| | TTATATACAG CTTTAGAAGC AGGTTTTGAA CCGAGTCGCA TCCATTTCCA TGGTAACAAT | 420 |
| 30 | AAAACGAAAC ATGAAATTAG GTATGCTTTA GAArATAATA TCGGTTATTT TGTTATAGAT | 480 |
| | TCATTAGAAG AAATTGAATT FATAGACCGC TATGCTFATG ATACGGTTCA AGTTGTATLA | 540 |
| 35 | CCGAGTTAAT CCCAGGTGGT TGrAAGCCAC mTrCaCaCgA aTTTATTCaA ACyGGGcaaG | 600 |
| | AAGGATAGGT TAAAGTTTTG GGATTAAnCC nnTTTCCCAT TAATGGGCC | 649 |
| | (2) INFORMATION FOR SEQ ID NO: 948: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 472 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 948: | |
| | TACAAAGCTT AAAAACAGAG CTTAGTYTCG TTGAACCATT AATTAGCCGC TTAGAATTAG | 60 |
| 50 | AAGAAGCTAA TGATAAACTA GCTAATATCA ATGATAAGTT AGATGACATG TATGATTTAA | 120 |
| | TTGAACATGA AGTTAAAGCT AAAAATGATG TCGAAGAAAC AAAAGATATC aTTACGGATA | 180 |

| AAAACTACTA TATAAATGAA TCTGATGCTC AGAGTGTTCG TCAATTTGAA AATGAATTC | 300 |
|---|-----|
| AAAGTTTAAT TTCTGTATAT GATGATATTT TAAAAGANAT GTCTAAATCT GCTGTGCGAT | 360 |
| ATAGCGAGGT TCAGGATAAT TTACAATATT TAGAAGATCA TGTCACAGTT ATTAATGACC | 420 |
| AACAAGAAAA GCTACAAAAT CATCTGATTC AATTGCGTGA AGATGNGCAG AA | 472 |
| (2) INFORMATION FOR SEQ ID NO: 949: | |
| (i) SEQUENCE CHARACTERISTICS: | |
| (A) LENGTH: 400 base pairs | |
| (B) TYPE: nucleic acid | |
| (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | |
| | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 949: | |
| AGAGGATCCC AGGCGTTTGT TGATCCAGCA GCCGATNCAG AATACATCTT CTATGCATAT | 60 |
| AAACGTTTCA ATTTCGAATT GAAAGATCCA AACTTCACTA GTGAAGAAAA TATGTTTAAA | 120 |
| GATGTATCAG ACAAACCATT AATACCTGCT CGTAAAGCTC AAATTACAAA TGCGAACTAT | 180 |
| AAACGACATG GTATGAAGTT GATGATTCTT GGGAATGACG AACCATATAA CAATGAGTTC | 240 |
| AAGAAAGATG ATCGAAAATG CGAAGAATGA GAAATTTCAA AGGTGCGCAN GTCAAGCCAT | 300 |
| GTGTCAGGGG GGCATATGAT TTCnGGTCAT CAGTAAGGAC TGTGTCATGC CATGGCCATC | 360 |
| TGTTGTACnG ATCTCTAATA GAATCTCAGA TGCCCGGCAA | 400 |
| (2) INFORMATION FOR SEQ ID NO: 950: | . " |
| (i) SEQUENCE CHARACTERISTICS: | |
| (A) LENGTH: 556 base pairs | |
| (B) TYPE: nucleic acid (C) STRANDEDNESS: double | * * |
| (D) TOPOLOGY: linear | |
| | |
| | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 950: | |
| AAAATCTTCG ATGACAAAGA AATCTAATGA TGTTTCTTTA AAATGACCAA ACTGCAACGG | 60 |
| AATGATATAA CCACACTTGA GATATGGCGC TTCTTTTTTC AACTTAGTCA TCACATCATA | 120 |
| ATCCAAAGAC ATCACACGAT ATTGATGTTC AACACCATGC TTTTTCAAAA TATCAATAAC | 180 |
| ACGTTGTGTA TAATCTGCTG GTTCTTTACC ATGTGGCTTT AACTCTACTA GTAGCTTCAC | 240 |
| ATTTGATTGT TTAGCCGTTT CAATAAATTC GTCTAAGGAT ACAAATTTTG CTTCATGTCC | 300 |
| ATTTTGACGC ATTTTCAAAC CGACGATATC TTTGAAATTA GATTCAGAAA TATTTTTATT | 360 |

| | CATAATTGTA TCTAACTCAA CGTATTCGAC ATTCGCTTTT GCAGCAGCTT TCAATGACGG | 480 |
|-----|---|-----|
| | AATAGAATTT TCAACACCTT TATCTTCGAA ACCACGTGGC CAATAATGGA GATATTGTAA | 540 |
| 5 | TTGATAGTAT TATTGG | 556 |
| | (2) INFORMATION FOR SEQ ID NO: 951: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 469 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 951: | |
| | TTGTGGTAAT GATGTTAATC AGTATATTTC TACTTTTGAC AATGACATCT AAAGGATTAA | 60 |
| 20 | GCAATCTTAG AGTAATAGAT GATGAGGCAA ATATCATTTC TTTTATTACT GAATTGAATT | 120 |
| | ATATTAAGTC GCAAGCTATA GCAAATCAAG GATATATCAA TGTTAGATTT TATGAAAACA | 180 |
| | GTGACACTAT TAAAGTAATA GAGAATAATA AAATACGATT TCTAAAATTA AAAGTAGGCA | 240 |
| ?5 | AAATAATTAA TGTTGCAAAA GTTGATATTA TTGCCTTTGA TAAAAAAGGG AATATCAATA | 300 |
| • • | AATTTGGTAG CATAACAATT TACAATAACA ATTCAATTTA TAGGÁATAAT ATTCCATATT | 360 |
| | GAAAAAGGCA AGAATTCGTT ATGAAAAGCT ATAAGTGTAA AGGTTCATTC TTAATAGATA | 420 |
| 30 | GTATGGCTGG nTTTTTGCCA ATTGGGATTG nATTACATTA CTATTGATT | 469 |
| | (2) INFORMATION FOR SEQ ID NO: 952: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 730 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 952: | |
| | ACATHTATAA THOTTATTTG CTTGCTCCTT TCACTTTTTA AGAGTAAAAH ATAACCTGAA | 60 |
| 15 | ACATAACTTT AACATCCAAG TTTCAGGTTA GTGTAATGTA AATGATTTAC TTTGTTMTAT | 120 |
| | TATGATTAAA CATCTAATTC TCTGCTTGTA AGTGCTTTAA TCATCTCTGG ATCAGCATGT | 180 |
| | GAGAAAAATT GGCTATTACT TTCTTCTAAT GTCGCAATTT GTTGTTTATC TTCTTCTGTA | 240 |
| 50 | AGTTCAAAAT CAAATATATC TAAGTTTTGA GCCATACGTT CTGGATTTAC TGATTTTGCG | 300 |
| | AGTACAACAA TGTCACGTTC TACTAACCAG CGTAAAATAA CTTGTGCAAT TGATTTGTTG | 360 |

| | AATGGTGCCC AAGCTTCTAC CACAACATTT TCTTGTTGAA GTGCTGCAAC TTGTTCTTCT | 480 |
|------|---|-------|
| | TGTTGATGGA ATGGATTAAT TTCTATTTGG TTCACTTGTG GTTGAATTTG ATTGTGAATA | 540 |
| 5 | CCTAAATCTA CAATTCGATC AACGCCGAAG TTAGATACAC CGATTGCTTT AAATTTTACC | 600 |
| | ATTTTCETTT AACTCCTCCA ATGCACGCCC ATGGAGCCAT ATACHGCCAT TGGTAAAGGT | 660 |
| | TGGGTGGAAT NAAGCACCTA GGATCCAGGA TAGGTCCCAA ATTTTAATCC GGTGGGNAAT | 720 |
| 10 | GGATCGGTTC | 730 |
| | (2) INFORMATION FOR SEQ ID NO: 953: | |
| | (2) INFORMATION FOR ONE 15 HOVE | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * |
| | (b) 10201001. 1=== | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 953: | |
| | ACAAATGACA ACGTACAATG ACGTCTTCAC AAACATGCAT TTTAGGAGAT TGATTATTAC | |
| 25 | AAATATCCAG TTTTTTGTTA CATCTATTTG CAAATCTGCA CTTATTAACG TGAAATGCTT | 120 |
| | GGATTGATGG CACAATTCCT TCTATCGTTT CAAGTCGTTT CTGCTCTTCT TTAAGTTTTG | 180 |
| | GAATTGTTGA TAATAATTTT TGGGTATAAG GATGTTTCGG ATTGTGTAGT ATTTCTTTTA | 240 |
| 30 | TGCCTCCAAA TTCTACAATT TGACCTGCAT ACATAACTAA GACTTTATCG CAAAACTCAG | . 300 |
| | CAACTACACT CAAATCATGT GTAATCATCA TAATTGCCAT TTGCGTTTCC TTTTGCAATT | 360 |
| .35 | CTTTTAATAA GTCTAATATT TGCGCTTGAA TCGTGACATC | 400 |
| . 33 | (2) INFORMATION FOR SEQ ID NO: 954: | * |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 251 base pairs | • * |
| 40 | (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
| | (b) TopoLogi: Timear | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 954: | 60 |
| | TAAATCTTGA GGACGTTTGG TCTGAAAGCG ATGCTCAACT GTTGATAAAT CCAATTCGAT | |
| | AACATCTGTA TAATTAGGAT CTTCTTTCTC AACATCAAAn ACATATGGTT TTGTTTCAAA | |
| 50 | TATTCTTTTA CTAGCGCGAT ATGTTCGTCT GATCTACCAG TTAACTTCAT ATATTTAAGA | |
| | ATTOTOATOA ACTGGGGAAG AATCCGCAAG TTGCTCCATA CTCTGGTGCC ATGTTTDCAA | 240 |

(2) INFORMATION FOR SEQ ID NO: 955:

55

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 514 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 955: | |
| | AAACATTTAC ACAAGTAGTA GAAGCAATTT ATGATGAAGA AGGTAACAGC TTaGamgCGG | 60 |
| 15 | CGCGCCATCC ATTACAAATC GTTCAAATTA AAGTGGATCG CCCGATATAT CCAAACAACA | 120 |
| 15 | TGATGAGAAA GGAAATTGGC TAATGAAAGC TACTACAATC ATTGGCATAG CTGGTGGATC | 180 |
| | TGGCTCAGGA AAAACAACTG TAACTAACGA AATTATGAAA AACTTAGAAG GTCATAGTGT | 240 |
| 20 | CGCTTTACTT GCTCAAGATT ACTATTATAA AGATCAAAAG CACTTGACTT TCGACGAGCG | 300 |
| | CCTAGAAACC AATTATGACC ATCCATTTGC ATTCGATAAT GATTTATTAA TTGAAAATCT | 360 |
| • | TAAAGACTTG AAAAATGGTA AAGCAGTAGA AGTACCGACA TATGATTATG CLAGTCATAC | 420 |
| 25 | AAGAAGTGGA CATTACCATT GGATTTTLAA ACCTAAAGAT GETTATTTAT CGTAGAAGGG | 480 |
| | CCTTTTTCGC CTTTAGGAAA ATAAGGGTAT TTAC | 514 |
| | (2) INFORMATION FOR SEQ ID NO: 956: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: | |
| • | (A) LENGTH: 388 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | , |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 956: | |
| 40 | ATTITAACGA ATATCTTGCC GTACGATGCC CAAGCTGCAT CTGAAAAGGA TACTGAAATT | 60 |
| | ACAAAAGAGA TATTATCTAA GCAAGATTTA TTAGACAAAG TTGACAAGGC AATTCGTCAA | 120 |
| | ATTGAGCAAT TAAAACAGTT ATCGGCTTCA TCTAAAGAAC ATTATAAAGC ACAACTAAAT | 180 |
| 45 | GAAGCGAAAA CAGCATCGCA AATAGATGAA ATCATAAAAC GAGCTAATGA GTTGGATAGC | 240 |
| | AAGCCATAAA GTCTCACCTG AATGACGGTC AAGTGTATAG CATAATAGTC ATGCTAAGTT | 300 |
| | AATGAGTCTC AATGTGTAGG GCACAAGTGC GGGCGTCTAT GCATGAATGT TGCCACGCTC | 360 |
| 50 | ACAACTGGGA AGTGTAAATG TGACTGTA | 388 |
| | (2) INFORMATION FOR SEQ ID NO: 957: | |

Port.

| <i>5</i> | (A) LENGTH: 394 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----------|---|------|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 957: | |
| 10 | AACAAAGTAC ATCGCAGTTA CGAGAAGAAA TAAATGCATT GTATAATCAA GTTATAGAGG | 60 |
| * | TTGGACAAGC GTTATCAAAG CAGCGTCGTA TAGTCGCTAG GGAGTTAAGW GACCACATTG | 120 |
| | TATCGGAAAT TCAAAACTTA CAAATGAAAG ACGCAAATCT TGAGATTTCA TTTAAAAAAT | 180 |
| 15 | TAGAAGAACC GAATATTGAT GGAATCGAAT TTGTAGAATT TTTAATCAGT CCAAATAAAG | 240 |
| | GGGAACCATT AAAAAGTTTA AATAAAATTG CGTCAGGTGG AGAACTTTCT AGAATTATGT | 300 |
| | TAGCGTTAAA AAGTATTTTT GTTAAALCGA GAGGTCAAAC TGCAATTETT TTCGATGAGG | 360 |
| 20 | TTGaCTCAGG TGTATCtGGr_caAGCTGcAC_CAnA | 394 |
| | | |
| | (2) INFORMATION FOR SEQ ID NO: 958: | |
| 25 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 503 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 958: | |
| | CCGCCATTTT TTTCGATTTC TTTTTCAAGT TTTTCACGGT CTTTTGAAGA TAGACTATTG | : 60 |
| 35 | AAATCTTTTG CACCACTATC ATCAAAATCA ATATCTGCTT TCAATTTTGT GCTAGATTTT | 120 |
| | AAAATGAAAT TAATTGGTTC TTCAGCATAL TTGATGCCGA TATYTAACGT AGATTTCTGA | 180 |
| | GTGTTATTYT TTACGTCAGA ATCTATATTA TTTTCAAAAG TGAATTCATT TTCGTCGCTA | 240 |
| 40 | TATTTATCTA ATGCGACAGT GATTTACCT TTATCTTGAC GTTTTGTGCC ATCTACTTTT | 300 |
| | TCTTGGTTAT CTAATTTGAT TTTTGATTCA TCATATTCTG TCTTTTTACC AAATTCGTAT | 360 |
| | TTATCATTAT ATTTATCATC TTTWTCTTTA GAAGATACGC CTTTAATTGT ATATTTCGCT | 420 |
| 45 | TCAGCATACG TGTATTTATC TTGATCGAAA TCAAGTGCGT AATCTAGTTT TAACTTATCG | 480 |
| | TOTTOTARAG TATTAGTACO TIT | 503 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 959: | |
| 50 | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 307 base pairs (B) TYPE: nucleic acid | |
| 55 | (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 959: | |
|------------|---|-----|
| | TCAAACGTAC AGAGCTTGTT AAGTGTTTAG ATTATTTACG AGAGAGCGAC ACATTAGTTG | 60 |
| 5 | TCTATCAACT TGATCGGTTA GGTAGAACGA CAAAACTATT AATTGAATTA TCACAATGAT | 120 |
| | TCGATGATAA CGGAATTGAC TTACCANATT AGTAACCTGA ACATTTCCAC GAAAGACCCC | 180 |
| 10 | ATGGGGCCAA AATGTTTTTA CCGATGATGA GTGCCTTTTT CCGGGTTAGA AGTTAATTTA | 240 |
| ,, | CTATGTGAGT GTATAAAATA GACTNAGCAG CCACAAGNCG AGAGGCCGAA AAAAGCGGGC | 300 |
| | GCCCTCT | 307 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 960: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 960: | |
| | ATAAGGACAT TTATAGTCGC CATATACGAC AACTAATGGT TTGCCGTTTT TCGAAGATGT | 60 |
| | CGTTGCTGAT TCTTTTTTAC CGCAAGCTGT TAAAATTAAC ATGCTCACTA TAAATAATGT | 120 |
| 30 | TAGTAATTTT TAGTCCATAA TTACTCCTAA TCCTAACCAN GTCnGCnAAA TTTCCTCCAT | 180 |
| | GATAATCCGC ATCATGTTGT TGATAATATC GTCTCGAATC AAAATCTTGC TTATATGATA | 240 |
| | CACGTTTATC ACTAAAATCA TATGCATAAT AATGCACTTC ATCATCATTA CTCAAAGGTT | 300 |
| 35 | TATAGCTAA AATGATAATT TTATCCTTAT CATAGACATA AATATTAGCA TCTTTGCGTT | 360 |
| | CAAAATGATC AACACGATCA CCGTGCCTTT TTTGGCAAGT | 400 |
| ‡ 0 | (2) INFORMATION FOR SEQ ID NO: 961: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs | |
| 1 5 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 961: | |
| 50 | ACAATTAGTT ATACCCAAAA GAGTTATGTC AGTGAAGTAG ACAAGCAAAA CTCAAAATCT | 60 |
| | COMPANIES COMMENTARIO AND CONTROL COMPANIES AND | 120 |

| | GCTCCTGATA ATCAATTGCC ACCTTTAGTT CAAAGTGGCT TTAATCCATC GTTTATCACT | 240 |
|----------|---|-------|
| | ACACTATCAC ATGAAAAAGG TYCAGTGATA CGAGTGAATT TGAAATTTCa TATGGTAAGA | 300 |
| 5 | ACTTAGATAT TACCTATGCG ACTTTATTCC CTAGAACTGG TATTTACGCn GGAAGGAAGC | 360 |
| | ATAATGCATT TGGAAATAGG AACCTTGTAN TTANGTATGG | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 962: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 358 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 962: | |
| 20 | CTTTTACAAA GACAAATTAG CGGTAATCGG TAANGATCGT TGTTGATCCA GTTGCACTAT | 60 |
| | TGAAAGAATT AGACGGATTA AATGAACGTG GCATTCCTAC AAGTAATTTA CGTATATCTA | 120 |
| | ATCGTGCGCA AGTGATTTTA CCATATCACT TAGCACAAGA TGAATATGAA GAACGTTTAC | 180 |
| 25 | TGGTGACAAT AAGATTGGTA CACTAAAAAA GGTATCGGTC CAGCATATGT AGCCAAGTCA | 240 |
| | CGTATCGGTA TCGTATGCAG ATTACTTGAA AAGAACATCG AAGATATTAA ATCAACATGA | 300 |
| 30 | TATAACCAGC TATTCAAGGA TGTTACGAAC ATGNCACATT GATGAANCTT GAGATATA | 358 |
| | (2) INFORMATION FOR SEQ ID NO: 963: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 258 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 963: | • |
| - | AGTGAGCAGG TTGAAGTAGT AGGGCCGATT CAAATGGAAA GAGATACACA TAAAGATGGT | 60 |
| 45 | AAGGTAAAGT GGCAATTGCT TTATATAATG AATCAGGATG ATGATGAAAT TAAGCCACCA | . 120 |
| | TTTTTTATTC AATGGGAGGA AAGTGATTCC ATTGCGTACT AAAAAATTGC AAAAATATTT | 180 |
| | TCAAAACCAT TTTCAATTGA AACTGTATTG TGAAAGTAAA ACCGTCACAA CAGTATCGAT | 240 |
| 50 | TGGTTGAAnT GGTTGnAT | 258 |
| | (2) INFORMATION FOR SEQ ID NO: 964: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 388 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|------|---|-----|
| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964: | |
| | TTATCAAACC GCCATAGCCA CATCTCGATT CAAGGATAAA TTTGTTTTCT CATATCTTAT | 60 |
| 10 | CTCTCATGAC AGTGCACGAT ATATATCTTT TCCAAATATT CATCACTTTT TTCCTGTTAA | 120 |
| 10 | AATCATTTCT ATTATTAATG CTTTAATGAC AACTTATTTA ATTTATTGCA TTTAATGCCC | 180 |
| | TGCTTCATTT TCAAATATTA ACTTTAATCG ACTAGCTCAT CACACTATTT ACCCTTTCCA | 240 |
| 15 | CCTATCACTA CTGAATTCAA AACGATTTGT TTACAAATCC CCTTATGCCA ACGGTCGAAT | 300 |
| | TTCATCATGT TTACATTTAA TTGCAAATGC CCTCTTGAAA TATTTTAAAA TTAATATTAT | 360 |
| | TCTTAGCATA CTAGTCGGAA TTATATTC | 388 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 965: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 602 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 . | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 965: | |
| | AAAGTGAGGT ATAGTCCGAC CATACTCTAA AAACGTAGCG AGATAAATAT ATTTCAATCC | 60 |
| • | TAACTTTTAT GTTTTGAGGC ACTTGCCATT TAGGATATTG TCGTTCGTAA TACGACACTT | 120 |
| 35 | GTTGTATAAA TACACCTAGT CCAAATGGCA GCATCATGAG TAAGATACTT CTTAAATAAC | 180 |
| | TTAAACCAAT ATCATGCCAT ATGTGTCCAA TAATCAATTG AAAGACAATG ATAGATACTA | 240 |
| | TTAAAACGAT TATATTTATT GTCACTTGTT CAAACGCACT CCTTTTCCAA ATAATAGAAT | 300 |
| 40 | TGCTGCTTGC ATGACAACCA TAAAACATAC AAACATAGCA GTTTTAAGCG TTAGACTTTC | 360 |
| | TAGAATGTGa TTTAGAACAT GTAAGGGCTC ATTAAAGAAA TAAACGGAAT GTAAGCGTAA | 420 |
| 45 | GAAACGACCA ATATAAATTC CGAATCCATT TAAAAACATT AGCACGACAA CrATTAATCT | 480 |
| | ATTAAGCCAA CGGTGAGAAG TCAATGLTAG TATTTCAAAA TAGATTHAAA TCATCACATA | 540 |
| | AACCGCTAAG AAGACACCAA GCAGTAAATA GGTAAAGTAT TTCCACTCAC TTAAATTTAG | 600 |
| 50 | TC | 602 |
| | (2) INFORMATION FOR SEQ ID NO: 966: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 744 base pairs | |

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 966: | |
|------|---|-----|
| | | |
| | GTCCTAAGGT AGATTTATCT ACAACTGTTG TTATTTTANC AATTATTGGA GCGATTTTAT | 60 |
| 10 | TAATGTTTGC TAGCATATAT TTTATNAAAA TTGTGACATC ATACTTTACT AAGAAACTTT | 120 |
| | TAGAAATTAA ATTTAATTCG AAATAGTATT TTCAATGAAG TGCTTCAAAG CTAAACTTTC | 180 |
| • | ATGACATTT TTTGAAACTA GAGAAAATGG CTCATCAACT TCTAGCtGAA TGCCTTCTTG | 240 |
| 15 | AAAATGTATT AATGTTGAAT TCTCTATGGC AGTCATACCA ACAATATAAT GTGCATTGAT | 300 |
| | ATAAATTTGT ATCGGTGCAC GTTTATGTTT TAACGGAAAA AGTATAGTTT TTGGGTTGAT | 360 |
| | GTAAATAGGA ACCAGTTTAT TAATATTTAG TATGTTTTTT GCAGTCTCAA TTAGCACACT | 420 |
| 20 | TTGTGATGAT AAATGCAATT TCGCATAATA TGYAACGAGT TTGTTAATTG GAACTTTAAG | 480 |
| | AATGTAATCG CAATGTAAAA AGACACAATT TGTTTCGAGA TGGTTTGAAG TAGCAGTTTG | 540 |
| | GATATAAAGT AGATATTTAG TAGAATTGTC TTGCAAATAT AGTACTCCTC GTTTAATAAG | 600 |
| 25 | TTGTTAATTT AATGGTTAAA ATAAATTTAT ATGAAGATGT TAGGGTGTTT CAACATCATT | 660 |
| | AACACATCGA CCGAAATTTC ACAATAAACT AATTAAAATT ATGTTGGCAT TTACGCTTAA | 720 |
| 30 | CGGACATCTT AATTAATTTA ATCG | 744 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 967: | |
| · 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 503 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 967: | |
| | TACTTTGCAG GAGCATTAGG TATTCTAGCA TTTATAATGT CAATTGTATT GATTCACGAT | 60 |
| 45 | CCGAAAAAGT CTACGACAAG TGGTTTCCAA AAGTTAGAGC CACAATTGCT AACGAAAATT | 120 |
| 45 | AACTGGAAAG TGTTTATTAC ACCAGTTATT TTAACACTTG TATTATCGTT TGGTTTATCT | 180 |
| | GCATTIGAAA CATTGTATTC ACTATACACA GCTGACAAGG TAAATTATTC ACCTAAAGAT | 240 |
| 50 | ATTTCGATTG CTATTACGGG TGGCGGTATA TTTGGGGCAC TTTTCCMAAT CTATTTCTTC | 300 |
| • | GATAAATTIA TGAAGTATTT CTCAGAGTTA ACATTTATAG CYTGGKCATT AWTATATTCA | 360 |
| | GTTGTTGTCY TAAWAWTAWT AGTTTTLGCT AATGGACTAT TGGGTCAATA ATGGTTAATC | 420 |

55

| | TTTTCCnAAn ATTGCnGGGG AAG | 503 |
|----|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 968: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 465 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 968: | |
| 15 | TACAGGTAAA AAAGGTGGTC CGTTTATCGA TTCATTAAAC CATCGTAGTT ACACGAAAGC | 60 |
| | ATATGITICA TCAGAAACCG ATATTCCATT TTATGCTGAA GCATTTGGAA TTAGAGAAGA | 120 |
| | AAATGTTGTA CCAACAGGTG TACCACGTAC TGATGTACTA TTTGATGAAG CTTATGCAAC | 180 |
| 20 | ACAAATTAAA CAAGAGATGG AAGATGAATT GCCAATTATA AAAGGTAAGA AAGTTATTCT | 240 |
| | | 300 |
| | ATTCGCACCG ACATTTAGAG GTAATGGTCA CGGTACGGCA CATTATCCAT TTTTTAAAAT | |
| 25 | TGATTTTGAA CGTTTAGCAA GATACTGCGA GAAGCATAAT GCAGTTGTGT TATTCMAAAT | 360 |
| | GCATCCGTTC GTAAAAAATa GmCTTAATAT TcaCgTGaAC CATAGACCAT ACCTTAATCC | 420 |
| | GATGTGGTCC AGATCCATCC GTGGAAAGTT AAACGGATAT TCCnC | 465 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 969: | 3 |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 300 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 35 | (D) TOPOLOGY: linear | |
| | | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 969: | |
| 40 | AATTCGGAAC AACGAGCTGG CAACAACATA AGATGACAGA GGCGAATGGT CAATCAATTC | 60 |
| | AAGTTAACTT AAATAATGCG CAANGCGATT TGGGATATTT AACTGCTGGT AATTACTATG | 120 |
| | CAACAAGAGT GCCGGATTTA CCAGTAGCGT TGAAAGTTAT GAGGGTATTT ATCGGTATTC | 180 |
| 45 | GTAAAGATGA TACAACAACN ATTTACTCAC ACCTATACTC TAAAAGATTN CACACGTCAT | 240 |
| | CACAACGGCG ACTTGAGCAA CATGGACAGT TCCTAATGAA CATAATCAAC GGTATTGTTC | 300 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 970: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 970: | ı |
|-----|---|-------|
| 5 | ATACGCGAGC GAACGGTGAA GCGACTTGCT GCTGCAAAAC GTCTGCGACC TTGAGCAACA | 60 |
| | ACATGAATGG TCTTCGGTTT CCGTGTTTCG TAAAGTCTGG AAACGCGGAA GTCAGCGCCC | 120 |
| | TGCACCATTA TGTTCCGGAT CTGCATCGCA GGNATGCTGC TGGATTATCA TCCGATTTTT | 180 |
| 10 | AAAACGTTAT TAGGCGTTGT CGTTGCAATT CAATTTACAG TACCTGCTTT GATTGGTGCA | 240 |
| *** | TTGGTTGCCA TGAAATTTGA CCTATCGCCA TTAGCAATTG CTGTTGTGGC AAGTGCAGCA | 300 |
| | TATGTAGGAA GCGGTGCAGC GCAGTTTAAA AATGGTGCTT GGATGATTAC GGGTATTGGT | 360 |
| 15 | GATTTAATNA ATACAATGAT TACAGCAGCG ATTGCAGTTG | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 971: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 20 | (A) LENGTH: 251 base pairs | · |
| - | (B) TYPE: nucleic acid | (1) |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 25 | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 971: | |
| | AAGTGTAAGA TTAGAATAAA AAATTTATAA ACGAATTGAG AAAGACCAAA GCTAGCAATT | 60 |
| 30 | ATTCAGAAAT TAAATCGAAG AGTCCTACAG TTAATGACTT ACCTGAACGA GATTTATCAA | 120 |
| | ACAAATCTCA GTATGACCAA TATGGCAAAT GCCGTGTCCA TGTTAACTGA TGAAAAGTAC | 180 |
| 35 | TTTGGTGGTA GTTTTGAAAG ATTACAAGCA TTGACGACAA AAACAACATT ACCCGTATTA | , 240 |
| | TGCAAAGnCT T | 251 |
| | (2) INFORMATION FOR SEQ ID NO: 972: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 414 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | · · |
| 40 | | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 972: | • |
| 50 | TGAAGCTCTT AATAAATCTT TTCTTGAACA CACACCAACA AAATCGTTAT CTTCATTAAT | 60 |
| 90 | AATAAATAAT GTACTTACAT CTTCTAAAAA AATTGTACAA ATAGCGTCAT AAACTGTTGT | 120 |
| | ATTCTCTCTT AGCACAACAG GTTGAGACAT ATAGTCCTTA ACCTCAAATT GTCGAAGTTT | 180 |

| | THE PROPERTY OF THE PROPERTY O | 300 |
|----|--|-----|
| | ATTCAACTTA TCTGCTATTT GTTCACCAGW AATGGGTCCT TTAGTTTTAA CAATTTCGAT | 360 |
| 5 | GATTCGTTCT TGTCTTTGAC TGAGTTCTrw AGGKCTTCAc CCCTTTtTAT GCnC | 414 |
| | (2) INFORMATION FOR SEQ ID NO: 973: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 747 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 973: | |
| | GAAATCGATA CTAATATCTT CTTTATTTAC ACCTGCTAGT TCAGCTTCTA AGTAATATAA | 60 |
| 20 | TTCGTCTGTt CATALATATE CGTLACAAAT GAAGGTGTLG AAAAGTAATT AAATACTTGT | 120 |
| | TTACCTAAAT CTTTAAATGT ATCACTTGGA TTACCGTTAA AAAAGTTTTG ATTCTCGAAT | 180 |
| | TGATTGAAGT TCALATCATC ACTTCCATTA TAGAAATTTG TATTACAAAG CCATTATATG | 240 |
| 25 | AGTAGTATTA AAAAAGTTAA AGTAAAAGGG GAGATAAAAA AGTAATAAAT GGGTAGATTT | 300 |
| | GTGCCTGATA AGGAATCAGG GCAAAAGAAC TGAGCATCGA GATTTATACA AGCAATAAAG | 360 |
| | ATAATGAATA AACATATCGA TGCATACTTC TGCCCATCAC CTTATGATAG GGAGTTATTT | 420 |
| 30 | TTTGTCGGAA TAGTCAAAAT TTTTAGAAAC AAAATTCCGC AAATTATTAA TTATATCTGA | 480 |
| | TGCTTCTCGT TCTGAAATGT TGAATTCATT AAAGACCTTA ACAGAAATTT CAGCAAGAGG | 540 |
| 35 | GCTTTTTATT GCTTTACCTT GTTCTGTTAG AGAAATTTGT AGGTTTCTTT CATCTTTCTC | 600 |
| | TTCACGTGTT CGAACAACGT AATCTTTCTT TTCTAATTTC TTTAGTAATG GKGTCAGTGT | 660 |
| | TCCAGAATCT AAGAACACAC GTTCACCTAA TTTTTTGATG TTAAGTTTTT CATCATTTTC | 720 |
| 40 | AATCGCCAAT TAAACCANGG TANCNGG | 747 |
| | (2) INFORMATION FOR SEQ ID NO: 974: | • |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 257 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 974: | |
| | TGCTTCCAAG TAATGTGGAC ATTTAATACG AGCTGGGATT GAGATACACC TTGCAATGCT | 60 |

| | TCTTGGRCAT TTGCATTGCT TCTCCCAAGT GAATGCCTTT AACAGCTTGT GTCATCATCG | 180 |
|-------|---|-------|
| | ATGACTTGCC ATTGAAATCG ACAACCTTCA CCTTCAAACT TAGCATCTTT TATAATGCCG | 240 |
| 5 | nCTTCTATAT CAAATGT | 257 |
| | (2) INFORMATION FOR SEQ ID NO: 975: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 451 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • ,) |
| 45 | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 975: | |
| | CAATGGAGCA TATTTTACGT TCGGCAATGG ACATTGATCA nACAACAAAA CATTATATAA | 60 |
| 20 | mTAATAAAGT AGAAGTTATC AAAGAAATTA TTAAAAAAGT AAGAGGGGGA AATCACGTGA | 120 |
| | CATCACAAAA TCCAGAAGTT AATTACGAAG CATTAGCTAA ATATGGCCGC GACTTAGTAG | 180 |
| | AAGAAGTTAG ACAAGGTAAA ATGGATCCTG TTATAGGAAG AGATGAAGAA ATTCGAAATA | 240 |
| 25 | CGATTCGTAT TTTAAGTCGT AAAACTAAAA ACAACCCTGT GCTCATTGGT GAACCAGGTG | 300 |
| | TTGGTAAAAC TGCAATTGTT GAAGGATTAG CGCAACGTAT AGTTAAGAAA GATGTGCCAG | 360 |
| | AATCATTATT AGATAAAACT GTTTTTGAGT TAGATTTAAG CGCATTAGTA GCGGGCGCTA | 420 |
| 30 | AATATCGTGG TGAATTTGAA GAGAGATTAA A | 451 |
| | (2) INFORMATION FOR SEQ ID NO: 976: | |
| 35 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 571 base pairs(B) TYPE: nucleic acid | |
| - | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . 4 |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 976: | |
| . • . | AACTATTAAT AATATTAAGT TCACTACAGA TGTTGCTAAT GGACCATAAG TTTTAAAGAC | 60 |
| 45 | ATCTTCACTT TTATAACCAA CAATCGCATC TAAAAATTGA ACTAAGATCA TTGCAATGGA | 120 |
| | TATAGTTATC AAAAATATAG CACTATGAAT GACTAAAGAA ANAATAGCTA ATAAAAATAA | 180 |
| 50 | AGGTAAGCTT CGACTAAGTG CATAATATGC ATTTATATTA TGGCTAGATG CACATGCTTG | 240 |
| | AATTGAATAA CCTAAACTTA CACTGGCACT GATTATTGTA AATATTGCTA AAACAAAATA | 300 |
| | CATGTTAATC CTTCTTTCTA TATTTGGATA TAAACAAGTA CTTGTCTAAA GTTATTTAAA | 360 |

| | TATAACTATG TCATAAACTG AATTTGTTGA AATTTTTCAT TATGCAAATT TATTAATAAC | 480 |
|------|--|-----|
| | AAACAGCTCG AACTATAGCA TCATTTTACT AATGAATGCA TTAAAGTAAC TATGACTAAA | 540 |
| 5 | AATGCATATT AATTATCATT ATTAAGACTA T | 571 |
| | (2) INFORMATION FOR SEQ ID NO: 977: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 10 | (A) LENGTH: 274 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 977: | |
| | CCCGAAAAA TTTAGACATT TTCAAACAGT AACATTTGAA GATTTGTCTA AGCTGGAAAA | 60 |
| 20 | | |
| 20 | GAGTAGTATG CCATCAGGGG TCGGTATATT AGGCTATGCT GTTGACAAAG GTGTTGCTTT | 120 |
| - | AAACAAGGGG CGCATTGGTG CAAAAGAAGG ACCAGATGCG ATTAAACAAG CATTTGCAGG | 180 |
| 05 | TTTGCCGGAT TTGAATCCAT GTGnACTTTA GTCnGATTAC CGGAATGTTT ATCCTGGTCA | 240 |
| 25 | TGGGGGAATT AATTGGATAC CCCAAAAAGG AATT | 274 |
| ·\$. | (2) INFORMATION FOR SEQ ID NO: 978: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 877 base pairs | • |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 978: | |
| | NTNTTACTTC TTCTTTTAAT ATTTCTCGTA TAGCTTCAAA TTTTTCACTG TCAAACAGTG | 60 |
| 40 | TTCTTAATAT CCCTTGCTTT TCACGACTGT TTGATATTAA AAAGCGTTTG AATTCACCTT | 120 |
| • | GAGGCAAAAT AAACAATTGT CGGAATTGAT CTGCATTTAC TCCTAATAAT TCAATAATGA | 180 |
| | ATTGGGTACC TGAAATTACT TTACTTTCTC TAATTTCATA CTTGCCATCC ACCATCTCAA | 240 |
| 45 | ATACATCAAA TTTAGCGTTC GTTTTTGTTG TATTACCTTC TTTGATATAA GGGCCTTGTC | 300 |
| | | |
| | TATGCACTIT ATAAATTCGA TGATTTAATT GAAATTCAAA TGTTACTGAC ATCGGCTGTT | 360 |
| 50 | TACCATCAGC GAAATGACTT CTCAAATCAT TTTCTTCTCT TTGTTCAGTT GATGCTTTAC | 420 |
| | CAAACAAGGC ATAAGTCATT GCATCAAAAA TCATTGTTTT ACCCGATCCA GTCTTACCAC | 480 |
| | TTATTAAAAA CAATTCATTA TTATCAATTT TAGAAAAATC AATTTCTTCT TTTAAAAAAGG | 540 |

27.2

| | CGTTTTCTAA AATATTTTTT ATCTTTTTAG ATTGGATATC CGATAATTCT TTATCAGTTA | 660. |
|-----|---|------|
| | TATGTTTATA AAACATTTCG ATAATTGACA TGTCaTCTTT TTCACTTATT TCYATAGCAT | 720 |
| 5 | TATTTTCTTC ATMGTAATTA AAAGTTTCAT TCGTCAGCGC TAAAGTATTA GGATAAATTM | 780 |
| • | GTTTTAAACT CATCATTGGA TCAGTAATAT GAGACATATT TTTAAGTTTA AAATGTAAAA | 840 |
| | TAATTATCGT TATATTTCAC ATGAACTTAT TCATTAA | 877 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 979: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 624 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 979: | |
| | ATTGGTACTA TACCATTTGT CCATTTTAGC GAAGACGTTA AACTATCGAT TAGCTAGTGA | 60 |
| | AGAAATTAAT CTCACTATAC CTTCTATACA TAAGCAAATT AAAAATTTAG AACAGCATCT | 120 |
| 25 | CAATGTGAAA CTATTGAAA CTTATAAAAA TCAAATTATC TTGACTGAAG ATGGTCATAC | 180 |
| • ; | ATTTCTTCCA ATTGCGCAAA GTTTTATTGA ACAATATGAA AGTGGCATCA AACATATCCA | 240 |
| | ACTTAAAAAA ACGATGTTTC AATCGAAATT AAATGTTGTC GTGTCTTCAT ATATCGCGAC | 300 |
| 30 | ATTCATTATG CCCAAATTTT TAAAATCTTT CTTTAACGAG CATCCTTTTA TCGATGTTTC | 360 |
| | TCTTCATGTC AAAAATGAAA ATATTGAAAA AGATATTAAT AATCATACGT ATGACATCGG | 420 |
| | GATTAGCAGA AATCAACCTA AACTAAGAGA AGTTCATTCT GAAAAAGTAT GCGAAGGTAA | 480 |
| 35 | AATTGTATTG ATTGCTCCCA ATAAAGAGAA TAATCATCTT CTAACTGAGG CATCTTTATT | 540 |
| | TGAAAAATAC AAAATAATAA GTGATAACCA TCCAGAATAT TGGGTCATCA CTTAAAAATA | 600 |
| 40 | ATATTITAAA TATTTATGAA AAAG | 624 |
| | (2) INFORMATION FOR SEQ ID NO: 980: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 457 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 980: | |
| | TTTGTCCTGT TGCATAAACT GCAGCTAGCA TAATGTTAAT TGTTGCACCT ACGCTAACCA | 60 |

| | INGALICATE AMILICAGEA CELAMAGELL IMANICELLI AMIA | AIGIIGA . | ICANIIGGAC | 100 |
|------------------------------|---|-----------|------------|-----|
| | GTGGCCCAAG TGGACATCCT CCCGGTAAAC CAATCACACA TTTT | TAAATT | CTACCTAACA | 240 |
| 5 | TGGCACCCAT CATATAGTAT GAAGCACGTA ATGATTCAAC TTTA | ATTATTT | GGtAATGCAG | 300 |
| | CATTTTGLAT TTCAGTTGTA TCAACTTCTA AWTCCGTACC ATTT | ragtgaw (| GCCTTAAtAt | 360 |
| | TTAAAtCtkC tAAtAAACTC aCTAAAGTTT TAACATCAGA GATT | Tngcgg ' | TAACCCTTCT | 420 |
| 10 | AATTTCACAT GTCCTTGAGC TAATAATGTT GCAGGAA | . • | | 457 |
| | (2) INFORMATION FOR SEQ ID NO: 981: | | | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 997 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · | * | |
| 20 | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 981: | | | (3) |
| • | ATTGCAGCAA CGCCCCCTGT AAAACTACGT ACTCTTACAT TTAT | rgaaacc ' | TGCTTCTTCA | 60 |
| 25 | AACATGCGCT TCAACTCTTC TTTTCCAGGA AAATTAAACG TAGA | ATTGCTG | TAACCATTCA | 12Ô |
| 25 | TATTCTTCTT TTGATTTTGC AAATAATTTT CCAAAAATAG GCAT | TAACAAA ' | TTTAAAGTAT | 180 |
| | AGTGCATACA TTTGTTTAAA GACTGGCAAA GTTGGTTGGC TCGT | TTTCAAG | ACATACCACC | 240 |
| 30 | ATACCACCTG GTTTAAGTAC TCTATTCATT TYTTTTAACG CGAC | CTAAATA (| GTCTGGCACA | 300 |
| 20 P 25 P 30 P 35 T 40 C P 1 | TTTCTTAATC CAAACCCAAT TGTTACATAA TCAAAAGAAT TGTC | CTTCAAA | CGGCAATTCC | 360 |
| 35 | ATTGCATCAC CATGAACAAG TTTAACATTT TCCATTGAAG CAGT | TTTTTTC ' | TTTTCCTACT | 420 |
| | TCTAACATAT TCTCACTAAA GTCAATACCA GTAACTTCAC CTGT | TTGGTCC ' | TACAGCTTTG | 480 |
| | CTTAATGCGA TTGTCCAATC ACCAGTACCA CAACAAACAT CTAA | ATGCTTT | CGTCCCTTTT | 540 |
| 40 | CTAACACCCA TGTCTTTCAT GACGCGTTTT CTCCATACTT TATG | SCTGCTC | AAAACTAATA | 600 |
| | ATATTATTTA ATCTATCATA TTTTTTTGAA ATATTTTGAA AAAC | CGCGATG | TACTTGCTCT | 660 |
| | TTATTTGCTT TATTGTCAGC CATGCTTAAT TACCTCTACT TTTT | PAAATAA | CTTTTTTGGA | 720 |
| 45 | TATCGTGTAA GTAATGCTTT ACTTCACTTT GATTATATTT CTTG | GAAGTAT | GATGGATAGT | 780 |
| | AATCAGACAT ATCTTCAAAT AAATAATTAT ATATTTCCGA CTCA | ATCAATA | TTGATACCGA | 840 |
| 50 | AATGAGATAA CGTAALATAT GGGAAAAGTG LTTCAATTTT TACT | PATTGCT ' | TGAGAAATTT | 900 |
| | CATAATCATT TAAAGCTTGA TGATGTAATG AAGATTTCAA TTCA | TTAATT | TCAACAATTG | 960 |

55

997

CTTTACTAAT TTCATTTTGA AATGATAAAT CATTGAT

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1118 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 982:

| | | - | | | | | |
|----|---------------|--------------|------------|---------------|------------|-------------|--------|
| 10 | CATTCCCTTT | ATCGGnACAA | TTATTTTAAA | TAATTGGTTA | ATAAGTTTTT | CTATTAATTG | . 60 |
| | CTGTTTTACT | TTCTAGAGCA | ACAATAAATG | TTTTCAGTTT | AAAATAATTA | AGATTGTCAT | 120 |
| 15 | TTACTAATTT | GCTTTTTCCA | TTCTTTAACC | ATAAATCAAC | TTGTAATTGC | CACTCAATAG | 180 |
| ,5 | GATGATTTT | TTAAATATAA | TGCTCTGGAA | AAATATAACC | ATAATTGTGC | ACTACTTCTT | 240 |
| | GATCAGTTAA | CTGTAATTGA | TACATTGCAC | TTAAAGTGGG | TTCTAAAACA | GAATTTTGCC | 300 |
| 20 | AGCGACAATA | TTTGATATAT | TGATTAATTG | CGAACTTTGA | TAATTTATAA | ACAGCATGAT | 360 |
| | AATCACAAGO | CGCCTCATTA | AACAACTCAC | TÄATTTTGGC | ATTTCTTTTT | TCAGCGACAT | 420 |
| • | ATTTGTGCCC | GCCTAAATAT | TGTATTTGTT | GAAACATCAT | TATTTGTTTT | TTCTCTAAAT | 480 |
| 25 | TGAACGTATC | AAGTTTTCGA | GTGAATGGAT | TAATAAACAT | ACTTTGAAAA | TGATTGAACT | 540 |
| | TCACTTTAT | T ATGACAATAA | TCAACATCAT | TTAMTAACCA | ACTTACTTTA | TATCCCATTT. | 600 |
| | TCTTKAAAC | TTCCGTTCGT | TGAAGAATCT | GTTTATAAGG | AATTGGCGAA | TACTGTAGCT | 660 |
| 30 | CAATAACAT | A TTTATTATTA | ATCAAAATAT | CCGGAATTTG | TTTTATTTCT | TTTAAAAATG | 720 |
| | GCTCTATCT | TACTTTACAT | CCTTGTTGCT | GTATCATCTG | TGCTAAAATC | AATTTACTTT | 780 |
| 35 | TATAATGTT | r aatcgtttca | TTATTAAAAC | ATTTTTGTTC | CGCTAAATGT | TTATGTGCAA | 840 |
| | ··· AATGACTAA | TACTTTGAG | CCACGCTTT | AAATAACTTO | CTTGCCACAC | ACCGGACAAA | 900 |
| | AATATTGTG | r ctttctcaa | GCAGTAGTT | CTAATACGC | TTCCTTTTCT | TCATTTAAAG | 960 |
| 40 | CTACTAACA | T ATCTTCACC | CAAAATATT | A. CACGTAAGTT | TAACTACTA | TACTTTTTCA | 1020 |
| | GCTTTGGAA | A TCCATTAAA | AAAAGGGAC | CCCAAAGGAG | GCCTCCTTTC | ATANGTGCGG | 1080 |
| | TGGCCTAAT | T AAATAATCC | TTAATTCCA | GTGGnCnC | | * x | . 1118 |
| | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 983:

- (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 269 base pairs

 (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

| | CATCCCCTGT TAAAAATTGn TATTTGTGTA TTGATGCTTC TCAGnCATTA TTACGAGTCC | 60 | | | | | |
|----|---|-----|--|--|--|--|--|
| | ATATTCATTG CTTCAGTGAA ATATCAGTAG CAATAACATT TAAATCCGGC TTTTCACATT | 120 | | | | | |
| 5 | TCAAGGTAAT TGCAGTACAC CACTACCCGT TTCCGATATC TACGGATTGT TGCATCATCT | 180 | | | | | |
| | TCTAACTGTT GGTAAGAAAT GCAACCATTA CTGCTTCAGT TTCAGGTCTG GTATCAAACA | 240 | | | | | |
| | ATTTGAGTTT ACATCAAACG GTCTACCTT | 269 | | | | | |
| 10 | (2) INFORMATION FOR SEQ ID NO: 984: | | | | | | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 298 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · | | | | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 984: | | | | | | |
| | AACCCAAGTG GAAnnGGTTT TGGTGGAAAA ATTTTAGGTC CTTTATCTGT CGTGCGAATC | 60 | | | | | |
| | ATTGTATTTT TTAAACTTTC CGCATAATCT TGATGGTCGA TTAACTTTTC GCGATAACAA | 120 | | | | | |
| 25 | TATTCAATCA CTTCAGAAAT CGCTTGCTCT GATATCTCTT CTTTTTGTAA ATATTGTATA | 180 | | | | | |
| | ACTTCTTTT CAGTTCTCTT TTTATATGAT AAATATTGGA TTGCTTTATT TAAACCTATG | 240 | | | | | |
| •• | CGATAATGAT CATACTTTTG AATCTCTGCC ATGTCAGCAG CnTCAAGTTG TnGCCCTT | 298 | | | | | |
| 30 | (2) INFORMATION FOR SEQ ID NO: 985: | | | | | | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 431 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | | | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 985: | | | | | | |
| | CCATGCGATT CCACCTATTA ATAGTAAGAC AATAATAATA GGAATTATAA TITTTAACTT | 60 | | | | | |
| | TTTAGACATT TTGCTTCCTC CCAATTATTT ATGAGTTAAT CATATCAGAA CAATACATTT | 120 | | | | | |
| 45 | TATTAAATGG TTTATTTTAA ATTTTGTTTA AATTAATAGA ATTTTAGTTA TAATAATGTT | 180 | | | | | |
| | TAATAAGTTA TTGG:AATCY AATAAACTAC MAAAAATAGT TTGATTACAT AATGATTCLT | 240 | | | | | |
| | GAAAAATGKT GGKTAACYTA ATAATATGCA TTTTTTKGGC GArGARGATT LATTLAACYT | 300 | | | | | |
| 50 | ATAAAAATAT KGAAGTAAGA TEGGGGAGAT EATGAATTEA TGGTATEGAA AGTCGATGAT | 360 | | | | | |
| | TTTGTAAAGA ATATAAAAAG ACCATACTTG ACTGTATTGG GAGTATTTGT AGTTGCAGTT | 420 | | | | | |
| | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 986:

| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs | |
|----|---|-----|
| 5 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 986: | 60 |
| | AAGGTTAGGN TGGAGTACCC AAAGTAGGTT TTAAAGGTTG GAAATACNAG GAGGATGAAT | |
| 15 | AACATGAATC AGTCAGTCAA ATTACTTAAA CATTTAACAG ATGTAAACGG CATTGCTGGT | 120 |
| - | TATGAAATGC AAGTTAAAGA AGCAATGCGT AACTATATAG AGCCTGTCAG TGATCAAATT | 180 |
| | ATTGAAGATA ACTTGGTGGC ATTTTTGGAA AGAAAAATGC TGAGAATGGT CAATACTCAT | 240 |
| 20 | TATGATTTCT GGTCTATGGA TGAAGTGGTT ATGGTAACAA GATGTAAACT GTTATTCATT | 300 |
| | ACGCGTGGTG TGTGATCAGC nGCACTCAA | 329 |
| | (2) INFORMATION FOR SEQ ID NO: 987: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 545 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 30 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987: | |
| | CATATTATTT nTATATGAGT TTACCAGTGT CAAAAAAACA ATTGCTTAAT GCCAACTATA | 60 |
| 35 | TTACATGCAT TGTTTTAACA TTAATTGGAA CGCTTGTTAT TAGTTTATAT GCTTATGAAG | 120 |
| | CAGATGTGAT TGAACCAAAT TCAATCTATT TTTCAACTGC ATATGCATTT GTCATATCTA | 180 |
| 40 | ACTICITGIC TATACCAATI GCATITAGIC AAITTACAGA ATIGCGIAGA GICAAAGIGC | 240 |
| 40 | CATATGGTAT ATACGTGTTT ACTATTATCA TTTTAGTTCC ATTTTTATTT TCAATTGCAA | 300 |
| | TAGTATTGGT GAATTATTTT GTTCTAAGTC AATCATCATT CCCAGATTTA TATTCATATA | 360 |
| 45 | TTTTAAATAT TGGTTTTCTA ATTATAAGCA TTGTTATACT TATTGTTAAT TATTTTAAAC | 420 |
| | AGCTCAATAA AATAAATACT AGAAAATTTA AAGGAGGCAG TCGATGAAAT TAGAACATAT | 480 |
| | TACAAAAAA TACGGCTCAA ATGTCGTTTT AAATGATATI GATTTTGACT TTGGCGANAG | 540 |
| 50 | | 54 |
| | TAGAA (2) INFORMATION FOR SEQ ID NO: 988: | |
| | (2) INFORMATION FOR SEQ ID NO. 388: | |

| 5 | (A) LENGTH: 607 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|----------|---|----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 988: | |
| | ACCTAGCATG ACATAATCAA ATATATCAAA AACACCTTTC TGAACTGATT CAACCGTTCC | 6 |
| 10 | AATAGTTAAT GGTCTTTCAG AATCAGATGT CTTTCCACCT TGAACAGTCA GATGACTAAT | 12 |
| | TAAAATATTG ACGGCATCTT CATCAATTTC CGGTGCTATT GTTTCAATAC AGCGCGTAAT | 18 |
| 15 | TCCCTGTTGA TGTGTTTCAA TGGTGTCATC TTCAAAGTAG TGTTTCATTT CGCTCACAGT | 24 |
| | AGCATAAGGG AGTGTATAAA AATTAACCCC ATTTATCTCT ATTGGTGAAT TAATCGATGT | 30 |
| | AAAATCTGTT CTTATAAATA ACTGATTATG TTCAAACCAA CTCGCCCCAT AGTTTAACCT | 36 |
| 20 | CTCTTTACCA TCGTGATTTC CACTAATAAT AATTATTGGT ATACGCAGTT CTAAATTTAA | 42 |
| | CTTTCCAATC GCTTGTTCTA ATAACATGAT TGCATCTTTA CTTGGATATG TTGTGTCATA | 48 |
| | TAAACTCCAG CTATCACAAT GITATCAGGT TCTTCTTCTT TCATTTTTTC TACGAACATA | 54 |
| 25 | TCTAAAATAT ACGCTTGaTC TTCTAAAAGC TGTTTGCCAT CTAATATTTT CCCTAAGTGC | 60 |
| | CAGTCTG | 60 |
| | (2) INFORMATION FOR SEQ ID NO: 989: | |
| 30 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 722 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 989: | |
| 40 | ATCGCGTTAA GCAACAATTA CAACAATCAT CATATAAGCT AACGCCACAA CGCGAACTAC | 6 |
| | TGTTAGAGTT CTAATTGAAA ATGAAAAAGA TCATCTAAGT GCTGAAGACG TATATCTGAA | 12 |
| | AGTAAAAGAT AAAGCGCCTG AAATTGGCTT GGCGACAGTA TACAGAACGT TAGAGTTGTT | 18 |
| 45 | AGCTGAACTA AAAGTTGTCG ACAAAATTAA CTTTGGTGAT GGCGTCGCTC GTTTTGATTT | 24 |
| | AAGAAAAGAA GGCGCAAAAC ATTTCCACCA TCATTTAGTA TGTATGGAAT GTGGTCGTGT | 30 |
| 50 | AGATGAAATC GATGAAGATT TGTTACCAGA AGTTGAAAAT CGAGTTGAAA ATGAGTTCAA | 36 |
| | TTTTAAAATT TTAGATCATC GTTTAACTTT CCATGGTGTG TGTGAAACGT GCCAAGCTAA | 42 |
| | AGGTAAAGGA TAGTAAATTG CGTAGGTTAA ATTAACCTTC GCTTTTTTTA GAGGTGTGGT | 48 |

| | TAACACAATT GGTGCTTATA GACGTGATTT GAAAAAGTAT CAAGATTATA TGACTGAACA | 600 |
|-------|---|-------|
| ÷ | TCATATCTCG CATATTGATT TTATAGATCG ACAATTAATT CAAGAGTGTn TGGGGCATTT | 660 |
| 5 | AATAGACCAA GGGCAATCTG CTAAATCTAT TGCGCGATTT ATTTCAACAA TCCGTAGTTT | 720 |
| | TC | 722 |
| | (2) INFORMATION FOR SEQ ID NO: 990: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: | |
| * * * | (A) LENGTH: 366 base pairs (B) TYPE: nucleic acid | |
| • | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | (b) Torologi. Timesi | |
| | | • . • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 990: | |
| 20 | ATCCAAAAA TACGAAAGCG CTTTCTATAT TGGTATGCAA GTATTTCAAA AAGAATAAAT | 60 |
| | TTAATTTTCC TACTTTCTA AACATTTATC TTTATGTATA ATGTTTTCAA GTAACTAAAT | 120 |
| | TATAAATTAA ATAAAGGGAG TGTTTATCAT GCTTACAATG GGGACAGCAT TAAGTCAACA | 180 |
| 25 | AGTAGATGCC AATTGGCAAA CTTATATTAT GATTGCCGTC TACTTCTTGG GTnATGACTC | 240 |
| | CAACTTATTG ATAGTGTTnT TATGTTTCAG ATAATGCCCG ATGACTTTGT CATGCCAGCT | 300 |
| | CCACCGATTT TGAGNAACGA CAGCGACTTC CGTCCCCAGC CGTGCCAGGT GCTGCCTCCA | 360 |
| 30 | GTATTC | 366 |
| | (2) INFORMATION FOR SEQ ID NO: 991: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 338 base pairs | • |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 991: | |
| | TGACTACAGT AACATTACCT GTAAATAATG ATTGAATGGC TTCATTTTCA TCATGAATAC | 60 |
| 45 | CTGTAATAAA TTCTAATTCT TCATCTGAAA CTTTTACAAT ATGCGCCAAT GGCAAAAAGG | 120 |
| • 0 | TATGAATAGT TTGTCTTAAA TCTTCAGCGT TATCCCATAA TGGCAATCTT ACATTAGGAT | 180 |
| | CAAATACGAC AGTACCATTT GCATTTAATG TTTTGGTAAT CAATTGATAA TGTGCATCTC | 240 |
| 50 | TCATCGGACT ATCGACCAAA TCAACAGAAC AAAAATGTAC TACATCATTT TCATTCACAT | 300 |
| | CaATATCATT CACAAAACTK GGKTCAAaTA aCATATCn | 338 |

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs

| 5 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 992: | |
| 10 | AGTTCATCGT ATTCTTAATA CCTATATGCT ATCGTTCACA AACTTTTGTT CTTTTCTTCC | 60 |
| | AACATACCGC CTATAATGCT CAAAAAGAAA TCAGCAGTGG AACCACTACG TTCCCTACCG | 120 |
| 15 | CTTTATCATT TTCAGGCTTA AATATTTTTA AAATTTTGTG AGGAATCCGC TTAAAAAAAAC | 180 |
| | TCATATCTTC AAAAAAATG ACAAAATTTA AATTTTTGAA TAACATCATT TTTTAGTAAA | 240 |
| | TGTTATAATT TCTTTATAAT ACAAATATCG AAAGAAGGCG ACTGACTTTG AAAAAAATTAT | 300 |
| 20 | GTTCATTAAT TGTAGGTAGC ATTAGTTTGT ATCCTTGCCA TTATCAGCTT GTGGNAAAGA | 360 |
| | ACNAACCNAA A | 371 |
| | (2) INFORMATION FOR SEQ ID NO: 993: | * 4 |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 530 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 993: | |
| 35 | ATAATGATTT ATCAATCGAT GTTAGATGCG GTTCAATTAT ATCCTAAGTC TATCGTGGTT | 60 |
| | GATTATACTG TGGATGGACA ATACAAAAAT GATTGTCACT ATTTCGGTCA ATCATCGATC | 120 |
| | AACATTGCCG ATTGGGCTCA AAACAATAAT TATTATCCTA ACCTGATATA TGCGATTCAA | 180 |
| 40 | CAGACTCTTG ATTTAATACA TTATTACTCT GTAGAAACGA TTTTCGATTT AGCTTTATTG | 240 |
| | ACACTTCTGA AAGGTGATTT ATCAATCGAT GGTCATGTCG TTTTTGATTT TAAAGCCCCT | 300 |
| | ATAGCAACAA GTGCTTCAAT ATGGGAAACT ATTAAAACTA TTGAAGATTT TGATATGATG | 360 |
| 45 | TCCAGTTTTL TTGALAAALG GCTTATATLG ATCATCATCC TATACCTTTT CGCAACCTTT | 420 |
| | TTATCGAGGA TTCAGAACAA CTTAATTCGC CAGATAATTG GTTGTATTCT ACCAAGTTTA | 480 |
| 50 | TGCTACCTAA ATGGGNTATA TAAAATAAGC AAAGCAACGT GCTGATAACA | 530 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 994: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|------|
| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 994: | |
| | | 60 |
| | TATTGGATTN TTNCCACCAA AGGCAACGGT TCCTTTTCTA ATTCTAATAA TCAAATCCCC | |
| 10 | ATTAATATCA ATCCCACTCA AATTCTTTCA CATCATTGAG TATAAAATAA TATGGTGATA | 120 |
| | TACGTTGAAG TTGATTNTCT TATTTAAGTA TACTCCAACA GTATTTTATA AAATTATTTA | 180 |
| | GTCATCATCT TCAGTGTTTA ATTCAAAAAT ATAGAATCTA CTGTATTGCA TAATAAATTG | 240 |
| 15 | AAATGCCACA AATTGTGTAC AAGCAATAAT AATGATACTT ACCATTATGA CAAACTTGGA | 300 |
| | TTCTACGACA TTGGGCACCA ATATATATTC GATAATTCTT TCAATATATA TAAATGCGCT | 360 |
| | CAACGCGGTT AATAATAAAC CGAAATGTGT TTTAGTTTTA CCACCCCAAC GTTTTGTYAC | 420 |
| 20 | TTTAGGTAAT TTTAATAACG TGAACATTCC GCCAATTAGT AATAACAAAT AACTAATTAT | 480 |
| | GATTGAAATC GTACCCATCA ACCAATAATT GAATAGGTCA TAATGATTTT GTACAGCAAC | 540 |
| | AAAATAATAA A | 551 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 995: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 729 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 995: | |
| | ATTCGCCACC ATTAGGTAGT GGAACACGAA CTTCATCATC TAAACCTTTA CCAATTAACG | 6 |
| | CTTTAGCCAT TGGTGATTCA TTTGAAATCT TACCATTAAA TGCATCTGAT TCAGCTGAAC | 12 |
| 40 | CAACGATTTG ATAACTTTCC TCTTCATCAC CTGGTAATTC TACAAACGTT ACTGTTTTAC | 18 |
| | CAATTITAAC AACGTTGTTA TCTCCAGTAT CTTCAATGAT TAATGCATTT CTTAACATAT | 24 |
| | GCTCAATTCT TTGAATATCT TGTTCGATGA ATCCTTGTTC ATCTTTTGCT GCATCATACT | 30 |
| 45 | | . 36 |
| | CAGAGTTCTC TGATAAGTCA CCAAATGAAC GTGCAACTTT AATTTTCTCT ACAACTTCAG | 42 |
| | GACGCTTAAC TGTTTTTAAT TCTTCAAGTT CACGCTCTAA TTTTTCAAAA CCTTCTTGAG | |
| 50 | TCATTGGATA TTGCTTTTGA TTTTCCATAT TGTCATCTTC CTTTACTGAA TTATACTATT | 4.8 |
| | GCTTGCTAAC TAAAGACTGA ATTITTGTTG TCATAATATC TATTGCAACT TTATTGCTCC | 54 |

CACCTTCAGG AATAATTATA TCAGCATATT TCTTAGTCGG TTCAATAAAT TGGTCATGCA

| | TIAGIATOTO GIGITGAAAC GGCGTAATAT NOTCAAGTOT GGCATOTGTA TCAACATATA | 720 |
|----|---|--------|
| _ | TnTTnAACA | 729 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 996: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 996: | |
| | GACAAATATA CTGCTTCTAC TCAAATATTA GTGAACATGA AAAAGTCCTC AAGTGATTTA | 60 |
| | GCTTTCCCAA AATGTTCAAA GTAGTTTGCA GTCTGTTAAT ACATATACGG ANATTATCAA | 120 |
| 20 | AAGTCCTAGA TTCTAGATAA AGTATCTAGA GAATTGATGG TCAGTATTCA ACAGCTGAGT | 180 |
| | GAAATCATTT TAAAAGTAAC CATCCAACCA ACTCTCAAAT TATTACTGTA CAGTTACACT | 240 |
| | GGGATAATCT GATCTGACAA ATGTATAAAT ACTAAGTTTT GCCAGCAGCT AAATAGAGGT | 300 |
| 25 | GTATGTACGA CTTCCANCTG TAGNG | 325 |
| | (2) INFORMATION FOR SEQ ID NO: 997: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 271 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 997: | |
| | CTTCAGTTGT CGGCAAATCT TCTATATTGG AAATACCAMA TACATTTAAA AATAAATCAG | 60 |
| 40 | TAGTAATTAA CTGTTGGCTA CGCTGTTCAT TAACCACTTT AGCCTCAACT AGTCCTTTGG | 120 |
| | CAATCAATGT CTTAACTGCA CCATCTGAAT TGALACTACG AATTAATTCA ATATCACTTC | 180 |
| | TTGATAATGG CTGGTTATAA GCAATAATTG GATAGTACTT CCATTGCTGC TTGTGALAAT | 240 |
| 45 | TTCATTTGTG aCTTTTGTTC AATTGAATTG T | 271 |
| | (2) INFORMATION FOR SEQ ID NO: 998: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 498 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 998: | |
|-----------|---|-------|
| 1 | TTTATGTGCT AATTTGTAAT TGAGATTCAT AATGGTATTT AAATCATTAT GGTGCGGGAG | 60 |
| 5 | TTATGGTATT GCCATAATAT GAGAGTGCAT CCACTTCTAT AAGTAATGCA TATTGCGAGT | 120 |
| | GCAGGAATGA ATGAGTGCTT GATTAAAATC CTTATGGGTG GTTGACATAA TTAAAAGAAA | 180 |
| | CCACATTTAA AATTTCTTAA TCACAAGCGG TTAACTAGGT ATAGTTTAGT TTTGAGTAAA | 240 |
| 0 | TCTTTTTAAA GGTGTACTTG TGCATTTTAC TTAATTAAAG ACATAAGACA TTTAATCGGC | 300 |
| | CTARARTARA TARARACTA CCTGTTTAGG TAGTTTTTTT ARTGTARTAG ATTARARCAC | 360 |
| 15 | TAGTTCATTT CTTATTAAAG ATGGATAGTT ATTTTATAGA TAAATTTGTC CTTTAGTGTA | 420 |
| | GCGGTAATTT TTAGGACTTT TTGGTGGhAA AAATGTTCTT AATAAAAGTA ATAGTCCTAC | 480 |
| • | TITACCGCCA AAGCCATA | 498 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 999: | |
| - | (i) SEQUENCE CHARACTERISTICS: | |
| 25 | (A) LENGTH: 568 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | *** |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 999: | |
| 30 | TGAGCTGGTT GTTTATTATC ATCAGTTTTC TTCTGATTAT CATCTGATTT ATCTTGAGAT | 60 |
| | GCTTTGTCAT CCTTATCTTT CGACTCATCC TTTGATGCTT TATCATCATT CTCTTCTTTA | .120 |
| | GCAGGACGTT GCTTTGTAGG TGCTTGTTGC TGAGGTGGCA CATATTGATA TTGATTCTGC | 180 |
| <i>35</i> | TGTGGCAATT GCTGATATTG GTTTGCTTGT GAATCTAGCT CATTCTGCTC TTTTTCCTCT | 240 |
| | TGTTGCTTTT TCTTTCTCTC TTTTTCTGCA TTTTCTTTTT GACGCTTTTC TTTTTGTTCC | . 300 |
| 40 | TGCTTTTGTT CGTTCAACAT ACGTTCTTTA GCTTTATTCG AATGATCTAC ATATGCAAAA | 360 |
| | ATTGCAAATA CTAATCCTCC GAGTAATAGC AATACCGTCG CAATGCTAAC TACTTTCGCT | 420 |
| | GTTGTACTCA TTTTCTTCTT ACTTCCATCT TCATTTTTAT TGTAGTCGTA ATTTTGATTC | 480 |
| 45 | GACATACTCT CCCTCACTTC AAACTAATTT AAATATAGAA ATTATCACGC AACCATTAAC | 540 |
| • | ATTTTCACAA CTAATTTGCG ACCHAGTA | 568 |
| | (2) INFORMATION FOR SEQ ID NO: 1000: | |

1786

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1000:

| 5 | AGTGTTTCTA | ATTGCAAAAT | TCCAAATACA | GTGTCGTTAT | TTACTTTTTT | CATGCTAAAC | 60 |
|----|------------|------------|------------|------------|------------|------------|------|
| 5 | ATCTCCCAAT | TAATAATCAC | ATATTTAGCT | ACTATACAAG | TATTAACAAA | CATCCCAACA | 120 |
| | ATCCCAAAAC | TTGTATGTGC | TAACTTATGC | ATAAAACTAC | AAGTGTAAAT | AAACTTGCTT | 180 |
| 10 | TCTATTCAAT | TGTCAAAGTT | GAATAAAATT | AAATAAGTAT | AAAAACCAAT | AATCAATAGA | 240 |
| | GTTAATATTT | AGAAATAAGA | TAATAGTACA | TAAAACAAAT | CACTCTATTA | CATATTAATT | 300 |
| | TTATAATTTA | TATACAAAGA | AAATATATCA | ATATTACCAT | TAAATTGCAA | CAATTCTACA | 360 |
| 15 | TATATTTCTT | CAAAAAAGAT | ACGCATTGAA | TTTTTATTAC | ATATAACTCT | CATGAAAATT | 420 |
| | GATTAAACTA | AATTAATTAG | TTAGCCTTAA | ATTTAACAAA | TTAAATCAAA | CCGAATGAGG | 480 |
| | CTAAATTGGT | TATTTTTCAA | GATATGATTT | GTATAAATCA | AAACATTTCT | TACAAATCAA | 540 |
| 20 | ATGTGTATAA | AATGTGATAT | ACATTTTCAA | CCTTAAAAAA | GTTCTAAAAA | AAGATGAGCA | 600 |
| | TCTACTGTCT | CATCTTTCAG | TTCTTTTTTA | CGGGTCTGTT | TTCTAATTTG | AGCACAATCT | 660 |
| 25 | TCGATTTCTT | TATCTAAATG | ACTACCAATT | AAATCTATTT | CTTCTATTGT | TAAATCGCTA | 720 |
| 25 | TCTCCATCTT | CTTTTATCTC | TGGTATTATT | TTTTCTTCAA | CTAAGTCACG | ATATAGTGTT | 780 |
| | TTTGAATTCT | CGTTCAATTT | CGATTCGTGA | TTŤTGAATAC | TTTCTTCCGC | ACCAATGTAT | 840 |
| 30 | ATCTATTGGC | ACTAGCTTCT | ACTTTTGTAC | CATCAATAAA | AATTGAATTA | TCATCAATAA | 900 |
| | GATTTTGCTT | TAAACATTGA | CTATAGAACT | GAATAAATAA | AGATTCAATT | AACGCATCAG | 960 |
| | TATTAGGATT | CACTCTAAAA | CGATTAATAG | TTTTATAAGA | AAGTGTTTGA | TCTTGGGCTA | 1020 |
| 35 | ACCACATCAT | TCGAATACTG | TCATGAAGTA | ATTTCTCTAT | TCTACGACCA | GAAAATACAG | 1080 |
| , | ATTGAGTATA | TGCATATAAG | ATGATTTTTA | ACATCATTTT | TGGaTGATAG | GATGTTGCAC | 1140 |
| | CACGATGATG | TCTGAATTCA | TCGAATTCGC | TATCAGGTAT | CGTTTCAACA | ATTTCATTAA | 1200 |
| 40 | CATATCGCGA | AATATCATTT | TGAGGAATTC | TAACGAAGTT | TCTATTGGTA | GTGTAAGTTG | 1260 |
| | GGGTCATGTT | ATTATTATA | TACATAAGGC | ACCTCTTTAA | TTTAGTTTAG | TAGTATTTAT | 1320 |
| | TAAATTATAC | GaAGGGACCC | AACACAGAAA | ATTCATTTTA | TTGAATTTTA | CATTTATGTG | 1380 |
| 45 | CAAGTTGGGG | AAAAATGTCT | TATTTTTCA | AAGTATTTAA | AAGTAAAATT | ACATGTTAAT | 1440 |
| | A | | | | - | | 1441 |

(2) INFORMATION FOR SEQ ID NO: 1001:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 587 base pairs

55

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----------|---|-------|
| | | |
| <i>5</i> | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1001: | |
| * * * | TAATAATATC TGTCATATTA AGTCTCCCTC ATTAGAACTC ATTATAAATG AAGTTATTGT | 60 |
| 10 | GTGTGTCGCC ACTGCCATAA ATTAAATATA AAGTAATAAA TATTGCCAAA TACAATAGTG | 120 |
| - 19 | TTAATAAATA TGGTTTGAAT GCTTCAACAT ATTTATTAGG TGGCTGTTTA CTTTTAGATT | 180 , |
| | TCATATTGCA CCTCTTAAAG TTCTTAGTAA AAACGCCTTT ATAAAGACCG TTCAATATAA | 240 |
| 15 | AATACGTTTT AAAATTTGTT TTTTACAATT CATTATATCG ATATTCATAA TGAAATTCAA | 300 |
| | TTTTAATTTT ATAGATTCAA CATAGTAATT GGTTGTCATC ACTCAAKTAT TGTAAATGAT | 360 |
| | ACACTTIGTT GAGRACATCA TTCATTTTAA AGGTTATTTA AACAATAAAC AATTACAGTC | 420 |
| 20 | TATATAACAA TTTTGTTATA TACGTCAAAA TCAAATAAAC TCATCACATT AATATGACGA | 480 |
| | GTTTATAATG TTATTGAATT ATCATCAGCG CAAATATATA CATTCGCAAG TCAAGCATAA | 540 |
| | CATATTTAAC AATTGCTTTG CTTGGTTTTA CCAATGGATT AAAAACC | 587 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1002: | (|
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 522 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · . |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1002: | |
| 35 | CAATTGTGTC ATAATTTTGC TGATGATAAC TAATCGTTTT GGAGTAGCTA TTTGATGAAG | 60 |
| | TTCGTCCAAT ACCTTTGTT GAATCGAATT TACCACCTGA GCGTATATGA AAATGTACTG | 120 |
| 40 | TCTACTTTTG CAGTTGAAAT TTTATTTTTC GGCAATTGGT CTAATATTTC AGTTTTACGA | 180 |
| | TITCTTTTTA CTTGAAAATC TACATGGTAC TCACTTGGAT ACTTTAACCA ATTTGAATTT | 240 |
| | TTTTCTTCTT TATGAGATTC AAACTTTAAA TTTGAATGAA TTGAGCCTTG TTTTTTAACA | 300 |
| 45 | AGTAATACAT TCTTGTCATA AGTTGGATCA TCGATAAAGT CGAATTGTAA ATTTTGGAGT | 360 |
| , | ATATTEGTWT TCTCATCATA TACTGTTTCA GTTCGTTTTG TGATTTTACC GTTTTTCCCA | 420 |
| | ATATCATCCG GTGCTGTTGA ATTTTTATCT TTATTAGTAA CATTACGTTG CTTTTGTGAn | 480 |
| 50 | TT 45002CTCARC CTTATCCARCA TT | 522 |

CTTATCAACA TGTCTTCTAT TTGGCTGANG CTTATGGNGA TT.

(2) INFORMATION FOR SEQ ID NO: 1003:

| 5 | (A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|------------|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1003: | |
| 10 | TCTTTGTTTG AGACATAATG TCATGTAAAG TTTTCACAAT GCGTTCTTCA ACTTGTTGCC | 60 |
| 10 | TTGCCTCTCC TTTGAAAGGA ACAATTCGAT CTCCGAATAA GTCCTCAGGC TTGTATAGAT | 120 |
| | TATCAAATAG ATAGACTGAC TCACCTTCAA ATATTCCAAA ATGCCATTCC TTCAGTCCCT | 180 |
| 15 | TAAAACGTTG ATACGATTGG WTAGGTGCAA CATTTTCAAG TGTGTCACTT GCGCGTTCTT | 240 |
| | GCGTTGATGA TGCATATAAA TCGAAGTTTA TCCCCTTAGT TTCATAATAA CTACGTGCCT | 300 |
| | TINGAGCTIG AGCAATTCCA AGT | 323 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1004: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 320 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| <i>3</i> 0 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1004: | |
| | TTCTAACTTG ACGTGACTGG GCATTTCTGT GNAAATNTTC TGACATTCTT TTTAATATCC | 60 |
| | GCAACGCAAT TGCTTCAGTT AAAGATTGAA ACTTGCAACA TTATTTGGTA CGAAAAAGTC | 120 |
| 35 | AGTTTTAATG TCGATATAAG ATTTATTTTT TTTGTTATAT AGTTTCGCAA CTACATTTGG | 180 |
| , | TTGTCTTACT TGATCATATT TTGCAACCGT ATCGAATGCC GTCTTTTCAA ACAGCTTTAC | 240 |
| | GAGATACGTA AACCATGACC CATCCATCGA AGTCCTTGGT AAAAACCCAG GGTTTCCGAA | 300 |
| 40 | GCCGTAGGGT TTGAAAGATA | 320 |
| | (2) INFORMATION FOR SEQ ID NO: 1005: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 305 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1005: | |
| | NATTAATGCT AGCCAAAACA GANTTGCAAN ATGTAAAGAC ATGTGAAACC CTCCTTATAT | 60 |

| | CGATATTTAT AAAAAATAAT ATTTCACTTA ACCAGTTTTT AGTTATCATT GCAATGGTAA | 180 |
|-------|---|-------|
| | AGGATACGAT GAGTATCACA CCACAAATGA TAATACCAGG CAGGAGCCAA CATAAATCAT | 240 |
| 5 | CTAAATCTTT ATTATATGTG ATTAAAATAT TAAAGATAAC AAAAGTGGTA GTAATAACTA | 300 |
| | TATTG | 305 |
| o | (2) INFORMATION FOR SEQ ID NO: 1006: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | • . |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1006: | |
| 20 | TTCAAGATAT CAGTATAAAT AAAAACTTAA TATGCTCATT ATAGACAGCT ATAACTATAT | 60 |
| 4 = 1 | TTTCTCGTCC CACTCTATAG AAATCAATTT CATTTATTAC CATTTTCTCT ATTTAAAAAC | 120 |
| | ATATTTTTGG TATTAACAAT TAAAAGTGGG TATATATATT TAATGAACCA ATTTTTTAGG | 180 |
| 25 | AAAGTAGGGC TAAACCTATG GAAAATAAAT TATACCACAT GGTGTCCTCT TTTACCATGA | 240 |
| | ACACAGTGAA TTAAAAAATA TTAANCAAGG TATTGGGGAA GTANCACCAG CATTAGGTCC | 300 |
| | AATTGGTAGC CACCTTCCAA TCCATTGGGG GnAA | . 334 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1007: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 565 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| ٠. | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1007: | |
| 40 | AGAAAATTTG TTATATTAGA AGCGAATAAT TTTAAAACAT ATTATGAAAT GTAAGAAGAA | 60 |
| | ATATTATGAA ACTAGGAAAA GTAGATTGTT GAAAATTCCA TACAATAGGN GANGTAAAGT | 120 |
| 45 | GAATAAATTC TGGTATTACT AAAGCTATTG ATTGTCCTAA TTGTAATAAA AAGTTGGATA | 180 |
| * | GTGTAGTTGA GGGGAGAAA ACTAAAATGC AAAAATATAT TCTCAATGGA TCATTATAAA | 240 |
| | TACCAATTAG ATTAAAGTAT TGCG&ACATT TACAATTAGA AATCAGTATT AATCTGCCAT | 300 |
| 50 | AGATAATTGT ATTAATGTAA AAMATAAAAT AGAATGAGAA TATACGGAAA TTTTTTATAC | 360 |
| | ATTTATAACC AATTCTGTTA AACTGTGAAG AGTAGAGTTA AAAACGAACT TTTTGTTTAT | 420 |

| | AATGATTGAA CGCTATTCTA GAGAAGAAAT GTCTAATATT TGGACTGATC AAAATCGCTA | 540 |
|-----------|---|-------|
| | TGAAGCCATG GTTAGAAGTG GAAAT | 565 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1008: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1008: | . * |
| 15 | CAACATTAGC GTCTAAACAA ATCTTTGACT AAACGTTCAC TTGAGCGACC ATCTTGATAT | 60 |
| | TTAAAATGTT TATCTAAGAA TGGCACAACT TTTTCAACCT CATAATCTTC ATTGTCCAAA | 120 |
| 20 | GCATCCATTA ATGCATCAAA GGACTGTACA ATTTTACCTG GAACAAATGA TTCAAATGGT | 180 |
| | TCATAGAAAT CACGCGTCGT AATGTAATCT TCTAAGTCAA ATGCATAGAA AATCATCGGC | 240 |
| | TTTTTAAATA CTGCATATTC ATATATTAAA GATGAATAAT CACTAATCAA CAAGTCTGTA | 300 |
| 25 | ACAAAGAGAA TATCGTTAAC TTCACGATGA TCTGACACAT CGATAAAGTA TYGTSTATGT | 360 |
| | TCACGTGAAA TAYYAAGTCY ATTETTTACG AACGGATGCA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1009: | • |
| <i>30</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 454 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1009: | |
| | TATTGTAAAA ACTGTGGTTC TTACAATGGC GAAGAAGTAG CAGCTAAATA ATTTTAGTTA | 60 |
| 40 | CTCAATATAA AAAGTCCCGC TTAAAATGAT TGTTTTAAGT GGGACTTTTT ATATTGCGAA | 120 |
| | AAATAATTGG CGAACGAGGT AACTGGATAC CTCATCCGCC AATTAAAATT TGTTAATTTA | - 180 |
| 45 | ATAATTAAAT ATAAAGACGA TITATTAGTT TTTACGTTTT CTAGGTAATA CGAATGCAAC | 240 |
| | GATGCTACTT AAAGCTAATA ATGCCATTAA TGGTAATGTC ATATCTnTAT TTGATTCTTC | 300 |
| | ACCAGTTTGT GGTAATGATT TTGCTTTATT TTCTTGTGTA TTTGTATTGT TTTGGCTTTG | 360 |
| 50 | GAGTGTGTCC ATCATTTGTG TTTTTAATGT TTGCTTnTnG TAATGGAGCA CTAATCTTTT | 420 |
| | GCCTCGCTAG AACCTGCCGG AGGTTTGGAA CCAC | 454 |

| <i>5</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • * . |
|----------|--|----------------|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1010: | |
| 10 | GGTACAACAA CTTTAGACAA TGAAATATTA AAAGATACGG ATGATAAAAA GTCGAGTAAA | 60 |
| | The state of the s | 120 |
| | ACTITIGITG GCGGAACAAA AGTIGATGAC CAACATGCTA GTATCGGAAT GGATTTTGAA | 180 |
| 15 * | AATCAGGACA AAACTTTAAC TGCCAAAAAA TCATATTTCA TATTAAACGA TAAAATTGTC | - - |
| 15 | TTCTTAGGAA CTGGCATTAA AAGTACTGAT TCATCAAAGG ATCCCAGTTA CCAACCGATG | 240 |
| | AAAATCCGCA AGCCGATGGG GAATACGGTA TTTTCCGGCC GTTAACCAAC CACCCATTCC | 300 |
| | GGTTATCCGG GAAACCATTC CATCCTTTTA GGAGNCNCCG GTNCCNAAAA GGACCTCGGG | 360 |
| 20 | TATCCTTTTT TTAACCAACC CGAAATTACT GGTAAAAAAG | 400- |
| | (2) INFORMATION FOR SEQ ID NO: 1011: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) Type: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | - |
| 30 | THE THE PARTY CHO IN NO. 1011. | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1011: | 60- |
| | TTAGGTATTC GCAAAAATGA TCTTCAATAT ATAGCTATGG CCAAAAGATG GGCTAAAGCT | |
| 35 | TATACAATTA CTGTAGCAGT GGGAGTTGTT ACAGGTACAA TTATAGGACT TCAATTATCA | 120 |
| | TGATTTGGCC TACATTTATG GAAATGGGTG GACACGTATT GCACTTCCCT TATTATGGGA | . 180 |
| | ACATTGCGGT CTCTTGGAGC TATTTCTTAA GTATATATTA TATACTGGGA TCGTTTAAAA | 240 |
| 40 | TAATGGCACA TTCTTAATAG TATACCAGTA ATTATGGGGC CTTCTCAGCA TCTCATACTC | 300 |
| | AGGAATCATT ATGAATACGC CTGCAGGTTT GAGTGAAGAT GGAAGTGGCC ATGTCACCTT | 360 |
| | AGAGCGTGTT ACCCACGTTA AGTCGTCATT nCGAATACAC | 400 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1012: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ; ; |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1012: | | |
|----|---|-----|----|
| | CTTTATGGGA TACACTACAA ATCGAGACTA TAAGGTTTTT TATTTTATTT | 60 | |
| 5 | TATCAATAGT TTTATAATCG AGCTTCAAAA CTTTAGAAAA TAGTAGAAAT AGCATTCAAT | 120 | |
| | ATAGTGCAAA AGTGCAAATT GATAACTTGA CACTTATCTC CTATAAACCG TACAATTAAT | 180 | |
| | TTGTATGATT TATATATAAT TTCATAAAGT CATATTGAAT TTCATATAAA GAGCAAACCC | 240 | |
| 10 | TAGAAAANGA GGTGTTGTGG AATTATTAAG CTCCTACTCA TTTGCGGGGT CATCTAGGGT | 300 | |
| | GTGGAGGATG TGTGCCGAAT TGTGCTCAAA NATCCCAGCA GCAACGCGAG TTGAACAGCC | 360 | |
| | TAAGACGCAA CAAAGGATCT GnnAAGGACC ATCAGGCACG | 400 | |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1013: | | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 353 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1013: | | |
| | GTCGTTGCTG ATACCACGCC AGTATTGGTT TTAAATGATA AAAAAATCTG TGAGATTGCA | 60 | |
| | TCATTGAGAC AAACATCGCT ATTTGAAATG GCCGAATATA TAGGGTTTAG CGAGCCACAG | 120 | ٠. |
| 30 | AAATTAGTAC AATTATTTAT TAACCATGAT AGGAAGGTGA GACGCCAATG AATCAATATA | 180 | |
| | ATACTATAGG TTTTCACCCG GGAAATAGTC GTATTCATCA ATTAAATGCG ACTGTTAAAC | 240 | |
| | TTTTATnCTT ATTAGTTGTT CTATTCTGCA ATGGTnCTAT GCACAGGTAT TNATTTAATT | 300 | |
| 35 | AGGCTCACAT TTATGGGCAA TTCTCAATGA TGAACAGTCG TTGTGTAATC TCG | 353 | |
| | (2) INFORMATION FOR SEQ ID NO: 1014: | | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 627 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| 45 | (a.i.) anaumyan pagantantay ana in ya 1014 | | |
| - | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1014: | مة | |
| | CAAAGCCTTC AACAAATAAT CUTTTATTAG TACTGATTGG TTGCACAACA TAAGTTACAC | 60 | |
| 50 | CAGGITCATC TITAAATGTA ACTICCITAT AGAAGAGACC TITITIAGCA CIATACTCTG TITITICTGA TITAATITTA TCTITIAGAT TITICCTTC CAAGTAACTG TCAATTAGIT | 120 | |
| | IIIIICIGA IIIAMIIIIA ICIIIIAMAT TITTCICIIC CAAGIAACIG TCAATTAGTT | 180 | |

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| | ATGAAATAAA TAATATAATG ATAACTTTAA TCGCGTTTTE TTTCTTCTTC ATTATGTAAC | 300 |
|----|---|---------|
| | TCCTTTTTGC TTATCTATTC AGTATGAACG AATCAATTTA TTTAATAAAG AGTTTTTACC | 360 |
| 5 | AGATTGTAAC AAATTTTTT ATTCTCAATA TTATTATAGA AATCGAATTA CATACACGAT | 420 |
| | GCTTTTAAAA AATTTAATAA CAAATTTTAT TTTACTATCT ATCAAAATAA TTGACTACTT | 480 |
| | TTAACAATTA AGGATGATAC AATTACATTT TTTTCAATTT AAAAAATCAG TCATATCAGT | 540 |
| 10 | AATTACCGAT GAAAATACTA AGATATCGAT ATATTTTGCA TTATTTAACA TTTAAATTCH | 600 |
| | ATTATAGACA ATTCAATAAT TGCGATG | 627 |
| | (2) INFORMATION FOR SEQ ID NO: 1015: | • • |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 462 base pairs | • |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 20 | (D) TOPOLOGY: linear | + + + . |
| | | · |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1015: | |
| 25 | TAGTGTGACA TTAACACTGG AACAAAAAGA AGCTGCAATT GCAGAAGTTA ATAAGCTTAA | 60 |
| | ACAACAAGCA ATTGATCATG TTAACAATGC ACCTGATGTT CATTCAGTTG AAGAAATTCA | 120 |
| | ACAACAAGAA CAAGCGCATA TTGAACAATT TAATCCAGAA CAATTTACGA TTGAACAAGC | 180 |
| 30 | AAAATCAAAT GCAATTAAAT CGATTGAAGA TGCAATTCAA CATATGATTG ATGAAATCAA | 240 |
| | AGCTCGTACT GATCTAACAG ATAAAGAGAA GCAAGAAGCT ATTGCTAAGT TAAATCAATT | 300 |
| | AAAAGAACAA GCAATTCAAG CGATTCAACG TGCGCAAAGC ATCGATGAAA TAAGTGAGCA | 360 |
| 35 | ATTGGAACAA TTTAAAGCTC AAATGAAAGC AGCTAATCCA ACAGCAAAAG AACTAGCTAA | 420 |
| | ACGCAAGCAA GAAGCTATTA GTAGAATTAA AGACTTTTCA AA | 462 |
| • | (2) INFORMATION FOR SEQ ID NO: 1016: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 235 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 1016: | |
| | TGATTGGTCC CATCGACTCG TTATAACAAA TTGAAGGTAC AAAAGTATCT TGTGATTTAA | 60 |
| 50 | TARATTCARG TARATTCGTA CCTGGTTCTA CAAGGTAATT CTTTTCCATC AAGTGTAACC | 120 |
| | | |

| | ATAAATTGCG CATATCCACC NAAAATAACG ATGCCCCACA CATCTTTCAG ATAGG | 235 |
|----|--|-------|
| | (2) INFORMATION FOR SEQ ID NO: 1017: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 227 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1017: | - |
| | | |
| 15 | GTTGAAAACT ATAAGATCAN ATAAAGGTAA AACAGTGGTT TGTGTCATTA GTGGTGGTAA | 60 |
| | TAATGATATT AATCGAATGA AAGAAATTGA AGAACGTTCA TTACTATACG AGGAAATGAA | 120 |
| | GCATTACTTT ATCTTAAATT TCCCTCAACG TCCAGGTGCA TTGAGAGAAT TTGTAAATGA | 180 |
| 20 | CGTATTAGGA CCTCAAGACG ATATTACTAA ATTTGAATAC TTAAAAT | 227 |
| | (2) INFORMATION FOR SEQ ID NO: 1018: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 25 | (A) LENGTH: 284 base pairs (B) TYPE: nucleic acid | - |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (b) Toronosi: Timear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1018: | |
| | GTCTTACTTG CACAAGGTAT TATTTCTATC TTACTCGTTG CTTTCGCAAT CATGCTATAT | 60 |
| 35 | ATCATTAATA TTTTAGATGC ATATCGTAAT GCTGAACGAT TTAATCGCAA TGAGGAAATA | 120 |
| | AAGGATCCGA AGCGCGTATG GTGGCACATG GGACAAGACG TTCCCATACT TACTAATCTC | . 180 |
| | ACCAGGTACA THOTTATTGA TATTGTAGTG TAATTCCATT ATATTATGTT GGAGTAGCAT | 240 |
| 40 | TACAATACAA TTATACACGC GCCTCGAGAC nACATAGATG GGTG | 284 |
| | (2) INFORMATION FOR SEQ ID NO: 1019: | |
| 45 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 779 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | • |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1019: | |
| | CAATCATCAC ACATAAATGT TCGAATAGGA TTGTTTTTAA GTCGTTTAGA CTCAGTTGTG | 60 |

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| TGAACCTTCT AACATGCAC GTTTTTATA TTTTATTTCT GAATTTAAAG TAGGCGGATT AGTTTGTCCL TCLAGGATAG CACGATTCCA TTCATGATTA TCTTCAAAGT CGATTGGTTT 480 TGAACCATCA AATACACCTT TTTCTAAATC TTCGATGCTA ACTITTCTAT CATCGAAAAT CCAAGTCGTA CTATCTAATG TTATAGGAAA CTTTACGGCT CCTTTAATTT GTATCATTTT 600 CCCACTCCCT ATCAATGTAT ATAGCATTAT TTTAACACAA ATTGCTAACG ACACATTTTA | | CACCTCAATA | TGAGTTACAT | GGTTGATTCG | ATATGAATAA | CCATCTTCTT | GATTGTAAAT | 180 |
|---|----------|------------|------------|------------|------------|------------|------------|-------|
| AGTAGTTGCA GAGTCATGTG GTTCGGAATG TTTGAAAAAT GGTGTCATAT TAATGACAAA 360 TGAACCTTCT AACATGGCAC GTTTTTTATA TTTTATTTCT GAATTTAAAG TAGGCGGATT 420 AGTTTGTCCC TCCAGGATAG CACGATTCCA TTCATGATTA TCTTCAAAGT CGATTGGTTT 480 TGAACCATCA AATACACCTT TTTCTAAATC TTCGATGCTA ACTTTTCTAT CATCGAAAAT 540 CCAAGTCGTA CTATCTAATG TTATAGGAAA CTTTACGGCT CCTTTAATTT GTATCATTTT 600 CCCACTCCCT ATCAATGTAT ATAGCATTAT TTTAACACAA ATTGCTAACG ACACATTTTA 660 | | AAAACTATCT | ACACCATTAT | CGCTGTAAAG | TCGTTTACCG | TCTTTTGCAA | ATTGGAAAAA | 240 |
| TGAACCTTCT AACATGGCAC GTTTTTATA TTTTATTTCT GAATTTAAAG TAGGCGGATT 420 AGTTTGTCCL TCLAGGATAG CACGATTCCA TTCATGATTA TCTTCAAAGT CGATTGGTTT 480 TGAACCATCA AATACACCTT TTTCTAAATC TTCGATGCTA ACTITTCTAT CATCGAAAAT 540 CCCAAGTCGTA CTATCTAATG TTATAGGAAA CTTTACGGCT CCTTTAATTT GTATCATTTT 600 CCCACTCCCT ATCAATGTAT ATAGCATTAT TTTAACACAA ATTGCTAACG ACACATTTTA 660 | <i>5</i> | TAAATAGGGT | AATAGATCTA | TCGGTATATC | TAAATGATCA | TGCTCATTTG | ATAATCGAAT | 300 |
| AGTTTGTCCL TCLAGGATAG CACGATTCCA TTCATGATTA TCTTCAAAGT CGATTGGTTT TGAACCATCA AATACACCTT TTTCTAAATC TTCGATGCTA ACTTTTCTAT CATCGAAAAT CCAAGTCGTA CTATCTAATG TTATAGGAAA CTTTACGGCT CCTTTAATTT GTATCATTTT CCCACTCCCT ATCAATGTAT ATAGCATTAT TTTAACACAA ATTGCTAACG ACACATTTTA 660 | | AGTAGTTGCA | GAGTCATGTG | GTTCGGAATG | TTTGAAAAAT | GGTGTCATAT | TAATGACAAA | 360 |
| TGAACCATCA AATACACCTT TTTCTAAATC TTCGATGCTA ACTITTCTAT CATCGAAAAT CCAAGTCGTA CTATCTAATG TTATAGGAAA CTTTACGGCT CCTTTAATTT GTATCATTTT CCCACTCCCT ATCAATGTAT ATAGCATTAT TTTAACACAA ATTGCTAACG ACACATTTTA 660 | | TGAACCTTCT | AACATGGCAC | GTTTTTTATA | TTTTATTTCT | GAATTTAAAG | TAGGCGGATT | 420 |
| CCAAGTCGTA CTATCTAATG TTATAGGAAA CTTTACGGCT CCTTTAATTT GTATCATTTT 600 15 CCCACTCCCT ATCAATGTAT ATAGCATTAT TTTAACACAA ATTGCTAACG ACACATTTTA 660 | 10 | AGTTTGTCCt | TCtAGGATAG | CaCGATTCCa | TTCaTGaTTA | TCTTCAAAGT | CGATTGGTTT | 480 |
| CCAAGTCGTA CTATCTAATG TTATAGGAAA CTTTACGGCT CCTTTATTT CAACACTAATG TATAGGAAA CTTTACGCTAACG ACACATTTTA 660 | | TGAACCATCa | AATACACCTT | TTTCTAAATC | TTCGATGCTA | ACTITICTAT | CATCGAAAAT | 540 |
| CCCACTCCCT ATCAATGTAT ATAGCATTAT TTTAACACAA ATTGCTAACG ACACATTTTA 660 | | CCAAGTCGTA | CTATCTAATG | TTATAGGAAA | CTTTACGGCT | CCTTTAATTT | GTATCATTTT | 600 |
| ANTICTACTTC CTTTTTAATA TTTAGTAAGA TAAACTITTA GTAAGACTTG AGAATTTATA 720 | 15 | CCCACTCCCT | ATCAATGTAT | ATAGCATTAT | TTTAACACAA | ATTGCTAACG | ACACATTTTA | . 660 |
| MATCHACITY CITITIMENT TITLES | | AATCTACTTG | CTTTTTAATA | TTTAGTAAGA | TAAACTTTTA | GTAAGACTTG | AGAATTTATA | 720 |
| TAGAGGGGGA GCGTGTCATG GCGAAACAAG CAACAATGAA AAATGCAGCT TTGAAACAA 779 | 20 | TAGAGGGGGA | GCGTGTCATG | GCGAAACAAG | CAACAATGAA | AAATGCAGCT | TTGAAACAA | 779 |

(2) INFORMATION FOR SEQ ID NO: 1020:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 950 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1020: 30 ·

| TTAATGGTCC ATTAAGAATA | ATGGCAGAAA | ACCGTTTGCA | TAAATCAAAC | CTTGATTCAC | 60 |
|-----------------------|------------|------------|------------|------------|------|
| TAACTTAAGT AATACTCGCT | TTTCnTAAAT | CCTTTAGAAA | GGAACTATnT | ATCATGATTA | 120 |
| CTTCATTCAG ACATTCTGAA | GATATAGATA | AACATATTAT | AAAAACACCA | TTAGATCATA | 180 |
| CAGCGTCATG GATTAATGTA | GTAGANCCAG | ACCGAGAAGA | AATTGAAAAT | CTTATGGAAC | 24.0 |
| AATATAATAT ACCTGAAGAC | TTTATACGTG | ACCCTTTGGA | CTCAGAAGAA | AGTTCCCGTA | 300 |
| TTGAATATGA CGAAGATACT | GGTTACTCAT | TAATCATTAT | TGATTTACCT | ATCGTCAATT | 360 |
| CAACTAATCG TAGCGTTCTA | TCTTTTGTAA | CGATTCCATT | AGGCATTATT | ATTGGCAACG | 420 |
| GTATTATCGT AACAGTTTGT | GACGCTGAAA | ATGAATTTTT | AGAAAATTTA | CCTAAGCGTG | 480 |
| ATATTAATTT AAAATTTCAC | AGCAGATTTG | CATTAGAAAT | TTTAACTACT | ATTGCCGACC | 540 |
| ATTATAATUG TAACTTACGA | TIACTIAATA | AAAGTAGAAT | TCGTATTGAG | AAAGAACTAA | 600 |
| AAAATAACAT TACTAACAAA | CAACTTTTCA | AATTAATGGA | AGTTGAAAAA | AGTTTAGTAT | 660 |
| ACTITITAGE TGCCTLAAAA | GGTAACGATA | CAATTATTAA | AAAGTTATTC | CGTTTACCTG | 720 |

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| | AAGCCATCGA AACAACAGAA TTACATCAAC GTATCTTAGA AAGTATCACA ACATCATACG | 840 |
|-----|---|-----|
| | CITCCTTATT ATCTAATGAT ATGAATACGA TTATGAAGAC ATTAACACTT TTCACGGTAC | 900 |
| 5 | TATTAACGTT ACCAAYACLC GTATTTAGTT TCTTCGGTAT GAATGTGTCG | 950 |
| | (2) INFORMATION FOR SEQ ID NO: 1021: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 10 | (A) LENGTH: 528 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | . : |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1021: | |
| Υ . | AATATATAAA ATGAATACAT TGTGAGGCAA TTATCAAATG AAATTTAATA AAGTAAAACT | 60 |
| 20 | AGTTATACAT GCGTGTGTAC TATTATTTAT CATTATTTCT ATAGCGTTAA TTTTTCATCG | 120 |
| | ATTACAGACG AAGACACATT CTATAGACCC AATACATAAG GAAACAAAAT TATCAGACAA | 180 |
| | TGAAAAATAT TTAGTGGATC GTAATAAGGA AAAGGTTGCG CCGTCTAAAC TAAAAGAGGT | 240 |
| 25 | ATATAATAGC AAGGATCCTA AATATAAGAA AATTGACAAG TATTTACAAA GTTCATTATT | 300 |
| | TAACGGTTCA GTAGCTATAT ATGAAAATGG CAAATTGAAA ATGAGTAAAG GTLATGGATA | 360 |
| | TCAAGaTTTT GAAAAAGGTA TTAAAAACAC ACCGAATACG ATGTTTTLAA TNGGTTCAGC | 420 |
| 30 | TCAAAAATTT TCAACAGGGT TACTGTTAAA ACAGTTAGAA GAAGAACATA AAATAAATAT | 480 |
| | CAATGATCCA GTAAGTAAAT ACCTTCCATG GTTTAAAACA TCTAAGCC | 528 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1022: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 713 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (b) Toronogr. Tilledi | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1022: | |
| 45 | GCATTnCGGT TAAAGTAKGt TTCAGCTTCT CTCaTTTTAG AAGTACCGAA AALTGGTTGG | 60 |
| | TTALCTGGAT TTAATTLCAC GATAAATATT GCTTACTTTG TTACTTTGTT AAATGTACCC | 120 |
| | ATTACGAGTC TCAATGTTAT TCCAATAAAT ATCACTTGTT GGTGCATGGT TTGGATATGC | 180 |
| 50 | ACAATGATTT CTTGAAATTG TTTGAACGAT TTCTAATGGA TCACAGCCAA ATGTACTGTT | 240 |
| | TARTACTTCA CACTCTCTCA ATACTCCACA ANDTGAAATA CAACTTCTCC ACTTTCCTAA | |
| | | |

| | CAR THE ANGEL AND ANGEL AN | 420 |
|----|--|---------|
| | AGTATCTTGC GTATAACCAG CCTCTATACG AACCATTTTA AATTTTGTTT GAATTAAATC | |
| | TGTAAAACTC TGTCTATCCA TTCTGTTATC TACCTTTCTG TTTGGGGAAT TTTATCCGGA | 480 |
| 5 | CACAAGAAAT TGCAATAATA CACATTTCTT GAAACACAGA TTACATCTTA ATATATTTTT | 540 |
| | AATAAAATGA AAAGAGTCAA TTTCACATTT GTATTAAATT TTGATCAAGT CAACAAGAGT | 600 |
| | TAAGTTTACT TTATAATGAA GCGAAAGTAA ATGAAGTAAA ATTTTATGCA TAATCACTAG | 660 |
| 10 | ATTTGATAAA ACTTACACTT TTATAATGAT ATCAAATTTA CAAAGGAAAA CTG | 713 |
| | (2) INFORMATION FOR SEQ ID NO: 1023: | • |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 15 | (A) LENGTH: 570 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | * | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1023: | |
| | AATAAAATAG AAATGATTAT GGGTACAATT ATCGCTATCA TATCCTTGTT ATTAATTATA | 60 |
| 25 | TTACAAGCAT TTAATATTAC TTGGGGCGTT ATACCAATTA CAAATTTTGG ACATCAATTT | 120 |
| | TTCTTTTTCA TTGGTATTAT TTTAGTAATT GCCGGCATAT TTTwyAAGCG ACTEGAGTTT | 180 |
| | TCGGGAATCG GGTTATTATT TTGTCAAAAA ACCGTCGATG CAATGATTCA TAATCCACAA | 240 |
| 30 | TCAGCCCAGA TTTTTCATT AATTATAGG ATATTATTAG TAGTTCTAGT TATATATTC | 300 |
| | ACAATTAGAT TATCTTCACG TACAAGATTA TAAATATGAT AAAACTATTC ACTTGATTAA | 360 |
| | TTGTATTAAT TGAGATGAAT AGTTTTTTTA TTGTTGGAAT AACTTTTGGT AATTTATAAA | 420 |
| 35 | TAATTTAAAA AAATTGTITA TAAAAGGAAG CGTATATAGA ATGAAGGTTG GGTATATAGT | 480 |
| | TTATTGAGGG AGGTGTCACA ATGAATAAAG TCACAATTAA TCCTCAAATC CAATTAACTT | 540 |
| 40 | ATCAAATTGA AGGTAAAGGG GATCCTATAN | 570 |
| | (2) INFORMATION FOR SEQ ID NO: 1024: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 487 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . * * . |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1024: | (· · |
| | AL DESCRIPTION OF THE PROPERTY CONTRACTOR CONTRACTOR CONTRACTOR AND THE PROPERTY CONTRACTOR CONTRACTOR AND THE PROPERTY CONTRACTOR AND THE PRO | 60 |
| | CTTTGTTGTG CTTGAGCATT ATTAAAAAGA GTATTTAAAT TTAGTTGTTG GTTTGTAATA | |
| | | |

| | TCAGAATTAT TAACACTATA TTTCCCTTTA AATAATGGTG ATTCGrAATA ATGCTTATCT | 180 |
|----------|---|-----|
| | TTATCTGCAG CTAACTGGAA TTKCCCTAAT GCAGAGTCTG CGATTGTTGG TTCAAGATTA | 240 |
| 5 | ATCATTGATT TCTCTTTTTT AGGATCATGT CCATATGACA tGTaATTTTC GATGCATTAA | 300 |
| | CAACAGATTT AKGAATGCCA AGCCCTTTAA CAATTTCATC TGATGCATCT GCGCTTAATn | 360 |
| | CTAATGAAGA TAAAAACGAL TALCTTTCAT CKKTTCTTGG AACTTCACTT CATTTTCAAA | 420 |
| 10 | ACGGTCATTA AAATAATCTT TATACATTTT TGCTGTTTGT TGTTCACTTT TTAGGTATGT | 480 |
| | ATTTTC | 487 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1025: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 364 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1025: | |
| 25 | ATATGTTATA AACAATTTTA CAGTTGTATC ATCTACTCGT TCTATTCTCA TATCATCTCA | 60 |
| . | CTCCTTACAG TCGATGAATA GTATCCACAT TGTATTAAAG CATCAAACAA AATACAATTT | 120 |
| | ATTTGTTTGA TTTCTTCTC TAAAMTATTT TGGTAACTTA TAATAACATA TTCGTTGTAG | 180 |
| 30 | CAAAACTATT TAAATGATTT ATACAGTTAA AGCATTAAAG CACTTTCTTA ATTTAATTTT | 240 |
| | ACCTTATCAT AGCAAATGTT TCATCCAAAA CACTCTAATA TAGAGCTATA TTAACAATTG | 300 |
| 35 | CACATTIGAT TTAAAAGATA CTAAGCAATT ATTGLAAAAT TAAAACCAAA AAAGCAACAC | 360 |
| | TATA | 364 |
| | (2) INFORMATION FOR SEQ ID NO: 1026: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | *. | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1026: | |
| | TGCCCCAGGG GAGTACNAAA AAAAAGNGGG GTGGGGAATT GGAAACCGGA ATTAGTGGTT | 60 |
| 50 | AAAGGGGTTT ATTGGATGTT GGGTCTAAAG TATTCCCAGA AATTTATCCA TChATGATTG | 120 |
| | A CONTRACT TO THE PARTY OF THE | 100 |

| | CTTATATAAA AATGGCACAA TTATTTCATG TACCAACAAG AACAATATTA ATACGTCATT | 300 |
|----|--|------|
| | TAACACCTAA AATTATACCG GCTATTATCG TTG | 333 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1027: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 450 base pairs | |
| | (B) TYPE: nucleic acid | |
| 10 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | - 1 |
| | (D) TOPOLOGI: Illieat | E-18 |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1027: | |
| | TGTTCCATTC GTTTTAATAA TGGTGATACT GTACCAGTAT CGAGTGCTAA TTCAGTTACG | 60 |
| | ACTITCTTGA CGTTTACAGG AGATTCATCC CATAAAATTG TTAAGACAAG AAATTGTGGG | 120 |
| 20 | TATGTTAGAT TGTACTTCTT AAAAACTTTG TTAGAGTAGT AGCGATTAAC TTGTCTTTGA | 180 |
| | GCATTGTACA AACTAAAGCA TAGCTGTTCT TTTAAATTAT GTTGATCAGA CATTAAAGTT | 240 |
| | CTCCTCCAGA CATACTATCC GTTTTTnTCT CTTTTCGGAT TGGTAATCAT TAAAAAGTTG | 300 |
| 25 | ATTGTTTATT AATTCACAAC TTTCTTTGAT TCAATGCCAT GCDAAAATTA AAGTATGTTT | 360 |
| | AAAGTTTAGA AGATATTTTT GATTAAATCA AGCAAAAAGA TAATTTAATA TATATGTGAT | 420 |
| | CATTTTAAA AATAACTGTn ATAGAAAAGA | 450 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1028: | |
| 2 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid | * |
| 35 | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1028: | |
| 40 | • | 60 |
| | TGCATCTATA CCTAGAACTT TAATTTCGGA TTTTATTGCG TCTGTAATAT CTTTAATACC | 90 |
| | ACTITICGATA GGGAAACTIT CGTCACCTTC AACATATITA ATACCAAAGC CACCACCAAG | 120 |
| 45 | GTTTAATAAT TCAACTTGAA TGCCTTGCtC TTTAAGCCAA CGTAAAmCAA TTTTAGCaGT | 180 |
| | TTCAATAAAL GCTTCTGTAC CTTCAALCTG TGYACCAATA TGACAATGTA CACCTTTTAA | 240 |
| | TTTTAAGTGT TTAGATTGTT GGACTTTGTC AATTGCTTTT TTAGCTAAGC CATATTGAAT | 300 |
| 50 | TGATAATCCA AACTTACTAT CTTCTTGCCC AGTTTGAATA AATTCGTGTG TATGTGCTTC | 360 |
| | aACACCTGGa TTAACTCGTA ALACAACTTG aACCGTATCA TTAGCATAGC GGTCTATTAA | 420 |

| | AATITCATGT TECGTTTTAT TGTTACCATG GAAATGGATG CGACTCGGTT CAAAA | 535 |
|----|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1029: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 359 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1029: | ٠. |
| 15 | GAAGATGATT GAATTATGGA ATTTTTTCG AGATATGTTA TTTCGGGGAT CAGATTTTGC | 60 |
| .• | GATTTTGCCT TGGATAGAGT AGTTGCGATT TGTAAATACG TTTTTCAGGT TCGATTCAAT | 120 |
| | TTCGTTGTTA AGATAATATG GATTAGTTTC ACTGACATGT TGATGCATGT CTTTTTTGTT | 180 |
| 20 | CTGATAAAGT ATAAAATGTT TACTTAACAT TACTTAGTAT GACACCTGCT AATTCAAACA | 240 |
| | TTATTTGAGA CATTCTTTTC AAATTAATTA TAAATTTTTA CCLATAGACT AGTTTGATAT | 300 |
| | TTATCTACAT CTCAAAATTC TCATCAACAA TCTGTCACAT CCAACATTTT TACTTHAGT | 359 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1030: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 341 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | , |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1030: | |
| 55 | TACATTGGTA AATAATTCTC ATAGTTTATG TCTCGTTGAT TAATCCAATC ATTGTTTTTA | 60 |
| | TCGGGTAAAA CATTCAAACT TTTCAAATTC ACAATTGATT GATGTTTCAT TAAAGTATCT | 120 |
| 40 | AATTTTTGCT CTCTAGTTAA ATATTCACCA ATGTCATTAT AATAGATATC GTGATTGTAA | 180 |
| | CTTCCATCTT TAACTAAAAT AGATATAGCT ATCGGTGCTC TACTTCCTGA TCCAAATATT | 240 |
| | TTTCCACCTT CTTTCTTGa TTTTTCACCC TGTGTTCGTT GGTCGCCTCT CAAATTAATT | 300 |
| 45 | ATGLACAGAT AGTTAAATTC ATCGATAAAA CTTTTCTAAA T | 341 |
| | (2) INFORMATION FOR SEQ ID NO: 1031: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 326 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | /-/ | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1031: | |
|-------------|---|-------|
| | GTCTAACTTT AATGTTTAAA AANCTTAGAA ATTTTCTACT CATAAATGGA TGCTTTATGG | 60 |
| 5 | AATATTATTA ACAGGCCCAG CTTCAATGCT AGCTATAGAA TTTGGATGGT TCTTAACAGA | 120 |
| | GATGGGTAGA CAGCCTTGGA TTGTTCGTGG TTATATGCGC GTGGCAGAAG CAGCAACACA | 180 |
| | GCAGCGGAAT AACCTTCGTT ACAATTTTAT TTGGCATATG TACATCATTT AAGTATACAG | 240 |
| 10 | TGCAACGTAT ATCGTAGTTA AAATAACCGC GTAGAGAGTA ACGTAGCAGA GCAGAGGAAT | 300 |
| | GAAANATTAG CTTATGNAAC GGTAGG | 326 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1032: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 263 base pairs (B) TYPE: nucleic acid | |
| 20 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1032: | . , . |
| 25 | ACAATCAGGC TTGTGAAGAA TGAATTGCAT GACGTTTGTG TAATTGAACT GCGAGGTTTA | 60 |
| | ATTTCTAAAA TGCTCCAGnC CTCCAATGTA ATCGCATCTT GATATAACAT AGCGATCGCT | 120 |
| | TGATTTGTCG TTGTATCAAC ACCTCTAAAC AACGTTTCAC CTATTCGGCA ATTCATTTAT | 180 |
| 30 | TTTACCCAAA TCATTATATA AAAGTTGTGG TAACATGCTC GAAATACCAC CTGAAATAAT | 240 |
| | nTCAATCGAT ATCCTATTTC TCT | 263 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1033: | |
| <i>35</i> ° | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 514 base pairs | |
| 40 | (A) LENGIH: 514 base putto (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1033: | • |
| 45 | TTTCTATAGA GGATCCTGTA GAGATGCAAA TTCCTGGTAT CGTCCAAATT AATGTGAATG | 60 |
| | ATAAAGCTGG CATAAACTAT GTAAATTCGT TTAAAGCTAT TTTAAGATGT GATCCTGATG | 120 |
| | TTATTTTAAT AGGTGAAATC AGAGATAAAG ATGTTGCCAA GTGTGTTATA CAGGCTAGTT | 180 |
| 50 | TAAGTGGTCA CCTTGTTCTG ACTACATTGC ATGCAACTGA TTGTAAAGGT GCTATTTTAA | 240 |
| | TOTAL TOTAL MATTER TACK ANTICATACA GGCAACTAAC TTAATTATAA | 300 |

| | AGCAACAACT CCGATATTTC TTTTCCCATA ATCATCATT ACCATCATCA TTTAAGAACT | 420 |
|-------|---|-----|
| | TAGAAGATAA ACTTGATGAT ATGACAAAAG CAGGTGTCAT TTGTGAAACT ACAATGCATA | 480 |
| 5 | AATACATTTA AACTACATTC TAAGAAGCGA CAAT | 514 |
| | (2) INFORMATION FOR SEQ ID NO: 1034: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 598 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1034: | |
| | TTTTTCACGA ACATTTTGT TTAAAATTTT CTTTCTTAAA CGTATACTTT CTGGTGTAAC | 60 |
| 20 | CTCAACAAGT TCATCATCAT TAATGAATTG TAACGCTTCT TCCAATGTTA GAATACGCGG | 120 |
| | TCTATTCATT GTTTGTGTTT GGTCTTTCGT TGCAGAACGT ACGTTAGTTT GATGTTTTGT | 180 |
| | TTTAGTGATG TTAACAGTTA AATCATTTTC ACGATTATGT TCACCAACAA TCATACCTTC | 240 |
| 25 | ATAAACTTCA GTACCAGGTT CCATGAAGTT TACACCTCTA TCTTCAAGTC CCAAAATGGC | 300 |
| , ->- | ATAAGTACTT GCAGAACCTT GATCCATTGA AATTAATGCA CCATTACGAC GACCGCCAAT | 360 |
| | TTGTGCTTTA ATACGTGGTC TAAATTCYTC AAATGTATGG TTAATAATAC CGTAACCTCT | 420 |
| 30 | TGTCATTGAC ATAAATTCAG TCGTATAACC AATCATACCA CGAGCCGGTA CATTAAAGAT | 480 |
| | TAAACGTGTA AGTCCATTAT CAGTTGTAGT CATATCAACC ATTTCACCTT TaCGTGCACC | 540 |
| 35 | TAAKGATTCa ATAACAGCAC CTGCATTTtC TTGTGGCACT TCACATTGCA CACGTTCA | 598 |
| 55 | (2) INFORMATION FOR SEQ ID NO: 1035: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 313 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1035: | |
| | AAACAGTGCT TCATTATCGG TATTGATATT GATCCACAAG CCGTTGACCT AGGGCGCACA | 60 |
| | ATCUTTAACG TCTTAGCACC AAATGAAGAT ATAACAATTA CGGATCAAAA GGTATCTGAA | 120 |
| 50 | CTTANAGATA TCANAGATGT GACGCATATC ATATTCAGCT CGACAATTCC TTTANGTACC | 180 |
| | AGCATTTAGA AGGAATTATA TGAnTTAACC AATGAAAATG TCCGTAGTGC CATGCGCCTT | 240 |

15.

| | AAGTGGGCCA TGT | 313 |
|----|--|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1036: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 235 base pairs | |
| ٠. | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| -0 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1036: | |
| 15 | AATAATGAGT AGGTTTTGAT TACTTACGAG ATAACATGGT GAATTATTCT GAAGATAGAC | 60 |
| | TAATGCGTCC ATTACATTTT GCAATCATTG ATGAGGTTGA CTCAATTTTA AATCNACGAG | 120 |
| | GNCGACGCCA TTAATTATTT CTGGTGAACT GAAAAGTCAA CGTCACTTTA TACACAAGCA | 180 |
| 20 | AATGTTTTG CGAAAATGTT AAAACAGGAC GAAGATTATA AATACGATGA AAAAC | 235 |
| | (2) INFORMATION FOR SEQ ID NO: 1037: | ý. |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 25 | (A) LENGTH: 263 base pairs (B) TYPE: nucleic acid | |
| _ | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1037: | |
| | NCAATATACC TCCTATCATC ACACAAAATG CGTTGTTTCG TATGATTTTC TCAACATCGT | 60 |
| 35 | AGACTAATGC AATCAGACAC AACACCATGC TCTATATCCA ATATTTGCTT TATTGCCTAT | 120 |
| 33 | CAATGAGCGT ACTGCGTGCT TTTAAATAAT CATCATCAAT TAATGACTGT ACAGGCACCT | 180 |
| | CATGAAAATT ATCATCCGCC AAGTATTGCG CACGATCACT ATATGCTAAA TGCATCGCTT | 240 |
| 40 | GTATCANATG ATGCAAGTAA TCA | 263 |
| | (2) INFORMATION FOR SEQ ID NO: 1038: | |
| | (i) SEQUENCE CHARACTERISTICS: | * |
| 45 | (A) LENGTH: 218 base pairs (B) TYPE: nucleic acid | • |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1038: | |
| | ATTGTACCTG GCACAATCTC ATTATGTATT GGATTATCAT CATTACGAGC GCCAAATATT | 60 |

| | ACCGITATGA CATGITGATC ATTITTAGTM AATGITAAAG CTATAACGTG TGATATTGCG | 180 |
|----|---|-----|
| | AGTCTGTCGG CATTCAATAT CTTCnAAATG CCCTACAT | 218 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1039: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 396 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1039: | |
| | GTTTAGACGC TAATGnTGGC ATATATTACT TGCCATGCAA ATGAGTCATA AGGCATAGTT | 60 |
| | TTCAAGAAGG GTTCTGACAA TGAAGTGAGC AACATGTCAT GATGAGAAGC AGGACTATAC | 120 |
| 20 | AATGAGAATA ACCTTTTGAT TTTTCATGCA TAAGGCGATT CAATCAAAAG CAATCACCTT | 180 |
| | CCAACTGAAT TGTCATTTTG TAAAATAAAA TAATCGATCC AATCGTTATC TAATTCATAA | 240 |
| | ATGTGTAAAC ACATACGTTA TGAATGGATA ACGATTTTTT GTTATGTTAA AGTGGTACAT | 300 |
| 25 | TAATCATGTA TTTCGTATGA TAATTAACGA CAAGTGTAAT GGTTAAATGT ATTTTATGGA | 360 |
| | TGGAAATGCn ATAATAGGCC TGGGTTACCA TGGnGC | 396 |
| | (2) INFORMATION FOR SEQ ID NO: 1040: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1040: | |
| 40 | AGCATTTTGT TTAAAAGCTG ATGAAGCAAT AATAAACTCT TCATATCCTC TGTCCATTAC | 60 |
| | AATTTGACCT TGATATACAA TTTCTTTAAA GTTTTCGATT TCTTTAAATT CTCTGCTATC | 120 |
| | ATTTAAAATA GGTGCATTCG TAATAACATT CGCTTCCTTC TTATATCCTT TAGATTGATA | 180 |
| 45 | ATATTCTTTT GCTGCATGAC TTACTGTTAC GAAGGCATTA ACACGATGTT TTACTATGTG | 240 |
| | TTTTTCTATA CTTTCTACAA ACTTTGAAAT AAGTGGAACT TTATTAATAA AGGCATTTTT | 300 |
| | CGCATATAT' TCATGCGCAT CATAAACAA' ATTAGCTTTT TLATAATTGC TTAAATAGAC | 360 |
| 50 | CATTAATAAT ACGTCGAAAT CATTTGCATG AATCACGTCA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1041: | |

| 5 | (A) LENGTH: 268 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-------|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1041: | |
| 10 | ACTTGCGTTT CTATTTAGCT CAGACAGGAA AAATATTCGC TGGAAATATG TAGGAATTTT | . 60 |
| | ACTTGCAATT CAGCTTATCT TTGCATTTAT CTTGCTTAAA ACTACAATGG GAATCAAGGT | , 120 |
| | TATTGGTGGT ATTTCAAACG GTTTTAACTA CTTATTATTA AAAGCAGCAG ATGGTGTTAA | 180 |
| 15 | CTTTGTATTC GGTGGTATTC AATATATCGT CCCTAAGCAC CCACCCATTC CTCCTCCGGG | 240 |
| | GAATAATAAC CAACNGAATT AATTCCGN | 268 |
| • | (2) INFORMATION FOR SEQ ID NO: 1042: | |
| 20 | (i-)—SEQUENCE CHARACTERISTICS: | |
| e) | (A) LENGTH: 277 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | (6) | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1042: | 60 |
| 30 | GTGAAGATAA GAAATTAAAG TTAAGACAAG GTTAAAAATA AGCAAAAAAT ATTGAAATTA | |
| | CAGATCATTG GAMTGGTATT CCAGAGGAAG ATCAAGATTC ATTITTGATC GCTTTTATCG | 120 |
| | ATGGATTAAA TCTCGTTCAA GAAGTCAAGC GGTAATGGAC TCGATTATCT ATTGCTCAAA | 180 |
| 35 | AAATCATCAA TTAAACGGNG ATCGATTAAA ATTAAAGTGA ATTAACAAGG AGCAACGTTA | 240 |
| | AATCTATTT AATCAGACTG AGACGTCATC AAGTCAT | 277 |
| | (2) INFORMATION FOR SEQ ID NO: 1043: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1043: | |
| 50 | TTATCATCAC AAGTGATTTT GAAAATAAAA AAATCGAAGA TGATGACAAT GATTCAGGTA | . 60 |
| 50 | GTGTGCCGAT ATTGCCGTTT ATTAAACGAG ACAAAGCATA TCAAATTATC CAGAATTTAG | 120 |
| | TACCAGATTT ATCTTATCAA CAAGTTAATG AAGGTATGCC TTTGTCAGGN TTCCACAGAC | 18 |
| | | |

| | AACCATTATT ATTGTTATTA CCGATATAAC CATAGTCATA TGGTTATTGT GATCCAAGGT | 300 |
|------|---|-----|
| | ACCTTATGTC AACAGCGGGT TAAAGCAGAG ACAATACATC AGATTCGGCA TGAACGAAAT | 360 |
| 5 | TATATTTAAn GCTnCTAAG | 379 |
| | (2) INFORMATION FOR SEQ ID NO: 1044: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1044: | |
| | ATATTGAACT TGAAGACCAT GCAGATATAA ATGAAATAAC ATATCGATTA TCAAAAATTT | 60 |
| 20 | TCGGTATTAA ATCTATTAGT CCAGTATTAA AAGTAGAAAA AACAATAGAG GCAATAAGTG | 120 |
| | CAGGGACAAT TAAATTTGCG CCATTNTGAA GAAAACAGCA CATTTAAAAT TGATGTGAAG | 180 |
| 25 | CGTGCCGATA AAAATTTCCC AATGGATACG TATGAATTAC AGCGTGAATT GGGTGGTGCA | 240 |
| | GTATTGAAGC ACTTCGACAA TATTTCAGTG aATGTCAAAC GTCCAGATCA TGGAAATTCG | 300 |
| 7 | AGTGGGMAGT TEAGGMTTAG ATGCCAATTT TATATGGTAT GNAAGAAGTT GGTTCCGGGG | 360 |
| 30 | TTCCAGGTGG GATTTACCNG TTGGGTACTG GTGGGTNAA | 399 |
| | (2) INFORMATION FOR SEQ ID NO: 1045: | |
| 35 - | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (wi) CEOUPICE DESCRIPTION, CEO TO NO. 1045 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1045: | |
| | ANGATAAACA GAGGAGCACA AAAATGAATN NAAATATAAT CATCAAAAGT ATTGCGGCAT | 60 |
| 45 | TGACGATTTT AACATCAATA ACTGGTGTCG GCACAACAGT GGTTGATGGT ATTCAACAAA | 120 |
| | CAGCCAAAGC AGAAAATAGT GTGAAATTAA TTACCAACAC GAATGTTGCA CCATACAGTG | 180 |
| | GTGTTACATG GATGGGCGCT GGAACAGGAT TTGTAGTTGG GAATCATACA ATCATTACCA | 240 |
| 50 | ATAAACATGT TACTTATCAC ATGAAAGTCG GTGATGAAAT CAAAGCACAT CCTAATGGTT | 300 |
| | TTTATAATAA CGGTGGTGGA CTTTATAAAG TTACTAAGAT TGTAGATTAT CCTGGTAAAG | 360 |
| 55 | AAGATATTGC GGTCGTACAA GTTGAAGAAA AATCAACGCA | 400 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 626 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-------|---|-----|
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1046: | |
| - Gen | ATAAACTTCT ACACCATCAT CTTTACCTAC AACATTTGTA GCTTTAACTT TTAGTCCAAA | 60 |
| | GTTATCTTTA AAGAATTGTT CACCTACTTT TTCAAATTCT TTACGATGCT TCTTCACAAA | 120 |
| 15 | TTCAATCGCA TCTTTTCTG CAGGTGGTTG AAAGCCTTGT CCTACATATT TTGAAGCTTC | 180 |
| | CATTTCTTCT GGTACTGATT TTGTTTCTGT ATTTGTTTCT GTATTTGTTT CTGTATTTGT | 240 |
| | GTCTTTTTT GATTCATTAT TCATCGCTGA ACATCCTGAT AACAGTAGCG TTGCTATTAA | 300 |
| 20 | GATTAATTTC GCCTTTTTAA ACATAGCTCA TCACCCATTT ATGTGKTTAT ATAGAATATT | 360 |
| | AAAAAGCATT TTAAAAAAAA TTTATTCATC TTTACGATAC ACTCCATATT CTATTGGATC | 420 |
| | ATTATCATCA TAAAAGGCTT TTTTAGTATT AATAGTAGGC TTTCCTATTT GAATTGTAAT | 480 |
| 25 | TGTAGATTTT TCTGGCTTAT TTTTAAAATT ATATAGTTTA TCACTCAGTT CAATTACATC | 540 |
| | ATCAACTGTA TTGTCTTTAG TAAAATTTTC CTTTGTACTA AACAATGTTG TTACTGTATC | 600 |
| 30 | TGTATTAGCA GCGNAATTCA CTTCTT | 626 |
| | (2) INFORMATION FOR SEQ ID NO: 1047: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 317 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1047: | |
| | GACGGCGTTC AAAATGCAAC GGTCAATTTA ACAACAGAGC AAGCTAAAGT TGACTATTAT | 60 |
| 45 | CCTGAAGAAA CAGATGCTGA TAAACTTGTC ACTCGCATTC AAAAATTAGG TATGACGCGT | 120 |
| 40 | CTATTAAAGA TAACAATAAA GTCAACGTCA CGCAACTGAA GCGTACAACA TAAATTGATA | 180 |
| | GRITATCATAT CAGCAGTATA TCTTACCACT ATAATGTAAT GTTGACACTT TCATATGCAT | 240 |
| 50 | ATACAGACTA TTACGATCAT GTCCATTATT TAGCHCACTG TCATTATATG GTGGCATTAT | 300 |
| ŕ | GAGGGTATAA ACTTAGn | 317 |
| | (2) INFORMATION FOR SEC ID NO: 1048: | |

| 5 | (A) LENGTH: 223 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|------------|---|-----|
| 3 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1048: | |
| 10 | ATACGNATTA TGCAAAAAAT AAAGTGAGAT TGGCATATGT GTAAATCTAA AATACTGTTG | 60 |
| | AAAAATATTT TTAGTGAAGT AATCAGAAGT TAAAGATTTA ACTGAAGTAA AAATATAATC | 120 |
| | AAGATTACGA GTCATTAACA TTTAGCTTTA AAGAGGGAAA CATATCAAAG TAGGTTAGCT | 180 |
| 15 | AAGNAAAACA CCGACTAAAT CGGGGATATT TCGTGACATG TTG | 223 |
| | (2) INFORMATION FOR SEQ ID NO: 1049: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 20 | (A) LENGTH: 608 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | * |
| 3 * | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1049: | |
| - | AAATATGAAT AATGCAATTG ACCAACGTTC GATAACGTTG CCATACCCAT ATTAAATTTT | 60 |
| 30 | GTATAACCTT GTTCTTTACT CCAAAGTAAC ATATGCAAGT ATAGACCATC CATTAATGGT | 120 |
| | AAATCTAACT CTGGCAACCA TCTAATTAAA TCGACTGAAA TGGCATCATT AAAGTATGTT | 180 |
| | GGCATTAAAC TACAAAATGC AATTACTTCA TTTTCTTCAT TTCGCATTAC ACCAATTGGC | 240 |
| 35 | GCTTTAGATA AGTATTCTTC ATTAAATnCA CCAACAGAGA AATGCATTTC CYGACGATTA | 300 |
| | TCTAGCCATA AATCACTTAC ATGTTGAAGE TCATTTALAA ATTCAGTTGr AAACGGEGGE | 360 |
| 40 | TCAATAATTT CGAACGAAAT ATTAAGTTCA TCGAATTMAT TTAAAGTCGC TCTAAATCCC | 420 |
| | ACGGCGTTTT TTACCTGAAG TTGAAAATTG CGTTAAATCA ATAATTGCTT CTTCACCTAA | 480 |
| • | TTTGAAAAAT TGGTTACCGG nATTATGATA TAAAGGCATG TGTTGATCTG TAACTTGATA | 540 |
| 1 5 | GAATATAACA TCATAGCCTA AATACTCAGC GTAATTATAG AATGCTTCTA ACAATTCATC | 600 |
| | AAAGGCAT | 608 |
| | (2) INFORMATION FOR SEQ ID NO: 1050: | • |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1050: | |
|----|---|-------|
| | TGTTTTTCTA CGCTAAACTA TATGATAAAT TGCCTATGTA TTTACTGGTG TTTATGGCCT | 60 |
| 5 | TTACAGCTGT AATTTTGATT ATGATGTACA TACAAGAGAA AAATGAAAAT TACAAAGTTG | 120 |
| | AAAAAAGATA TGTGGTTAGA TATCTCACAC TTAACGTTAT TGTGGGATAT ACTTTGCCAT | 180 |
| | TGCTTTTGT ATCTATTTAC GTTTTTGGTG TAGTCGGTTT TGGATTTGAT GTTTTCAATT | 240 |
| | ATTGTCTAGG TAKTATCTTG ATGTYATWTA TTTCTTGGTT TAGGTnTATT nT | 292 |
| | (2) INFORMATION FOR SEQ ID NO: 1051: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 734 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | · · · |
| | (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1051: | |
| | TAAATCHTCA AAGATTTCTT CTAAAACATT ATAATCTTCA ACGATACTCG AATAATAATA | 60 |
| 25 | CAGCTCATCA TTTCTGGGCT TGGTATAATA AAATATAACT TGCCCACCTC CATCGTCCAC | 120 |
| | ATATGCAATT ACATATACCT TTTCCCACTC TACTGGTATC ATTTCATTGA TCTCATTTGC | 180 |
| | AATTTTATTG TACATTTCAC TTAATTTTTC TTCGAAATTC ATGTTATCGC CTCTATTGTT | 240 |
| 30 | CAGCTTCTTC TTGCTCTTTA ACATATTGCT CGATTTCTTT AACTTTATTA ATTTCATATT | 300 |
| | CCGTTTCTGG TAAAATTCCA AATTTTCTAT ACTTATAGTA ATTTTGTCGA CCTACTTGAC | 360 |
| 35 | CARATTCTGA ATTTATCCAA TCAATATAAT CAAATGAAAC TTTTAATTCA CCTTCTCTTG | 420 |
| | TAAAGTCAAA TTCGCATGAT GTCCATGGTT CATGTCCTTC TTCTTTAAAT AAATTCCTTA | 480 |
| | AATTITGAAA TIGITTATAC AACTCATACA CIGAATCCAT AAATTCCGAT TCCGATATAT | 540 |
| 40 | CATATTATT TAATACACTA GTATAGTAGT ATAATTCATT ACTTCCAGGT TCTGTGTAAT | 600 |
| | AGTAGAACAC TICTCCTCCT CCGTCATCTA TATATGCCAT TGCATATACC TTTTCCCACT | 660 |
| | CTACCGGTAT CATGCTGCTA ATCTTATTCG CAATCTCGCT ATACATTTCA CTTAATTTTT | 720 |
| 45 | CTTCGAAAGT CATG | 734 |
| | (2) INFORMATION FOR SEQ ID NO: 1052: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 775 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1052: | |
|------------|---|------|
| | ATTTTTAACC AAAATTGCTT TTTTATCTGA AAAGAAAGGC AATGTTAATG TTTCTTCAAC | 60 |
| 5 | AATTGGTGCA ATCTCTGTTT CGTATAAATT ATATTTCACA AAGTTAAAGT CATCTCTATC | 120 |
| | ACTITICAAA AATTGTGATA TGATTTCTGC ACTITGTTTT TCAACCAATT CAGGCACATC | 180 |
| | TCCATAAATA GCTACAATAT TGTCGCTCAT TCATTACACC CTTTCATTCG TTTGACACAT | 240 |
| 10 | CAATAGATTA TATCATGTTT CTGTATCTAT AAACCACTTG CATTTCCATA AGAGCTTGAA | 300 |
| | TCAACTTTTA AATTATCATC TAAGTCAATT GTAACTTGAC CGTTTLGTTG ACTATTGTAA | 3,60 |
| 15 | ATGCGLACTG CGAATCCTTT GCAATCGTTL AACAACTTCT ATATTAGGAA GWTGATACAT | 420 |
| | ATTGTTCTTC CCAGAAGAAA TCAAACTTAT TTTAGGCTTA ATCATCTCTA TAAATTCTTT | 480 |
| | AGAACTACTT GTCTTGCTCC CATGATGTCC TACTTTTAAA ATATCAATCT CCGGCAAGTT | 540 |
| 20 | ATATTTTTT AGTAGTAAAG ATTCATTATT TTTACTAGCA TCGCCCATTA ATAAAACTTT | 600 |
| | TTTATTTTGA TATGTAATCA TAGTAATAAT CGAATACTCA TTTTTATCTC GGCTATTTGG | 660 |
| | AATAAAACTA TCAAAAAAAT AGAAAACTAC TATCTCCAAG TTTAAAACTA CTAACTTGTC | 720 |
| 25 | TTACATCCAT AAGTTTAATG GTTGTACTTA TGGGCTTAAT TTCCGATAAT AACCA | 775 |
| •• | (2) INFORMATION FOR SEQ ID NO: 1053: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 234 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · . |
| 35 | | |
| .• | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1053: | |
| | GAGACCAATC ATCATAATGA ACGACAATCA TGTATTTAAT ATTTAATAAA ATACTGAATA | 60 |
| 40 | ATGCTATAAC TGCCATTAAT TGAAGACCAA TCGCATCTAA TGCGACAACA CGATCGGCAA | 120 |
| | GTGATGGGCC TAGCACAACG CGAATGAGCA TAGCTAACAT AGGANGTGAC AÁCTATGATT | 180 |
| | AATGCAATAA CGATGAATAA CCTTGATGAn TCATTATAAT TCGCCCACCT CTCT | 234 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1054: | |
| 5 <i>0</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | CTACTGGTAT CATCCACTGA TTTCATTTGC AATTTCATTG TACATTTGAC TTAGCTTTTC | . 60 |
|-----|---|------|
| | TTCGAAAGTC ATGTTATCGC CCCTATAGTT CAGCTTCATC TTGCTCTTTA ATATATTGCT | 120 |
| 5 | CGATTTCTTT AACTTCTTCC ATTTCGTATT CCATTTCTGG TAAAACACCA AACTTTTTAT | 180 |
| | ACATATAATA GTTTTCACGG CCTAATTGAT CAAACTCTGT ATTTATCCAA TCAATATAAT | 240 |
| | CAAATGAAAC TTTTAATTTA CCTTCGCTTG TAAAGTCAAA TTCACTTGAT GTCCATGGTT | 300 |
| 10 | CAAGCCCTTC TTCTTTAGAA AGTTTCTCTT AACTTCTTAA ACAATCTATA TAAATCCGTC | 360 |
| · S | CACAAATCAT AAAATACTTT TTCAGAGACA TTATACTCTC | 400 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1055: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1055: | |
| 25 | GRGGCATATA TAGCGTTGGC GGTATAACAA AGAAAAATGT GAGATCAGTG TTTGGATTTG | 60 |
| • | TAAGTAATCC AAGTCTACAA GTTAAAAAAG TTGATGCTAA AAATGGCTTT TCGATAAACG | 120 |
| | AGTTGTTTTT TATTCAAAAG GAAGAAGTAT CATTGAAGGA ACTGNACTTT AAAATAAGAA | 180 |
| 30 | AACTCTTAAT CGAAAAATAT AGATTGTATA AAGGAACGTC TGATAAAGGT AGAATTGTTA | 240 |
| | TCAATATGAA AGACGAAAAG AAGCATGAAA TTGATTTAAG TGAAAAATTA AGTTTTGAAC | 300 |
| 35 | GTATGTTTGa TGTAATGGaT AGTAAGCAAA TTA | 333 |
| | (2) INFORMATION FOR SEQ ID NO: 1056: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 347 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1056: | 60 |
| | TGGGCAGTTA CATTTATGAT TATCAGCACA TGTTTAGCTT ATAAATTTT ACGAAAGTTT | 120 |
| 50 | AGCCGTTTAT AAAGCACATG CATAATGAAA CGAGTATTTG CCACTTGATT AGTACTICAT TATTATGTCG AAAATAAAAA TAAGTGGTAT TTTTAATATA TTAAGAAGCA CTCATAATCG | 180 |
| | GCTGTTAATT AATAATATT TTCATAAGTA TTGATTCATC ATTTTCTTTA TGTTAAATAT | |
| | GCTGTTAATT AATAATATT TTCATAAGTA TIGATICATO | |

•

| | TAATACAGAT ATCAATATGG CNAAAGTGTT NNATGAATCA GAGGTAA | 347 |
|-----------|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1057: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 312 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | : |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1057: | |
| | TCCAAAACGG AGAGCCAAGA GTTAACTCTA CTTATATAGG ATACGCGCCA ATTGATGATC | 60 |
| 15 | CAAAATTAGC GTTTTCAATT GTATATACAA ATCAGCCTGT ACCACCACCA TGGTTAACAG | 120 |
| | GTGGAGACTT AGGTAGAGAT GTAATTAACT ACTACTTTAA GCAGTTAGGT AAAGATGATA | 180 |
| 20 | AAAATAAAGA CAAAGACAAA TAAAATTTAA CCTGACGATT GTGTAGCGCA TGGTTGTAAA | 240 |
| | ATTTTAACTT TGCMAATATT ATAGATGTTG GTATAATAAT AAAGTCGTAT TLAGAAATGA | 300 |
| | TWAGGAGGGA AT | 312 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1058: | |
| <i>30</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 404 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| - | | . • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1058: | |
| 35 | GCCATTTTGC GATGCTAAAT CCATTGAAAA TGCAATACCT GAAAGTCCAC CAAACAAAGA | 60 |
| | ATTGTTATAT TGACCACTCT GTAAATATGG TGCTAATTTC ATGATGTACT TATGCACAAT | 120 |
| 40 | TTGCTCAGTA TTAATATCGA AAACTTTTEG ALAAGCATCT AAAAACAAAA TGATACCTGG | 180 |
| | TATACCATGT GATAAAGTTG AAGGTTCAAA ATAATCGGTT TCAGTAGATG CTTTTGAAAT | 240 |
| | GAAATCATCT ACTTCTGAAA TCTCTTGAAA CTTCTTCTTC AATATTAGAT TCATATCAAT | 300 |
| 45 | CATTTTEGTC ACCACCAA TGCTTTTGAG TTTTAACAAT TTCTTTTACA ATAGATAAAA | 360 |
| | CAAATGTTTC TTGATCCTTA TCAATGCCAA ATATTCGATT GnAG | 404 |
| | (2) INFORMATION FOR SEQ ID NO: 1059: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| • | (xi) SEQUENCE DESCRIPTION: SEQ 1D NO: 1059: | |
|----|---|-------|
| 5 | ATGTACATAG GNATGACATA AGTGTGCCTT CTTTTTCAAG ACCCTCCATA GAAATAATAC | 60 |
| • | ATGGATGTGC ACCACGNTAC TACCTCTTTA ACGTTACCAG AATTGATAAA TTAACTTTCT | 120 |
| | CTTGTGTTGC TAAACCTACA ACTGGTGTAC CTTCTTCGAT TAAGGCAATT GTACCATGTT | 180 |
| 10 | TAAGTTCTCC ACCAGCAAAA CCTCGCTGAA TGTAGAAATT CTTAAGTTTA AGT | 233 |
| | (2) INFORMATION FOR SEQ ID NO: 1060: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 295 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | • |
| | (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi)-SEQUENCE-DESCRIPTION:_SEQ_ID_NO:_1060: | |
| | GCACCACTAC TGTTAATAAC ACACCTAAAA AAGTCGAAAT ATAAGGGTTA ATCGCTGTTT | 60 |
| 25 | TAAATGTATA TCCTAGTGCG ATTGCCATTA ATTATCCGAT AGCTTTTTCT GCTGCTTCCA | 120 |
| 25 | TAGTCATCTC ACCTAATGTT GGATGTGCAT GGATTGTTAA TGCGATATCT TCAGCATTCA | 180 |
| | TACCAGCTTC AATTGCTAAA CCTAATTCAG AGATAATATC TGATGCACCA GTACCAACTA | 240 |
| 30 | CTTGAGCACC GATTAAAGTA TCATCTTCTT TAGTGTAATA AGTTTAACAA ATCCG | 295 |
| | (2) INFORMATION FOR SEQ ID NO: 1061: | •• |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 413 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1061: | · (¥) |
| | CAATGCCTCT CGTGTTGCAG CTTCTTCCGG TGAAAAACCA ATATTTTCAA GTGCAATAAT | 60 |
| | TTGATCTAAG TCCTGCATGA TTACTTTTCT TAATACCATA AAAACACTTC CTTAGCCCTA | 120 |
| 45 | TATATCAAAA GTAATACCTT CATCTTTATA TTCATTATTT TCAAACTACC TTCACTATAA | 180 |
| | AAAACGAGTC TTTTTATTGA AAGCCATTCG CCTTAATCAA TTAGACAAGT TGTATKATAC | 240 |
| 50 | GAATTAGTAA ATAATCATGA TTATAATTCA TTTTAAGCAT ACTCAAAAAG ACTGGTACAT | 300 |
| | GTATACCAGT CTAATTCGAA AAAATATATT TAGTTAAAAC CATTTCAAAA ACGACTTCAC | 360 |

(2) INFORMATION FOR SEQ ID NO: 1062:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | , |
|----|---|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1062: | |
| | AAGCTGCATA CTCTCCAAAC TTAGAACCAC CGAAGCGATT CACAAAATAT TTATTAGCTA | 60 |
| 15 | AAAAGTCGGC ACATAAAATT AATATTGTTA GCAATGCCAT AGATACATAA AACACCCATG | 120 |
| | ATAAATGCTG ATTATGAAAG CCAAATTGAT AGATTAAAAA GCCAACCCAT AATACTAAAA | 180 |
| | CAGAAGGAAT AATCGGCTTA ATCAACCCAA CAAATGCTAA CATGAAGGCA GCGATGATAA | 240 |
| 20 | GTAGCCATAA AATAATTGTC ATGTTGATAT CACATCCTCT TTTGTATTTT TTGATTTTTA | 300 |
| | GTAAAGAATA TAAGTATCAT ACCTAACATG GTTGATGCTG CTGGATACCA AAANATACAT | 360 |
| | TTTCCCAAAC CTTACCCAGT GGACTCCTAG GCACCACCTT | 400 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1063: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1063: | |
| 35 | TGGATCAGAA GGAATCTGGA TGCCTATTGA TGACAAAGGA TACTTTAATT TTGACTTCAA | 60 |
| | AACGAAACGT TTCGATGATT TAGAGTTAAA GAAAAATGAT GAGATCTCAT TAACATTTGC | 120 |
| 40 | ACCTGATGAC GAAGATGAGG CATTGAAGTC ATTAATTTTC AAAACTAAGG TAACGAGTTT | 180 |
| | AGAAGATATT GATAAAGCAG AAACTAAATA TGACCATACT AAAGTGGAAA AAGTAAAAGT | 240 |
| | ATTGAAAGAT GTTAAAGAAG ATTTACATGT AGATGAAATT TACGGAAGCT TATATCATAC | 300 |
| 45 | AGAAAAAGGT AAAGGTATTC TTGATAAAGA AGGTACTAAA GTAATTAAAG GTAAGACTAA | 360 |
| | ATTCGCAAAT GCAGTTGTGA AGGTAGACTC TGAACTAGGT | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1064: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 434 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1064: | |
|----|---|--------|
| 5 | GTGGTCGTGA AGCAACTGAT TTCAAAGAAG AAGATATCGA GCTTTTCAAA GACATTGCCG | 60 |
| | ACAAAGTAAA ACAAACAAAT AGTTATGATC TAGCGTTTGA TGAATTAGAA AAAGAAAAAG | 120 |
| | ACTTCCTGCA AGTCATTGTC AAAAACGATG ACAAAAACTT ACCTACTAAT CAAAATGTCG | 180 |
| 10 | CTCAACTAGT AGAAGATTTA CGCCTAGAAA TCCAGAAAAT GCGCGAAGAA CGTCACCTAC | 240 |
| | TTGGTCAAAT GATGAATCAA GTACATCAGC AACAACAAGA ATTAAAAGAA CTTCAAAATC | 300 |
| | AACTTACATC TAAAATCGAT TCAAATAGCG AATCCTTAAA AGCCATCCAA ACATCACAAG | 360 |
| 15 | AGGCTATCCA AGAAGCGCAA GCCTCTCAAG CAAAAGCATT AGCTGAATCC ACCAATAAAG | 420 |
| | TTGGAAAGAA TGCT | 434 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1065: | ·. : . |
| 20 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 239 base pairs (B) TYPE: nucleic acid | |
| 25 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1065: | • |
| 30 | TAAAACATAT GGCTTGATAT TGCAGAAGAA TTGAAGTTAT CGTACCAGAA ACGGTACATA | 60 |
| | ATCATGATTA TATGGAAACG AAAAAAATAA AAATGGGTCA TTTAATATAG GAGGATTTAA | 120 |
| | CATTGAATTT TGAAGGTAAN TAATTGGAAA AGATTTGAAG TTGCATCGTT ATTATCGTTT | 180 |
| 35 | AATGATTTTA TCACTGGAAG ATTACTTGAA GGTGCAAAAG ATACNTTGAT TCGACATGA | 239 |
| | (2) INFORMATION FOR SEQ ID NO: 1066: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 202 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1066: | |
| | AAATATCTAT AGACCTTTAT TCGGAAATGG TTCGTCTCCA GAATGGAAGG ATGAAGTACC | 60 |
| 50 | GAGTATTGAA AGGTAGAAGG TCTCCAAACT TTACCTGNAC GTGCACGANA TCTAACTGAA | 120 |
| | GATGATTAG CAATTGAATT GAAACAGCCA ATTGTCGGTT GTAATAACTT AGGAGAGTTA | 180 |

(2) INFORMATION FOR SEQ ID NO: 1067:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 749 base pairs (B) TYPE: nucleic acid | |
|-----|---|-----|
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1067: | |
| | CTACAATTCG ATCAACGCCG AAGTTAGATA CACCGATTGC TTTAATTTTA CCATTTTCTT | 60 |
| 15 | TTAACTCTTC TAATGCACGC CATGAGCCAT ATACGTCATT GTAAGGTTGG TGAATAAGCA | 120 |
| | CTAGATCAAG ATAGTCCAAA TTTAATCGTT GTAATGATCG TTCGATTGAT TTGATAGTAT | 180 |
| | CTTCATAGTT AACATTTCA ATCCATACTT TAGTCGTAAT GAATAGTTCA CTTCTATCAA | 240 |
| 20 | TACCTGAAGC TTCAATACCT TGACCTACTT CAGTTTCATT TAAATAACTT TGTGCTGTAT | 300 |
| | CAATATGTCT ATAACCCGCT TTAATTGCTT CTTTAACCGC TTCTGCnGTT TGTTCTTGAG | 360 |
| | GAATTTGAAA TACTCCGAAA CCTAATACTG GTATCTTTAC ATCTTTACTT ATTTCAATAT | 420 |
| 25 | GATTCATAAA ATGAACCTCC TTTATCTtGT ATGTCCACTA TAAACCATGG AGCGAACTCT | 480 |
| | ATAGCAAGCC ATAGGTTTAC TTTCTCTCCC AAAGACGTTC AACATTGTCA TCATAATTAT | 540 |
| . · | CACTAGCATT GATTTTAGCA ATATGATTAT CATAATTATC AATTTTATAT TGTAGTAAAT | 600 |
| 30 | CTCTCGCATC ATGAATTGTC TTTAAGTTTT CATTTAATTC TTCGAGTTGC TTATTTAAAA | 660 |
| | TTTGCTTTTG CTGTGCTTGA ATATTTTCAT TTTTAGGCAA nTGCGCTAAC CTGCAAAATT | 720 |
| ' | CGATAAGCGA TTCAATACTG ACGCCTGCA | 749 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1068: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 436 base pairs (B) TYPE: nucleic acid | |
| 40 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (5) | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068: | |
| • | TCCTCGAGAT AGACAAGAAT GGTGGTACAA TGTTTTTTAT GACGATGGCA AATATMATAA | 60 |
| | GAANATAA11 AAGAATGACA TGTCAAAAAT TAGGCGTAAT TTTTAGATTT ATCTATATAT | 120 |
| 50 | TTATGCCACC GCTCAAACTT TTATnAAAAG TAAAAAGACA ATATTTATAT TGAACTTGTG | 180 |
| | ACGTGAATTT CTAAAACACA ACCAACAATC CACAAGGAAA CTAGTAAATA AGTTTAAATA | 240 |

| | TACTGACTAA AAAGATTTTG AAAGIGATTA AGTATTTAAA ACAGGCCAAT | |
|------|---|-------|
| | TATTGACAAA TATGAAGCGG AACCACCGTT GTnTTTCTTT TnCAGGTCCA ATTGAATAAA | 420 |
| 5 | TGTTGATGAA TAGAAT | 436 |
| | (2) INFORMATION FOR SEQ ID NO: 1069: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 4 2 2 |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1069: | |
| | TTCTCAAGTA ACAGGTATTA TTGTTACTGG TACAATCAAT AGAGAAAAAT ATGGCATTAA | 60 |
| 20 | CTTTAACCAA GCACTTGAAA CTGGTGGCGT AATGCTAGGC AAAGATGTTA AATTCGAAGC | 120 |
| * | ATCAGCTGAA TTCTCAATCT CAGAATAATC TCATTACACA ATCCTCATTG TTTTAATATA | 180 |
| | TATACGAAAT GCCAACTATA TCATCCCTAG GTATAGTTGG CATTTTTCGT TTAACTCATG | 240 |
| 25 | TGTAACAAGC ACTAACTGTT CACCCTAATT TTAGACGCCT TTCATTCAGG TAGGTCTTAT | 300 |
| | TGAAACTGAA AACTTTGATG ACCTTTTGCA AAGCCATTAA CTGTATAAAG CATAGATCCT | 360 |
| | CCGCCCATTT CTATATCATT GGAACAAATG ATGAGTTGAT TTGTTCCAGG TATAAATTGC | 420 |
| 30 | GGATGAGTAG AACGTAACAT ATGCCCTTCA TCTCGGCCTG GTATCAATAT TTGTCCTATT | 480 |
| | GGATAACCCC TTTTATTAAA AACTAACACT CGACCTTGGA CCATACATTG CTACGGATAA | 540 |
| | ATTATCGGCA C | 551 |
| · 35 | (2) INFORMATION FOR SEQ ID NO: 1070: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1070: | |
| | TATNATGGTA ACGCATGANC CTGTTGCAGC ACGCTATGCA AATCGAGTAG TGATGCTANA | 60 |
| | AGATGGTCAA ATTTTCACTG AATTATACCA AGGGGATGAC GATAAACATA CCTTTTTCAA | 120 |
| 50 | AGAAATAATA CGTGTACAAA GTGTTTTAGG TGGCGTTAAT TATGACCTTT AACGAGATAA | 180 |
| | TATTTAAAAA TTTCCGTCAA AATTTATCAC ATTATGCCAT CTATCTTTTT TCGTTAATTA | 240 |

| | CAGAGTCATA TCCAATTATA CnGGC | 325 |
|----------|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1071: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 771 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1071: | |
| 15 | TAAATGCCGC AATTGGATAG CTTTAATATA ATTAATAGTC AAGGTATTnC CAACAAnAAT | 60 |
| | ATATTATCCA CCCGAAGGAA GCGGGGTATn TTTGTTACTG ACGTCCCACA AGAAGCACAn | 120 |
| | ATATTAGATA GTGCTTACTC TGAAATTAAA AAATTAAGAG ATTATGATGA AAAACTAATT | 180 |
| 20 | ATCCCAGGAT TTTTTGGCGT ATCTCATGAA GGATATATAG TTACATTTCC ACGTGGCGGA | 240 |
| | TCAGATATAA CTGGCGCCAT CATATCAAGT GGTGTTAGAG CCACAATTTA TGAAAATTTC | 300 |
| - V | ACCGATGTGT CTGGTATTTA TAAAGCTAAT CCAAATATCA TCAAAGATCC TGAATTAATC | 360 |
| 25 | GAAGAAATCA CTTATCGAGA AATGCGTGAA TTATCTTATG CTGGTTTTAG TGTTTTCCAT | 420 |
| | GATGAAGCCT TACAACCACT TTATAAAGAT CGCATCCCTG TGGTGATTAA AAATACGAAC | 480 |
| • | CGCCCTCAAG ATAAGGGTAC ATTTATAGTG CATGATAGAG AAATAAATGC GAAAAATGTG | 540 |
| 30 | ATTAGCGGTA TAAGTTGTGA TAAAGATTTT ACCGTTATTA ATATCAAAAA GTATTTAATG | 600 |
| . | AATAGACAAG TCGGCTTTAC TAGAAAGATA TTAGGTGTCT TAGAGGATAA TAATATTTCA | 660 |
| 35 | TTTGATCATA TGCCTTCAGG TATTGATACT ATCAGTATCG TTATGCGTTC AAAACAAATT | 720 |
| | CAAAATAAAG AAACAAAAGT ATTAAATGAA ATTCGTCAAA AATGTGATGT T | 771 |
| | (2) INFORMATION FOR SEQ ID NO: 1072: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 237 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1072: | |
| 50 | CGGTGGATCC GTTTGATCTT GAGTGAGGTG CCAATGAAAG TTATGAGCCA CGTTGTCGCG | 60 |
| 50 | CGCACCATAT CGTAGCACCT AGTGATAATA ATAAGGAGGA ATTATAAGTG TTTGATCAAT | 120 |
| | TAGATATTGT AGAAGAAAGA TACGAACAGT TAAATGAACT GTTAATGACC CAGATGTTGn | 180 |

(2) INFORMATION FOR SEQ ID NO: 1073:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 733 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ě |
|----|---|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1073: | |
| | CTTCTTGTGA GGGCGTTACA TCACCGGATG GATGATTATG AACTGCGATG ATTGCATTGG | 60 |
| | CATTITCTCT CACCGCAATA CTAAAAATTT CACGTGGATG TACAATCGAA CTATTTAATG | 120 |
| 15 | TACCTTTAAA AACACAGGTT TCTTTAATCA CTACATTTTT TGAATTTAAC AATAAAATGA | 180 |
| | CAAAATGTTC TTGTGTTAAA TCTTTCATTG TTGGAATCAT ATAATCAGCA ACATCACTTG | 240 |
| 20 | GTTGCGTTAT TTKTATACGA TTATTTTCAG CTCTTCTCCC CATCCTTTCC CCTAACTCAA | 300 |
| | ATGCTGCTTT TAAAGTAATT GCTTTTTGTA ATCCAATCCC TTTAACTTTT ATCAAATCGT | 360 |
| | TAATTGAAGA TITTTTCAAT TCATTCAGAT TCGAAGCAGA TTTAAGCAGT TCATTACTAA | 420 |
| 25 | TGTCTATGCT CGAGAATCCT TTTCTTCCGG TGTTAATTAA TATAGCTAAT AATTCTGTAT | 480 |
| | TCGAAAGACT TTTTGCACCA TGGCTTAACA AACGTTCTCT TGGCATTTCT GAAGTTACCA | 540 |
| | TTTCTTTAAT TTTCAAAAAT ATACGCCTCC TAAAAATTGA TGGATATCAT TATAAAAAAG | 600 |
| 30 | TGAATTGATA AAAAAGGAYA TAAATATAAA TGGAACAAGG GGTAATAGTT TAATCGGCTT | 660 |
| | AAATATCATG GTAATTAAAG CAACTAAACC AGCAATGACA AATGTAAATA ANATGACATA | 720 |
| | AATAGTGAAT TGG | 733 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1074: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 768 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1074: | |
| | ATGGTTATTT TTTATGCTCT AAATCGTATG TGTTTATAAG GTTCAATTTC TTGCCATTAT | 60 |
| | TAATTTTGCC GAGCAGTAAT GGGTTGTTAA AGTATCCATC AATTATGCTT AGCAATATTG | 120 |
| 50 | AAAAATTTAA ATGAAAAAGC GGTTCAATTC TTGAAAAATA GTGTATATTT ACATTTTGGT | 180 |
| | AATAACTAAC TATAATTTAC ATAAGGAGGT TGTCATTTGG TAGTATTGTT ATCTTATAGT | 240 |

| | TATTTACATA GAAGATCGAA ATGTGATTAT TGTAATTCGT CACTCAAAWG GTATGAATTA | 360 |
|----------------|---|-----|
| | ATGCCGATTA TTAGTTTTTT ATTATTAAAA GGGCGATGTC GAAACTGTCG AAAGCGTATT | 420 |
| 5 | TCCCTAACAC ATTTCTTAGG GGAAACCTTT GCTTTAATAC CTATCGTCTT TATTAAGTAT | 480 |
| | GATTTCACAT ACGTAAATGE ACGCTATTTA TAACTACATA TGTTETTCTG CTTATTTTTA | 540 |
| | CTATGACCGA TATCACTTCT TTAATGTTAG ATTGTCGCTT AATTATAATT TATTGTATCG | 600 |
| 10 | TTTCTCTCTC GTTAAGTATG ATTTATCCAG TAGCTTTTAT CATTATTAGT ATGACCACGC | 660 |
| , | ATATATTCTA CTTTTTATTT CGGGCATATA TTGGTTATGG TGACGTTTTA CTAATATCTG | 720 |
| 15 | CACTTTCTTT GTTTTTCCCC TCTCCAATTC ACTATTTATG TCATTTTA | 768 |
| | (2) INFORMATION FOR SEQ ID NO: 1075: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1075: | |
| | TCATATTCAT TTAAAATACC ATTCATCTCA GCTTTTCTCA TTTTCTCTTT ATAAAGTTGT | 60 |
| 30 | ATTTCGTGTC TTAATTCTGG CTCAGACATC TCACTCAATT TCTTCTGTTC CATCGGCAAT | 120 |
| | ACCACTTTCT TCTAATTTAG CTTTAATTTT ATCATATTTA TATCCTTTTC TCATAAGGCC | 180 |
| | .TTCGATAGTT TTTGAAATTA ATTTCTGTTG CGTGTACTTC TTTCGATTTT TATTATAAAT | 240 |
| 35 | TTTTTCTAAA TCTCGTTGTA ATAAATCGTC TAAAACCGCT TCATCTTGTG TAAAATCCAT | 300 |
| | TTCATTCAAT ACAGCATGAA TGGTTTCCAT TTCAAACCCT TTTTGAATTA AAGATTGCAT | 360 |
| | TACTTTTGCn TnAACTnTAT TTTGTGGCCC nTTTTTTGTT | 400 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1076: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 753 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| - 0 | (xi) SEQUENCE DESCRIPTION: SEQ 10 NO: 1076: | |
| | TTAGGTCAAA ATATGTTTTA TCCAAAAGGC ATTTTATCTC AATCTGCTGA AGCAAAGAGT | 60 |
| | ACAACATATA ATGCAACTAT AGGTATGGCG ACAAACAAAG ACGGAAAAAT GTTTGCATCA | 120 |

| | CAAGGCATCG AAGAATTACG TGATTTATGG CAACAAAAA TGTTGCGTGA CAATCCAGAG | 240 |
|-----|---|------|
| | CTATCAATCG ACAACATGTC ACTACCAATT GTTACGAATG CATTAACACA TGGTTTATCT | 300 |
| 5 · | TTAGTTGGCG ATTTATTTGT AAATCAAGGT GACACTATCT TGTTACCAGA GCATAATTGG | 360 |
| | GGTAATTACA AACTTGTTTT CAATACGAGA AATGGTGCAA ACCTTCAAAC ATATCCTATC | 420 |
| | TTTGATAAAG ACGGGCATTA TACTACTGAT TCACTTGTAG AAGCTTTACA ATCATACAAT | 480 |
| 10 | AAAGATAAAG TCATTATGAT TTTAAATTAT CCTAATAATC CGACAGGTTA CACACCTACG | 540 |
| | CATAAAGAAG TGACTACCAT CGTCGATGCA ATTAAAGCAT TAGCTGATAA AGGTACAAAA | 600 |
| | GTTATAGCTG TTGTGGATGA CGCATACTAT GGTTTATTCT ATGAAGATGT GTATACTCAA | 660 |
| 15 | TCATTATTTA CTGCATTATC TAATTTAAAT TCAAATGCAA TATTACCTGT TCGTTTAGAT | 720 |
| | GGTGCAACAA AAGAATTTTT CGCATGGGGA TTC | 753 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1077: | |
| | (2) 211 010 2 | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 405 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | ** |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1077: | * |
| 30 | AGAAGCGATT TGACAATAAA ACAATTGAAA AACTTTTGGA AAGCAAGTGG TGGGAGAAAA | . 60 |
| | CGCCTGACAA ACTAAAAGGA TTTTCGGTTG AATATTTAAA TAAAAAGGAT ACTTAATGAT | 120 |
| 35 | ATGAGAATIT TAAATATTGT ATCGAGTAAT ATTGTTCAAG ACCCAAGGGT ACTTAAACAA | 180 |
| 35 | ATAGAAACAA TTAAAGGCGT TACGGATGAT TATAAAATTG TTGGAATGAA TAATTCACAA | 240 |
| | CTACTAATA AGCGATTGGA AAATTTAGAT TGTAATTATC GTTTGTTAGG TAGCAAGGTA | 30 |
| 40 | GATCCAAAAA ATATTCTTTC TAAATTAATT AAGCGTATAA GATTTGCAAC AGGTGLTATC | 36 |
| | CGAGAAATTA AAGCTTATAA ACCTGACGTG ALTCATGCAA ATGAT | 40 |
| . : | (2) INFORMATION FOR SEQ ID NO: 1078: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 504 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | * |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1078:

50

| | CATATTCACA CCTCAATATT CCATAACTTT TACTTTAATA TCAATCCACT TAAATCCATT | 120 |
|----|---|------|
| | CACATCATTG AGTATAAAAT AATATGGTGA TATACGTTGA AGTTGATTAT CTTATATATA | 180 |
| 5 | AGTATACTTC ACAGAATTTA TAAAATTGTT TAGTCATCAT CTTCAGTGTT TAATTCAAAA | 240 |
| | ATATAGAATC TACTGTATTG CATMATAAAT TGAAATGCCA CAAATTGTGC TCCAGCGATA | 300 |
| | ACCAACATGC TCACAATAAT TATAAACTTA GATTCTACGA CATTAGGMAC CALATATATT | 360 |
| 10 | CGATAATTTT TTCAATATAT ATAAATGAGC TCAACGCAGT TAATAATAAA CCGAAATGTG | 420 |
| | TTTTAGTTTT ACCACCCCAA CGTTTTGTTA CTTTAGGTAA TTTTAATAAC GTGAACATTC | 480 |
| 15 | CGCCAATTAC TAATAACAAA TAAC | 504 |
| | (2) INFORMATION FOR SEQ ID NO: 1079: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 645 base pairs (B) TYPE: nucleic acid | |
| 20 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1079: | |
| | CATTCTTAAT CAACTTCTTC ATAATGGGAA TTTGGCATGG TANCGAAGTG TATTACATTG | 60 |
| 30 | TTTATGGTTT ATACCATGCA GCATTGTTTA TAGGTTATGG CTATTATGAA CGTTGGCGTA | 120 |
| | AGAMACATCC GCCACGTTGG CAAAATGGTT TCACAACAGC ACTTAGCATT GTGATTACAT | 180 |
| | TCCACTTTGT AACATTTGGC TTTTTAATCT TCTCAGGTAA ACTTATATAA TAAAGGAGAA | 240 |
| 35 | TTTAATTATG GAATTTAGAG AACAAGTATT AAATTTATTA GCAGAAGTAG CAGAAAATGA | 300· |
| | TATTGTAAAA GAAAATCCAG ACGTAGAAAT TTTTGAAGAA GGTATTATTG ATTCTTTCCa | 3.60 |
| | AACAGTTGGA TTATTATTAG AGATTCAAAA TAAACTTGAT ATCGAAGTAT CTATTATGGA | 420 |
| 40 | CTTTGATAGA GATGAGTGGG CAACACCAAA TAAAATCGTT GAAGCATTAG AAGAGTTACG | 480 |
| | ATGAAATTAA AACCTTTTTT ACCCATTTTA ATTAGTGGAG CGGTATTCAT TGTCTTTCTA | 540 |
| | TTATTACCTG CTAGTTGGTT TACAGGATTA GTAAATGAAA AGACTGTAGA AGATAATAGA | 600 |
| 45 | ACTTCATTGA CAGATCAAGT ACTAAAAGGC ACACTCATTC AAGAT | 645 |
| | (2) INFORMATION FOR SEQ ID NO: 1080: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1080: | |
|-----------|---|-------|
| | AGATGCCAAA ATCAAAACCA ATAATTTGGC AACAACATAT AAGTCCACTT TACCGGACCT | . 60 |
| 5 | NTAAACTTAT CGTACTGTTA AGAACCAAAC GACTGCCATT ATTTGGTCCT AAAGCCACGA | 120 |
| with | TGGTGGTAGC CNTTGTAATA ATGCTGGCGT AGAAATTAAC CGCCACCCCT AACACCGAAC | 180 |
| | TATAACGCGG ATAAACCAAT AAAATTATGA TATAATCATC CGTTAAGTCA ATCCATAGTT | 240 |
| 10 | TAACATCCCT TATGTTTAAT TTACTCT | 267 |
| | (2) INFORMATION FOR SEQ ID NO: 1081: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 441 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1081: | |
| | | . 60 |
| 05 | ATATTTGTCC ACTATTAGAA GATTGTAGAG AAGGACAAAA ACGTTATAAA GCTAGTTTGA | 120 |
| 25 | AAGAAGCGTG ATAACATGAC AAATATTACA AAAGAGGTAT TTGATAATTT AGAACAAGAG | * |
| · · | ATTGATTTAT TTGCCAAAAA TAAGACATTA GGTTCTAGTG AAGCAAAGCC CTACTTGGAT | , 180 |
| | GAATACCATA GTAAAATTAT TGATTATTTT AAGCAGGTTA ATGACATAAC TGGCAATATT | 240 |
| <i>30</i> | GATTTGATA AATTAAATCA ATATCCTGTT GTGCCAATGA ATTTTAAAGA AAGATATGAT | 300 |
| • | TATATGATTG AACGTAAATA TCATTTTATG GGCTATCGAC AAATGAAGAC CTTTAAAACT | 360 |
| 35 | GAATTGATTA AAATGNATGC TAGTTATCAA ACAAGGTTAA AGAATAAGCA GGTATNGACA | 420 |
| | AGATTGATCA TTTCCTAGTG T | 441 |
| | (2) INFORMATION FOR SEQ ID NO: 1082: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 410 base pairs (B) TYPE: nucleic acid | • |
| 1 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1082: | : |
| 50 | AAAATTTCTT AGETGATGGT TATTGTTGTT GATTTGAATA ATTTGTAGCG AATATTTTGT | 60 |
| | AACAGGGCTA CTAAGAATTT TTATAACAAG AAGTGATTTC AATCGTACTA ATTTTCAGCG | 120 |
| | TTTGATGACA AAAGTGTATG TCCAAACTTA AATAATGGCG ATAAAATTTA AGTCATGGGT | 180 |

| | GITCHAIRTE ANTARAGAT INGCARGITA GITCHARATG GCIAIGIAIT GITTIIGAA | 300 |
|------|---|-----|
| | ATACATAGGT TTGAAATCTA TATTAATTAT GCACCAAATA ATTTAATTAG ACTCTATCGA | 360 |
| 5 | AAATTTCCAA ATTTTGCTTA CTATCTTTCT AATTTTACTT TTATATTGTG | 410 |
| | (2) INFORMATION FOR SEQ ID NO: 1083: | . • |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 586 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| , | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1083: | |
| | CAGATATTCC CTTCTATTTA CAAGTTGGTA ACCCATATTT ATCAGACAGC GTAGATAATC | 60 |
| 20 | ATACCGAAAA GTTGTTAGAA CGCTACGAGC AGTTGGTGGA TTTAGTTATG YAAAGTAATG | 120 |
| | ATATGAATCA CGTTTATGTG TTACCACAAC TTCATACATT ACTTTGGAGC AATAAAAAAG | 180 |
| | GTGTATAAAG GATAACTTAT TTTACTTTTT GCAAGTCATA TCTAATGAAT AACAATATAT | 240 |
| 25 | TAATTGATAT AATAGTTGAT TGAAGTATAA CGAACAGGAG TCCATCATGA TTGTATATAT | 300 |
| | ATTAATTAAT ATTGCTATCG TCGTACTTAT AACTGGATTC AATTTATATA GGCATCAAAT | 360 |
| | GCAACATTTA TCATTAAGTG CAATGTTGTL ATCTATTACG ATAAACGCCT TTATAAATAC | 420 |
| 30 . | ATTCATAATT GATAAATATA ACTTTATTAC TCTGTGTACT ATAACGATGT TTATCATTTG | 480 |
| | GACGATACTA CAGTTTTACA TTGATAAAAA ATTAAAACCT GTATACATTA CAGACCAAAA | 540 |
| 35 | ATTTATTGCT ATCATATTAA CGATTGTTGT CAGTTTAACG CAACGT | 586 |
| | (2) INFORMATION FOR SEQ ID NO: 1084: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 638 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1084: | |
| | AACACAAGGT AGCGTCATTA GCATTTAGAT TTTATTGCCA AATTATATAA CGATTTATAC | 60 |
| | ATCAATAAGA AAACAATAGA TGATGTATCT GCAGTTTCTG AAGTGAAATA TGATATTAAA | 120 |
| 50 | TCACAAATGA GTGATGATGA GATTAAGCGT TTAGAGGAAC AAGGACTTCA AGCTATTAAA | |
| | | 180 |
| | GAAGGACAAT TTGCAGTACT TTTGATGGCA GGTGGTCAAG GAACAAGACT TGGTTACAAG | 240 |

| | TTAAAAACAT TGAATCATCA ATCTGGACAT ACGATTCAAT GGTATATTAT GACAAGTGAT | 360 |
|----|---|---------|
| | ATCAATCATG AAGAAACTTT AGCTTATTTC GAAGCACATA GTTATTTTGG ATATGATCAA | 420 |
| 5 | GAAGCAATCC ATTTCTTTAA ACAAGATAAT ATTGTGGCGC TTAGTGAAGA AGGGAAGTTA | 480 |
| | ATTITAAATC AACAGGGTCG TATTATGGAA ACGCCGAATG GTAATGGTGG CGTGTTTAAA | 540 |
| ٠. | TCTTTAGACA AGGCAGGATA CTTAGAAGAA ATGTCTAATA ATGGCGTTAA GTCATATTTT | 600 |
| 10 | CTTGAATAAT CATCGACAAT GTTTTCAGTA ACATGTTG | 638 |
| | (2) INFORMATION FOR SEQ ID NO: 1085: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 15 | (A) LENGTH: 618 base pairs | |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 20 | | * 1, 1, |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1085: | • |
| | ATTGCAATAT TATCCGCTTG GTTCAACACG TCATCTTTaT tAATACCATT TATTGGAAAT | 60 |
| 25 | tCCACCCATT TCCCGGGCTt CTtACTTCCc TTTATAAAAC TGCCCATTTA ATGAATACTG | 120 |
| | TTTAGCTTCA TCTATTCGTA CTTCCACTAG TTTACCAATC ATTTCTTTAG GCGCTTTGAA | 180 |
| | ATTAACTAGC TTATTTTTAT CAGTGTAGCC AGCAAGAACC TGATCATCTT TTTTACTACT | 240 |
| 30 | TCCTTCACAA AGTACTGTTA CAGTTTGTCC TTCGTACTTA CTCATAGCTA TTTGTGAATA | 300 |
| | ATGACCAACT TTTTTATTCA AACGTTGCAA TCGTTCCTTT TTGACATTTA AAGGTACATT | 360 |
| | ATCTTTCATT TTAGCAGCAG GCGTACCATC ACGTTGTGAA TACAAGTACG TATATGCATG | 420 |
| 35 | TTCAAAACCA ACTTCATCAT ACAGAGTTAA AGTTTCTTCA AATTGTTCCT CTGATTCATT | 480 |
| | TGGATACCCT ACAATAATAT CTGTAGTTAA TGCTACATTA GGAATTCTAT CTTTGATTCG | 540 |
| 40 | TTTTACTAAA TCCAAATAAC TTTCTCGTGT ATATTTTCTA CCCATTATHT TTAATACTGC | 600 |
| | ATTATTTCCA GATTGAAC | 618 |
| | (2) INFORMATION FOR SEQ ID NO: 1086: | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1086:

1826

| | CAGCAATATC ATGATCAGTT TAATTCATCA AGAAAGTCTA TCTATACTTT TACAGAAACA | 120 |
|----|--|-----|
| | GTTCAACCAA ATCGTGTTAT TTATGATTTT TATGATTATG ATCCGTATCA ATTAGCAGCA | 180 |
| 5 | AATAATGCGA AAGCATTAAA GGATCATATT GAACAAAACT TTAACTTTAA AGTCCAAAGT | 240 |
| | ACCGGTGTTA KTTACTTTAG TGATGGTACA GTTAATATCA TTCAAGGTTC TGAAGAAAGA | 300 |
| - | GATAAATATG TTGATACAGT TTCAACAAAA TCTTCGTTAC GACGTATTAT TAGCGAACCA | 360 |
| 10 | NAGAGCTATC TAAACACCCT TTAAATAAAG AACAGGTTGA NCAAATCACA GCTATATTCA | 420 |
| | AGTARARTCA AAGGCATAAT AATCCATTAC GCTCGATACG CACTATGGTT ATTATGCCTT | 480 |
| 15 | TAAATTATTT CTATATAA nT | 502 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1087: | ٠ |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 429 base pairs (B) TYPE: nucleic acid | |
| 20 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1087: | ., |
| | TTGCCTGATG GACGATGGCC ATCACAGACT GAGTTTAGAT TGTCTTTAAT GCAACAACTT | 60 |
| | GCTGTAAACC AAATTACGAG TGGTAATGAA AGAATAAGTT CAGTTAATGG GCCACCAGGT | 120 |
| 30 | ACAGGTAAGA CTACTTTATT AAAAGATATA TTTGCTCATC TAGTAGTTGA mAGAGGTAAA | 180 |
| | GAGTTAGCTA AACTAAATAA TCCTAAAGAT GCATTTGTCA ArACAAAAAT TCATGAAACG | 240 |
| | GATGATAAAT ACGTATACTT ACTAAAGGAN NTATTGCCAA ATATAAGATG GTAGTCGCAT | 300 |
| 35 | CTAGTAATAA TGGAGCTGTT GAAAATATAT CTAAAGATTT ACCGAAAATT GAAGAAATTA | 360 |
| | TAAGANATCC CGAAAAATGT AAATTCCCTA AATATGAACA GAATTATGCA AATTTAGCAC | 420 |
| 40 | ATGAATTAA | 429 |
| | (2) INFORMATION FOR SEQ ID NO: 1088: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 611 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 50 | (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1088: | |
| | TAAGACCTAA TATTTTGGnC CAATACTATG GTGCAGGTnA TTTATATATG ACACCAACAG | 60 |
| | · | |

| | ATCCATTATT ACATGAGTTT GGTACGAAAA AGTATCCAGA TGAATATCGA TATGGTTTCT | 180 |
|------------|---|-----|
| | ATGCTAAGCC AACATTGAAT AGACTTAACG GGGGATTCTT TGGACAAGTC TTTACTGTTT | 240 |
| 5 | ACTATAATGA TAAGTATGTA GTTGTACTTG CATTAAATGT AAAAGGAAAC AATGAAGTTC | 300 |
| | GAATCAAACA TATTTATAAT GATATTTTAA AACAAAATAA ACCTTACAAT ACGAAGGGTG | 360 |
| | TTATTGTTCA ATAATTAATA TAGAAGATAT AACATGTATA TGGCATTAAG GCATCGACCT | 420 |
| 10 | TATCTGACCA GTATACGAGT TATATCTTCT TTTTTATAGT GGTAAAAAGT TTAAAGTATA | 480 |
| | AGGTTGAAGA AGGATGAGTT TAAAAATATG TGTTAACTGA TAAAAGGGGA NATCATTTGG | 540 |
| | TGAGTTGGCA TCAGNCTAAA NTGAATGAAG ACGAATACGT TGGTCCATGC GTGGTGTGAN | 600 |
| 15 | TGTTTCTAA A | 611 |
| | (2) INFORMATION FOR SEQ ID NO: 1089: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 20 | (a) LENGTH: 644 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (C) STRANDEDNESS: GOUDIE (D) TOPOLOGY: linear | |
| | (b) Totoboot Comme | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1089: | |
| | CTGGATAATC GCTTTAATAT GATCAATTIG CTTTTCACTC ATATTAAGCT TATCTAGCCC | 60 |
| 30 | TTTCATTTA TTCATACCTG GAATCATTTT CATAATATCA TCCAGTGGTC CTAGATTTTT | 120 |
| | CACCYGWTCA AGTTGTTCTA AAAAATCATC TAAAGTAAAC GATGACTCAC GCATCTTTTT | 180 |
| 35 | CTCTAAATCT TTTGCTTTTT CTTGATCCAC ATCTTGTTGC GCTTTTTCAA TTAAACTTAA | 240 |
| 3 5 | CACATCACCC ATACCTAAAA TACGTGATGC CATACGTTCA GGATGGAATA GCTCTAAACC | 300 |
| | ATCTAACTIT TCACTCATAC CAACAAATTT AATTGGTTTT TGTGTCACCG AACGAATAGA | 360 |
| 40 | TAAAGCTGCA CCACCACGTG tATCACCATC TAATTTAGTT AAGGLAACAC CTGTGACATC | 420 |
| | AAGTTGATCG TCAAAAGATT CTGCAACATT GACAGCATCT TGACCCGTCA TTGAATCGAC | 480 |
| | AACTAACATA ATTTCGTTTG GTTTAGCAAT GTCTTTTACT TCTTTTAATT CGTTCATCAA | 540 |
| 45 | TGCTTCATCG ATGTGTAATC GACCTGCTGG TATCAATGGA TTACAAAGTC TAAATGTTCT | 600 |
| | TCTTTAGCAn GTTTTAATGC ATTAGTTACA ATTTGGTGTG GGCC | 644 |
| | (2) INFORMATION FOR SEQ ID NO: 1090: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 207 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1090: | |
|-----------|---|-------|
| | | |
| 5 | GATCCTATCG TTTTAGTGCA TGGTTTCAAT GGGTTTACAG ATGATATTAA TCCTTCAGTG | 60 |
| | TTAACTCATT ATTAGGGCGG TAATAAAATG AACATTCGCC AAGATTTAGA AAAAATGGTT | 120 |
| | ACAAAGCTAT GAAGCAAGTA TAAGTGCTTT TGGAAGTAAC TATGACCGCG CATTGAACTT | . 180 |
| 10 | TATTATTATA TCAAAGGCng TCGngTA | 207 |
| | (2) INFORMATION FOR SEQ ID NO: 1091: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 212 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1091: | |
| | GACTCTAGAG GATCCCCGCT CAAATGCCAT TTGGTGATAT TCGTGAAGCT GCTGGCGAAA | 60 |
| | AAACATTTAA TCCAGTGGAA GATCGTTTCG TAATAAAAAA ATAATCAATA TATTGTTAGG | 120 |
| 25 | AATGGGACAG AAATGATAAA GATTCATTAG TTATTCATTA TGTTGTAGTT CTTACACATT | 180 |
| | AGCCGCTGCT AATnGCAACT TAAGAnTAGG TT | 212 |
| | (2) INFORMATION FOR SEQ ID NO: 1092: | |
| 30 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 208 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| · · · · · | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1092: | |
| 40 | TGGACCTGCA ATTGGTTGCC AGCAGCAACT TTAGCTTCAT AGCTAGCTTT GTGAGCAAGT | 60 |
| | GGTAAACCTG GAACGATATC ACCAATTGCA TAGATATTGC TGATAGACGT ACGGCTTTGT | 120 |
| | TTATCAACnn CTAATAATCC ACGTCAGCGA ATTTAACACC TAATTCTTCT AGGCCTAATT | 180 |
| 45 | CGTCGTGTTT GGACGACGAC CTACATTA | 208 |
| . () | (2) INFORMATION FOR SEQ ID NO: 1093: | * |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 902 base pairs (B) TYPE: nucleic acid | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1093: | |
|-----|---|------|
| | CTTAAAAGTT GTnTCAATAA TGATTGTATT AGTTGCATGC TTATTATATA TGAATCATAG | 60 |
| 5 | TATTGATTTA CCTACCCTTA TTATGATTTC AATTTTTTCA TTTGTGATAT TTGATAGTGT | 120 |
| | TGAAAATATT AATAGTGCTG CACACGTACT TGAAATGATA GATATGACGA TAGATGATAT | 180 |
| | TGMAAAGATA AAAAATGCTC CAGAACTGGA TGAGAATGGA AAAAATTTGA CGATTAAAAA | 240 |
| 10 | TGAAAATATC GCTTTTCAAA ACGTGAACTT TTCATATGAT GATAAACAAG TGATAAAGAA | 300 |
| | TGTGAATTTT GAGATACCTA CACAAACATC AACAGCAATA ATTGGACCTT CAGGAAGTGG | 360 |
| 15 | GAAATCTACA TTATGTCACT TACTCTTGCG CTTTTATGAT ATCGATGATG GAAATATTCG | 420 |
| | CATCGATGGT GTTGATATTA AAGATATGAC ATTAAGTACG TTAATGTCGA AAATTAGTGC | 480 |
| | AGTATTICAA AAGGIGIATI TATITAATGA TACGATTGAA AATAACATAT TGTTTGGCAA | 540 |
| 20 | TCCAGGTGCA ACGAAGAAG AAATTATTCG TGCCGCGAAG CAAGCATGTT GCCACGACTT | 600 |
| 347 | CATCATGTCA TTACCTGAGG GATATCAAAC AATGCTAAAT GAAAAAGGTA GTAATTTATC | 660 |
| | TGGCGGAGAA AAGCAAAGGA TTTCTATTGC TAGGGCGATA TTAAAAGATG CACCAATAAT | 720 |
| 25 | TATTTTAGAT GAAGCAACTG CAAGTATTGA CCCTGAAAAT GAACAGCTGA TTCAAACGGC | 780 |
| | AATTAATGAA TTAAGTAAAG GCAAAACAGT AATTACAATT GCACATAAAC TTGAAACTAT | 840 |
| | TAAANATGCA GATCAGATTA TAGTGCTCAA TGNAGGTGAA ATAATTCAAA AAGGTAGTCC | 900 |
| 30 | TG | 902 |
| | (2) INFORMATION FOR SEQ ID NO: 1094: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 632 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1094: | |
| | ACGCAAGGGA TATGATTAAA CACCATAATA TACAATCACC TTTTTTATAC ATGAAAGCAC | . 60 |
| 45 | TAATAGAATC GATTCATTTA AACATAAAAC ATGATTTTAA CCAGCAAGAT TTGATTGAAA | 120 |
| | TACCAATTGT GTATGGTTCG AAATATGGTC CGGATTTAGA ATCACTTTTA AAACATTACA | 18 |
| | AAATCAAGCT AGAAACTTTT ATTGAATTAC ATTCTAAGGC GCAATATTTT GTTTCGATGA | 24 |
| 50 | TGGGATATTC ACCTGGGTTL CCTTATTTAA CTGGATTAAA TAAGAAATTG TATATTAATC | 30 |

| | GCGGTATTGT AACTACGGAT ACAATTAATG ATTGGTTAGT TATTGGTTAT ACACCATTAT | 420 |
|----|---|-----|
| | CACTTTTTAA TCCGAAAGAA TCAGATTTCG CACGCTTAAA GTTAGGCGAT AATATTAAAT | 480 |
| 5 | TTAGACCTAT CAATGAAAAT GAATTAGAAG TAGGAGCGTT TAAAGATGTC AATCATAATT | 540 |
| | GAAAAAAGTG GCTTATTCAG TAGCTTTCAG ACTTTGGCAG AAGGGGATAT GAACATGATG | 600 |
| 10 | GTGTAATTCC ATGTGGTGCA CTTGATACTT TA | 632 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1095: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 212 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1095: | |
| | GCAACACGAT TGCTAAAAAA TGATATACTT ATTAATTGTT GCAACACTTG TTTATGTGAT | 60 |
| | ATACTGATCA TGGCATTGTG GCGGATTGAT GACCATACAC ATGACGTGAC AATGATAAAT | 120 |
| 25 | CATTGCCACT ACTTGTTAAA ACAGCAATTT CTCAAGTGGA AGCTGGTGCn ATATATTnCG | 180 |
| | CCAATAATAT GATGGATGGT TTGTTGCTGA AA | 212 |
| | (2) INFORMATION FOR SEQ ID NO: 1096: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 466 base pairs (B) TYPE: nucleic acid | |
| 35 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1096: | |
| 40 | AATGAACTGG GTATTMCTTT TGCCATGCTT GCCCACTGCC ATGCATTTGC TGAAGAATGT | 60 |
| | TTTTGTAGAA CCGGCTTAAG AATTTGAAGT TTGTAGTAGT ATCTAAAAAG ATTACTTGGT | 120 |
| | GATACTCAGG ATGAATTCCT TGTTCATTAT TTTCAGCTCC TTTGCCCTGA ACCATCTGGA | 180 |
| 45 | ACAGAGTTAT TTGTGAGTTT TTACCCAATA CTGTGTAATT ATAAAGGTAA TTAATTCAAA | 240 |
| | ACGCAAGCCC CTATATAATG TTTATTAAAT TATAGGTCGA CCCGTTTTAG TACTTTCTTC | 300 |
| 50 | TGCAGACTTT TGTAGCTGCT TGAAGAAATC TECATTATTC TTAGACCTTT TAAGTTTGCG | 360 |
| 50 | AATAAATCTT TCAGTAAAGT CAGTTGAGTC AGTGAATAGA TTTCTTAATT GCCATAATGT | 420 |
| | GTCTAATTCA GATTTACTTA TCAACAATnC TnCTTTACGC GTTGAA | 466 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 208 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|------|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1097: | |
| 10 | TTTTGATTCA ATAGGCGGTT CCGTGTTATC ACTGACAACT TTAGTTGTAG CTTCATCTTT | 60 |
| | ATGTATTTCT TCGTTAAATC CTTCAAGTTT TTAGTCGTGG GATTTTAACC TCAGGATGTT | 120 |
| | CCATCATGTC TTGACTATCA AGTCCTTnTA CACGTGTCTT TATGTGATGC TTGATTGCGT | 180 |
| 15 | nCCCTTACTT TTTGAATAGG GGTAGTAA | 208 |
| | (2) INFORMATION FOR SEQ ID NO: 1098: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | |
| - | (A) LENGTH: 571 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | , , |
| | (6) 1332-1333 | • |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1098: | م نہ |
| | CCTTCAACGA AAATAGCATA TTGACCATAA ATATTATGAA TTGTTTGTTC AACATCTTCA | 60 |
| 30 | GTTATTGGAT CTTGACTCAA AAATACATTA AATACTTCAA TACCAAATTT ACGTGACATT | 120 |
| | TCTACAGCTT CATACGTATC AATAATACCA TCTTGACTAT AATTAAATGC AGACGGTTCG | 180 |
| | CCGTCTGAAA ATANGATTAA AAATCGTTGA TGTTGATTTC GACGCATTAA TCGTTCACTT | 240 |
| 35 | GCAACTCTAA TAGCAACACC ATCACGATTA TCATCTTGAG GTTCAAGTGC CATAATACGT | 300 |
| | GGGCCATCTT TTTCAAAGGT TGAGTAATCA TAGTTAATAA TTTCATTAAT GATATTTGGT | 360 |
| 40 | TGTGCATGCT CGTCTGAATC AAAGGCATCC TCACTGAATG ATAAAATTTC ATGTTTAATG | 420 |
| 40 | TTCAATGCTT TTAACGTCTC GTGGAATAAC ACTACACCTT TCTTCGTTTC AGCCATTTTA | 480 |
| | TCATGCATAC TTGCTGGACG CATCAATTAA CAATGTAAAT GTnCGCATCA AATGATTNAC | 540 |
| 45 | TTAAATCTTG TTTTTTGTAA AACAATTTAT A | 571 |
| | (2) INFORMATION FOR SEQ ID NO: 1099: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 214 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1099: | |
|----|--|-----|
| | TGCAAGTGAA CAAGTCATTA ACTTGTTTAA TACACGTGGG GCACAAGTCG AAGAAGTTTG | 6 |
| 5 | GGTGAAGGGC CATGAAATTA CAGAAACTGG ATTAACGGCT GGTCAACAAA TACTTGGGAA | 120 |
| | ATAACAGTTC TATTAAGAAG CGGACAGATG GAAAAGATTT TACCTTTCAT CTGCCGCTTT | 180 |
| 10 | TTGATTTGAA GGCCGGACCn AATTTACCAn GGAA | 214 |
| ,, | (2) INFORMATION FOR SEQ ID NO: 1100: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1158 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1100: | |
| | CACCGTATTG TACAAAGAAT TTAAAGTTTT CGATTTCTTn TCTTAATTTA TCATCAGCTA | 60 |
| | TCGGTTTGGT TGGGATAATT TTATTATGTT CCATTTTTAC TGGATATTCT TTTTCTTTAC | 120 |
| 25 | TACGTGAGTA TCCTnTTTTA TCTTCCCATA ATTCCCTCAC AATAAATTCA CCTTTTGTCG | 180 |
| | TTCTGGTATT GCGGTCTACA TACAGGACCA ATCCTCTGGA TTCCATATTC TTTCCATTTG | 240 |
| 30 | TTTCTATTGT CATTTTAGAG TGAATTATCC AAGTGCCTTT GTCGCCCTTT TCAAACTCTT | 300 |
| | GATCTCGAAA GCCTTCCTTA TCATAAAAGT CTTCAAGATT TTTAGTTGGA TACAGGCTCA | 360 |
| | ACGTTTTGTT GAAGTTTTCT TTAATTTGTT TATCTTTACT GCTTTCTTCC TTTTTCATTC | 420 |
| 35 | CGCAAGCCCC TATAAAAACA GCTAATAATA CTAAATACAG CCAGAGCCTC AACCTTTTTG | 480 |
| | AGTGAATCAT CATTTCACAT CCCCATTTTT ATTTTTGATG CAAAGTTAAG TECAAATTCC | 540 |
| | AATATTAATA ATATTAGAGG AAALTTLATG ATTAAATCCT CGTGGATTLT AATTGTTAGT | 600 |
| 10 | TGTATTTTTC ACATATCAAC ATCACAAATT ATTTAAAAAG CGCAAATATC TTTATAATTT | 660 |
| | TTATTGGCCT AACCAACTAA TTAATTAAGA TAAATTGCGC TTATATTTAA AATAATAACA | 720 |
| 15 | CTGAAACTCA ATGTATTTAC TTATTAAAAT TGATGTTTAA ATACAACTTT ACTAACATTC | 780 |
| | ATTTTTCGGT TTACATTAAT TKGTTAGATA ACGATATATA TCALCTCTTA CAGCTTTATC | 840 |
| | CAGTGCTAAA TCCATCGTTA CTACGTTTGA ACCATTCGGC ATTTTATCTT GCTTTTCTGA | 900 |

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50

960

1020

1080

ACCTTCTATA TATCCAGCAG TTCCTAAATA ATAAAAATAT ATACCATCAT CATCTTTTTT

CTGTACAAAA ATATACATTT TAATTCCTTT TGCTCTATGG GACAAAATTT TCTGAACTTC

TTTTGATTCT AGCGTTCTAT TAGATTTAGT AAACCATTTT AATTCATCTT GACTTAAAAA

| | TGGCATTTCT TGGCTTTT | 1158 |
|----|--|---------|
| | (2) INFORMATION FOR SEQ ID NO: 1101: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 353 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | * * * * |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1101: | |
| 15 | CCAAATGCTA TAAATGCAAA AATMGCTAAT GCGATATTIT TATAGAAAAT ATCTGGTCCT | 60 |
| | AAATTTTGTA AATACGTGGT AAACGTTGCG TATGACAATA AGCCAATCAC TACAGCGTAA | 120 |
| | ATATGTGAAA TAATTAAACC GAACCGTCTC GCTCTTTCAA AAACAAGTGT TGCTAAAATA | 180 |
| 20 | ATAATCAGTA ATCCAAATGA CAAGGGTTGT CGCCAACTTA ATGGTAAAAA CTGACCTAGA | 240 |
| | TAGCATCCTA TGCCAAATAT AATCCAATAA TACATAAAAT AAAGCCACAC TTTACTTACT | 300 |
| | GATTGAGCAT GCTGGTTTTG ATGATAATAT GAATGATTTG TATTTTGCGA CAA | 353 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1102: | |
| * | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 194 base pairs (B) TYPE: nucleic acid | |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| • | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1102: CCCACACGTC TTCCACCGGA TAGGTTTCGA GCTCGGGCGA ACCGGGCAGG GCGGTGACCA | 60 |
| | CCCGCGCGG TGTCTTCTTG GCCAGCTTGT TTGCGAGCTT GGCCAGCGTC TTCGTGGGGC | 120 |
| 40 | CAATGCCCAC GCAACACGGG ATGCCCACCC ATTGGAGGAT CTGGGCACGG ACCTGGCGGG | 180 |
| | CCATCGCTTC GnTG | 194 |
| | (2) INFORMATION FOR SEQ ID NO: 1103: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 220 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |

1834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1103:

| | TCGCTTTTGC TTTTGCATCA GGTATTGCTG CTATTTCAGC ATACTTTTTG ACTTTCAAAT | 120 |
|----|---|-----|
| | CTGGTGATCA TGTCATCTTA CCCGATGGAT GTATATGGGC GGTTACTTTT CGTCTCACTG | 180 |
| 5 | TGGCAAATTT TGGATCGATT TAATATTGAA TTTTACAACC | 220 |
| | (2) INFORMATION FOR SEQ ID NO: 1104: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 235 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1104: | • |
| | GGACATTGTA TCGACATTTC AAAGATAAAA GCGATTTATG CTACTACGTC ATACAAAGAG | 60 |
| 20 | ACCTTGATAT TTTTATCACT CATTTTAAGC AAATTAAAGA TGACTATCAT TCTAATTATG | 120 |
| | AGGTTATGCA AGTGTCGTCA TCGCTTTTAA ATAAGTCATA ATAAAAATCA AATAATTCTT | 180 |
| | GATAAAATGC GCTTTGGTAA AAACGTAATT TATTGTTGCC TGCTTCAATA CATTG | 235 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1105: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 229 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1105: | • |
| | GCGGGGCAG GTAAATCCAC TTTGACACAT CTTATTGCAG GTGTTTATCA GCCAACAATA | 60 |
| | GGTACTATAA GTACAAACCA GCGTGATTTT AATATTGGGA TACTTAGTCC ANAGCCCTAT | 120 |
| 40 | ATTTCAGGCT CTATAAAAGA GGATATTACG ATGTTTAAAG nTATAGAAAA TAATACTAAT | 180 |
| | GAAGAAGTGC TAGACGAAGT AGGGTTTATT AGACCAAGTG CCATCCTTC | 229 |
| | (2) INFORMATION FOR SEQ ID NO: 1106: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 596 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | | |

1835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1106:

| | PAATTAAAAT CAAAATTTGA TGAAGTAAAT GTAATCGCGT CAACAAACGG TAGAAAGTTT | 120 |
|-----|---|-----|
| | ATTANTGGTG AAATATTAAA GCAATTTTGC GATAACTATT ATGACGAATT TGAAGACCCT | 180 |
| 5 | TTTTTAAATC ATGTAGATAT AGCAAATAAA CATGACAAGA TTATTATTTT ACCTGCGACT | 240 |
| | TCTAATACGA TTAATAAAAT TGCMAATGGT ATATGTGACA ATTTATTATT AACTATTTGT | 300 |
| | CATACAGCTT TTG:AAAACT TTCTATATTT CCAAATATGA ATTTACGAAT GTGGGAAAAT | 360 |
| 10 | CCAGTTACTC AAAATAATAT TCGATTATTA AAAGATTATG GTGTATCAAT ATATCCAGCA | 420 |
| · | AATATTTCAG AAAGTTATGA ATTAGCGTCA AAAACATTTA AAAAGAATGT TGTCGCACCT | 480 |
| | GGAACCATAT AAAGTTCTGG GAATTCATTT GAGATTAGAA TATGGAAAAT CATAAAGCGC | 540 |
| 15 | GCKATTGATT AGTTTAATGA ATGATTGGAG TCNTTTGAAG ATNCGATTTA CAATGG | 596 |
| | (2) INFORMATION FOR SEQ ID NO: 1107: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 673 base pairs | |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| , | (D) TOPOLOGY: linear | |
| 25 | | |
| . * | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1107: | |
| | ACTAGCTAAA AATAATATTC TATTCTTTTT AACATGGGCA GTTCCAGCGG CAATTAGTGG | 60 |
| 30 | TATTTATATT AAATATATAA ACAAGGCTAC GGTAGAAAGA TTTTTTAAAT TAGTATTTTT | 120 |
| | CATATTTTCT GTTTCATTTA TTTTTGTAAT TTTAATACCA AAACTTACAG GTGAGATACC | 180 |
| 35 | TAGCTATATC AATTTTGGAC TTATGAACTA TCAAAACGCT TCGTACCTTT CAGCATTTAC | 240 |
| · - | TGCCGGATTA GGCATTTATT TCATTATGAA AGGTTCAGTT AAACATAAGT GGATATATGT | 300 |
| | TCTATTTACA ATAATTGATA TCCCTATTGT GTTTATACCA GGAGGGCGTG GAGGTGCTAT | 360 |
| 40 | TTTATTAATT CTTTACGGCT TATTTGCATT TATACTTATT ACGTTTAAAA GAGGAATACC | 420 |
| | TATCGCAGTA AAAAGCATTA TGTATATTTT TGCATTAAGC ATATCTAGTG TATTGATTTA | 480 |
| | CTTTCTTTTT ACAAAAGGTT CGAATACTAG AACATTTTCA TATCTACAAG GTGGAACACT | 540 |
| 45 | TAATTTAGAA GGTACTTCTG GGAAGAGGAC CGATTTATGA AAAAGGTATT TACTTLATTC | 600 |
| | AACAAAGTTC GTTATTAGGC TATGGGCCAT TTAACTATLA TAAACTAATC GGAAATATAC | 660 |
| | CACATAACAG CAT | 673 |
| 50 | | |

(2) INFORMATION FOR SEQ ID NO: 1108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

| | \cdot | |
|------------|---|-----|
| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1108: | |
| | TCACAGTGGC GGCACAAAA GTAAGTGGAG ATTATTTAA TTTAATTGAC CATAACGATG | 60 |
| 10 | GCACAATGAG CTTTGCTGTT GCAGATGTCA TTGGAAAAGG TATACCAGCT GCTTTAGCAA | 120 |
| | TGAGTATGAT AAAGTTTGGC ATGGATTCTT ATGGACACTC ACAATTACCG AGTGATGGTT | 180 |
| | TAAAACGTTT AAATCGTGTT GTTGAAAAGA ATATTAATCA AAATATGTTC GTCACAATGT | 240 |
| 15 | TTTATGGTTT ATATGAAGAA ATGAACCATT TATTGTATTG | 300 |
| | CTGGATATAT TTATCGCGCT GAAAAAGAAG AATTTGAAGA AATTTCAGTT AGAGGTAGAG | 360 |
| | TGTTAGGAAT CAGTTCACAA ACACGATATC AACAACAAGA AATTCCAATA TACCTTGATG | 420 |
| 20 | ATTTAATTAT CATTTTAACG GATGGTGTGA CTGAAGCTAG AAAAGTGAAG GTACCTTTAT | 480 |
| | AGATAAACAA AAACTTTTAG AATATA | 506 |
| | (2) INFORMATION FOR SEQ ID NO: 1109: | |
| ?5 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 552 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| 3 0 | | |
| , | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1109: | |
| 35 | TGATATTGAA AAAGATGTCA TTGTTAAAGC ACAAGAAAGT AAAATTGCTC AAGTTATCAC | 60 |
| | GAATTTGTTA ACGAATGCAA TTAACTATTC TTATGAAGAT GGAGATATTA ACGTTCGTGT | 120 |
| | GTATCGAGAT GACTTTCGTG TCATTTTCGA AGTACAAGAT TTTGGTATAG GTATTAAATT | 180 |
| 10 | AGAAGACCAA CAACGTATIT TIGAAAGATT TTATAGAGTA GATAAAGCAC GAAGTAGAAG | 240 |
| | ATTCTGGTGG GACAGGTCTT GGATTATCAA TTACAAAGCA TATAGTAGAS GCCCACCAAG | 300 |
| ; | GCAATATTGA AGTGAATAGT CAAGTTGGCA AAGGCTCAAC GTTCAAAGTT ATTCTAAAAG | 360 |
| 15 | ATTATAAGA ATAANAATTA AAGTGGTAAC AGCGCGTGTA TTTTTCACGA AGTTGTTGCT | 420 |
| | GCTTTTTTAT TTCGTTCAAA TCTCTATTGG TATTAAATTA GAGTTAATGA AGTGGAATAA | 480 |
| | ATTCGGTTGT CAATTITGTC ATTTGTATAT GTCGATTTGT AAGTTATAAG TAATAGATTG | 540 |
| 50 | TTGTGAATCA nG | 552 |
| | (2) INFORMATION FOR SEQ ID NO: 1110: | |

| | (A) LENGTH: 244 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| 5 | | |
| | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1110: | • |
| | AACAGATCAA CAATTGCAGA TCAATTACTC GTCATATTGA TCAATTATCT CTGACAACGA | 60 |
| 10 | GTGATGATTT ATTACGTCAT TGATTGATCA TCACAAGATA AGTCGCTATT GATTTCTCAA | 120 |
| , | TTTTACAACG ANATTAGGAA AGCTGNAGCA GATAATTGGC TAAGTTGGAC GATAAAGGTT | 180 |
| 15 | ATCAATCGCC AATCGTTGCC ATTGAAGAAC TTTTGCTCAC TGGCGCACGC TTCAGATGAT | 240 |
| | ATTT | 244 |
| | (2) INFORMATION FOR SEQ ID NO: 1111: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 825 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1111: | |
| | AGTATTGAGT GTTTTGATTT AAGAGACTTG GAAAGTGAGT CAATAATCAA AATCTTACTC | 60 |
| 30 | AATACTTTTA TTTTGGTACT CGCAATTTAG ATTTGTTAAC TAATTTTTTC GCTTATTATA | 120 |
| | AAACGAAACA ATCAAGTAAA CGATAAAGCC TACAAAGATA CCCAATAAAA TAGATAGTAC | 180 |
| 35 | TGCCGTCACT ATTAATGGTA ATTTGAAAAA TATTTGTAGG AAAATmCCAA TGATAATTGC | 240 |
| 55 | GATAATTACT GCAALTAATG TGACTGTATT TTCATTTGAA ATGTTCATLT ATLLTCACTC | 300 |
| | CTEAACAATA ACATTATATC ATGCTATAGC TTTCCAAAAT ATTGAAATAT GTAGATATGG | 360 |
| 40 | CTATTGACGA TATTTCTTAA CTTTTATATG ATTAATCGGA ATGAAAAAAG AGAAGTAGGT | 420 |
| | GGCAATATGA AGTCAAATAA ATCGCTTGCT ATGATTGTGG TAGCCATCAT TATTGTAGGT | 480 |
| • | GTATTAGCAT TTCAATTTAT GAATCATACG GGTCCTTTCA AAAAGGGGAC GAATCATGAA | 540 |
| 45 | ACTGTACAAG ATTTAAATGG TAAAGATAAA GTACATGTTC AAAGAGTTGT GGATGGTGAT | 600 |
| | ACATTATTG CAAATCAAAA TGGTAAAGAA ATTAAAGTTA GGCTTATAGG GGTTGATACG | 660 |
| | CCAGAAACGG TGAAACCGAA TACGCCTGTA CAACCATTTG GCAAAGAAGC ATCAAATTAT | 720 |
| 50 | AGTAAGAAGA CATTAACAAA TCAAGATGTT TATTTAGAAT ATGATAAAGA AAACCAAnTC | 780 |
| | GCTATGGTAG ACCATTGGCG TATGTATGGA TAAGTAAAGA TCGTA | 825 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 621 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: doubl (D) TOPOLOGY: linear | |
|-------------|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1112: | |
| 10 | TCCCTATARA TCCCCACARA ARRAGGGTAR ATCCGRACGT CREATTTCAT CTCTTTATGC | 60 |
| | CAATCAACGA TCGATTTACC TTTTAAAATT TAAAATGTAT CTGTAATACT CTTAGCAATA | 120 |
| 15 | TTTGTATATG CTGCATCTTC CATAGGTGGA TTGTGTAATC CTGCACGCAT GTCACGATAG | 180 |
| 15 | TAACGTTGTA ATGGTCGATT CATTTCTAAG CTTTTAGCAC CAACTATTCT CATCGCTAAA | 240 |
| | TCAATCACTT CAAGCCCTTG ATTCATTACC ATCACTTTAC TCGCACTTGT TGGATTTCTT | 300 |
| 20 | ATCTGACTGT CATCTTTATA TTGTTGATAC CCTTTTGCTG TACTCCATAA AAATTGTCTC | 360 |
| | GCACATAACA ATAGCGTTTC CATTTCCCT AAATTTTGTT GCACAGTTGG CAATGTTGCA | 420 |
| | ATCGTTCCTT CAATACTATT AGGGCTATGT TGGATTGCAA AGTCTACAGC ATAATTTCTA | 480 |
| 25 | GCAGCTTGTG CTATACCTAA ATAACAGCTT GGTATATGCA ATATCCAACC ATTTGGCGCT | 540 |
| | TTACTTTTCT CTGTTTCCAC TAAATGTTTT AATGGTACTT TTACATCATT TAATATTAAA | 600 |
| | TCATGACTTT CTGTCGCTCG C | 621 |
| 30 | (2) - INFORMATION FOR SEQ ID NO: 1113: | |
| <i>35</i> , | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 619 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1113: | |
| 40 | GTACCTTGTT TTTCAGTGTT AATTTCCCAA ATATAACCTG GTGTAATACC GTATTGTTTT | 60 |
| | GAGAAGTACT TGAAGGCACC TTCACTTGTa ATCATGGCAC GTTGTTCTTC TGGAATGTCA | 120 |
| 45 | TTAAATTTGT CTTTACTGTC TTTACTGTCA TTATTTAATT TTTCCAATTG AGCAATGTAT | 180 |
| | TIGITACCIT GCTTTTCATA ATCTGCTTTA TGTTTTTTGT CGTTATCGAT AAATGTTTGT | 240 |
| | TGAATTGTTT TTACGTATTT AATACCGTTA TCTAAACTTA ACCATGCGTG TGGATCTTGT | 300 |
| 50 | TTATCTTTGT TGCCTTCTTC ACCGTTTAAA TAGATAGGTT TAACATCTTT TGATACTGCG | 360 |
| | ATAACTTTT TATCTTTTAA TGATTTACCA GCCTGTTCTA AGGCTTTTTC AAACCAACCG | 420 |

| | ATATCYTTAG GTTLAACYTC ATAWTCATGA GGATCTKGAC CAACAGGIAC AAIACIATGA | 340 |
|--------|---|-----|
| | ATATCGACGT TGTCTCCACC AACATTTTTA GCCATATCAG ATAGAATTGA ATTCGTCGnT | 600 |
| 5 | ACTACTTTNA ATTTGCCAT | 619 |
| | (2) INFORMATION FOR SEQ ID NO: 1114: | • |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 549 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1114: | • |
| . ~ | GAAAACCGCA CGACAATGAA AAAAGATATC CGGTTAAAAT GGTCGATAAT AAAATCATTC | 60 |
| 20 | CAACAAAAGA AATTAAAGAT GAAAAAATAA AAAAAGAAAT CGAAAACTTT AAGTTCTTTG | 120 |
| * | TTCAATATGG TGACTTTAAA AATTTGAAAA ATTATAAAGA CGGAGATATT TCATATAATC | 180 |
| | CAGAGGTGCC GAGTTATTCG GCTAAATATC AATTAACTAA TGATGATTAT AATGTAAAAC | 240 |
| 25 | AATTACGCAA AAGATATGAT ATACCGACGA GTAAAGCTCC AAAGTTATTG TTAAAAGGTT | 300 |
| | CAGGGAATTI AAAAGGCTCA TCAGTTGGAT ATAAAGATAT TGAATTTACG TTTGTAGAGA | 360 |
| | AAAAAGAGGA AAATATATAC TTTAGTGATA GCTTAGATTA TAAAAAAAGC GGAGATGTAT | 420 |
| 30 | AATCATGGCT CAATCAGAAT ATGAAATCAA TCCCGGAAAA AGAGAGTGAT GAAATGATAA | 480 |
| | AACGTGTAAA TAAATTAGTG CTTGGTATTA GTCTTCTGTT TTTAGTCATT AGTATGCACT | 540 |
| 35 | GCTGGTTGT | 549 |
| 33 | (2) INFORMATION FOR SEQ ID NO: 1115: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 317 base pairs | |
| 40 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | • • |
| | (D) TOPOLOGY: linear | |
| .= | 270 TD NO. 1115 | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1115: | 60 |
| | TGTTATTGCA ACTATTAAAA ATATMAAAAA CAAAGACTTA ATTGATTATT CTTTATATAT | 120 |
| 50 | TAAAAAAGGT TTAGTGGAGC CATTTATTGT ATTCTATAAT CAAGAAAATA TATTCTACAT | |
| 50 | TAGCAATGCT GTTATAGATA TCATCAGTGT ATCCAAAGAT ACTCTTGATT ATATAAAGTC | 180 |
| | AGAATTCAAT GATCACTGTG tTCGCCATAC TGATTTTATA GCACAGAGAA AAGCCGTAGT | 240 |

| | TTATCATCTT CGATGAA | 317 |
|-----------|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1116: | • |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 10 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1116: | |
| 15 | ACTATGACTG CAATGCCAAC AATGAATGTT ATTGCATAAA GCATATGCAT TTAATCAAGC | 60 |
| | TTATGTTATT TAGCAAGGGC AAGCCACTTC TCGATTCATG GCTTGCCTTA TTTTATTGTA | 120 |
| | TATTTTTAAT TATCGTTGCT GGGCCCTTGA TTGACAATCG TATTAAAATG GCCTTATTAA | 180 |
| 20 | GTCAACTTIG TCTATACGGT TIGGAATCTT CTACCCAATG TCTTATAAAA GACAATCCCG | 240 |
| | CACCTGAAAC ATAACTCATG AAnATAAGAA NATGGTATAC CATTAATNTG AATCCATTTC | 300 |
| | CANTITATAA CGTTGTAAAT GACACATAAT TAGAATCATA AAGTTTTTCG TGGGATATTG | 360 |
| 25 | AAACTTTACC CATACGAGAC ATCATGGATA AAAGCGAGGC | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1117: | |
| <i>30</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 696 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | * | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1117: | |
| | TGCATATAAT GTTCAAACGG CAATGATTCC ACTGTATAAA CCTCTTGTCG TGGATGATCT | 60 |
| 40 | TTAATTTGTT GTTTTAATAA CTGAACTCTT TTTTCATGTT CATAATGAAC ATAAATAAAT | 120 |
| | GCACTAAGAT ATATCACAGC TAAAACTAGT GATGCACCTT TAATAAAATT AACATTGATT | 180 |
| | GACTTATATT TCCGAAATTC TTTTAATAAA ATAATTAAAA TGATTACATG TATCGTATAA | 240 |
| 45 | ACAATCAAAA AATTACCTGG TTCTATTGGA GTAACAATGA CTAGTGTCGA CGCCGAAACA | 300 |
| | CATATTGCAA TAAGTAAGGA ATATAAAGTG ATTTGTGTTT TACGATCATT AATAGACAAA | 360 |
| 50 | TAAATACCTA CAAATATCGA AAACGCAAAG TAACCACATA CAATTACGTT CACAAAACCA | 420 |
| | ACCAATCCAA TATCTGTATT TTTATTTAAT AAAAACTGAT TGTAAAATAG TAAATAATAA | 480 |
| | AGCGGTAAAG TGATAAATCC TATCATAATG ATACGACGCT TTAATATTGT TAAATGTACA | 540 |

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| 3 | ATCTGACTGA AAATGACACC ATATGGAAGT GACGTTGATA TCATTTCTGC AAATTTTGAA | 660 |
|----------|---|-----|
| | AAGATACCTT GATTATTTGA AACTTGTTGA TATTCT | 696 |
| <i>5</i> | (2) INFORMATION FOR SEQ ID NO: 1118: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 223 base pairs (B) TYPE: nucleic acid | |
| 10 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1118: | |
| | GCAGTGACAA TCAATAATTT GTAACTAGAA GATAATAAAG AGAACGCTCT ATAGAGACGA | 60 |
| | ATTGAAGGTT TGATTTTAAT GTCTGTTAGT AAGAATCATA TCAATGAGAT GCCTATAGTA | 120 |
| 20 | CTCAGANTAT ATTAAATTAA AACCGTCATT AATTGTTTTT CCGAAAACCA TTTGTAACCA | 180 |
| | TTTNAATGTA GTTGGACCTA CCTACGTTCT CCAATAATCC ATT | 223 |
| | (2) INFORMATION FOR SEQ ID NO: 1119: | • |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | - |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1119: | |
| 35 | CTGCTTTACC TTTTCCAACT TTAGAAATTG CTACATAGGG GCCTTCTGCT TTACCGCCCC | 60 |
| | AATTCCAATT CCACATTTTC AAGAAATAAG GAGGCAAAAA TGTTCATATA TGAATTGGAA | 120 |
| | TTATTTGTTT TCTTATTAGG CCGAGATGCG CCGCGTGCGG CTGCTGGAGA TGGCGGACGC | 180 |
| 40 · | GATGGATATG TTCTGCCAAG GGTTGGTTTG CGCATTCACA GTTCTCCGCA AGAATTGATT | 240 |
| | GGCTCCAATT CTTGGAGTGG TGAAT | 265 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1120: | |
| - 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1120:

| | CATGACATTA CATGCTTATT TAGGTAGAGC GGGAACAGGT AAGTCTACGA AAATGTTGAC | 120 |
|-----|---|-----------------|
| | CGAAATAAAA CAAAAaATGa AAGCAGATCC GCTTGGAGAT CCAATCATTT TAATTGCGCa | 180 |
| 5 | ACTCAAAGTA CATTTCAATT AGAACAAGCC TTTGTCAATG ATCCGGAATT AAATGGTAGT | 240 |
| | TTAAGAACAG AAGTGTTGCA TTTTGAACGA TTAAGTCATC GTATTTTCCA AGAAGTTGGT | 300 |
| | AGTTATAGCG AACAAAAGTn ATCTAAAGC | 329 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1121: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 252 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1121: | |
| | ACACCTCTTT TTTAATATAT GTGAACTATA TATAGTGTAT AGAGAGGTTA CTTGTTACTC | 60 |
| | AATATAAACA AAAATCAACT TTGTCAAAAT AAATGTGACA AAATTAAATA AAGTGTCATC | 120 |
| 25 | AATGTGACAG TATAGATCAT TTTGCAAAAA GTCAAAACAA AAAAATTGTT TTAGGGATTT | 180 |
| * A | TTCAAAATTT TCATTGTGGA AAATGATTTG nCAAAACAAA ACAACACnTT GTGAGCAATG | 240 |
| | AAGCTTCAAT GG | 25 ² |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1122: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1122: | |
| | NAATAATAGG CGCCACCTAA TAAACCAGCT GGAATGCCTA TCATTGGTGT TGTGAATGAG | 60 |
| | CTTAATACAA TAACAAGTAT TGTTAAAGCA ATGACGTTAT ACCAAGTTAC AGTCAAATTT | 120 |
| 45 | TTCAAATCCT CATATGATTG TTTTACTAAT TCTCTAAATT TCATGATTCA ATCTCTCCTT | 180 |
| | TTCTTAAATC AATTAATAGT TATACTGCAT TGCTTAAAAT CAANATATCT AATGAAGCAT | 240 |
| 50 | CTTTTAATCG TAAGTGTTAA ATGGTTTTCT TAATCAATTT GTTTGAATGT ATAANAGCAA | 300 |
| | TTAAAGCAAA AGTAATGTAA ATGAGGGTGT ATACAACAAT TACTACAATA ACCGGCATGA | 360 |
| | AGGAAATATT ACCCATCAAT TTCATAAATG CGATTGCGGC | 400 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 270 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-------|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1123: | |
| 10 | | 60 |
| | AATACAACCT TTTATCATAG TGTAAATGTA TTCTACCAGT ATTGAGAAGT TTTCATATTA | 120 |
| | TTCAATACCT GAAATCGCCA TAGTAATATT ACTAAATGCA CACTGCATAT GTTGTTTAAC | |
| 15 | AACACAACTT TAAAAATATA TTCTAACTCT ATCTACGAAT GTACTTAAAT ATCATAACAA | 180 |
| | TCTATTCCAA ATCNAATTAC ATTATTAGCT ACCTTAAAAA CCAAACCGAG GCCTTAGGCC | 240 |
| | TCGGTTTAAA TATATATAC GnGCGACATG | 270 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1124: | |
| | (i) SEQUENCE CHARACTERISTICS: | n |
| • | (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid | |
| 25 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (b) lopologi. linear | |
| | 270 YD YO. 1124 | - |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1124: | |
| | GGTCTTCTGT ATCAAATTAT ATTATGAGAG TTAGACTCAG TATTAATGAA ATCGTTGATA | 60 |
| | AAGATCAAGT GCTTGCATCA CAAATAGGTG GATTACTATG ATGTTTAATC AAATTAATAA | 120 |
| 35 | TAAAAATGAA TTAGAAGAAT CATATGAATC TGAGAAAAAA CGTATAGAGA ATGAACTGCA | 180 |
| • | AAATTTAAAT GAACTTAGGC ATAGAACTCG AAAAGAAAAT GAACGTAGTT ATGATGTTTT | 240 |
| | TCAATATTTG AAGCACGAAA TGAATTATAG TGAAGATGCC CAAAGGAAAA TGACGAGAAA | 300 |
| 40 | TATAGAAGCG TATGAGCAAG AAATCAATGA GATAATTAGA AAGCAAGAAT GGAAATTAGG | . 360 |
| | AAGAATATAA AGAAGACTTA AAAAAGTCTT ATGAAAAGCA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1125: | |
| 45 | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 377 base pairs | * |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 50 | (D) TOPOLOGY: linear | |
| | | |

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1125:

| | AAATATAYTC GATCATTGAT AATATGTGCT TTACTATTCC AAATAACTTT CAAATTTTGA | 120 |
|----|---|-----|
| | TAATATCAT CAATACTCTC AATATAACTA ACCAGTTTAT ACAACCATTC GCCATCGACT | 180 |
| ش | | |
| 5 | TTCACATATT TTTGAATACT ATTTCCAAYT TLAAGACGTG TTGGTTCATT TACAAAATGC | 240 |
| | CCCAAATTAA TACCACTTAA TAATCCAAAT GGAGTTGGAC GTGTTGACAT TCTAATTAAA | 300 |
| | TATTTTAATA AACTTTCTTT AGCATCTCTA ACCTTCTTGT TATCGCCATC AAAATTTATT | 360 |
| 10 | nCnTGTAAAG TACAATA | 377 |
| | (2) INFORMATION FOR SEQ ID NO: 1126: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 227 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1126: | |
| | GTTACATTAC TGTTCATGTC CACAACGTTT GTCAGCGATT ATCATCATTG TGTTATATCT | 60 |
| 25 | TATTTATAGC AAGTGCATGG TCTGGATAAG TAAAGGTATT CATACTTAAG TAACTTGAAC | 120 |
| | ATTGGTTTAG GACTATTTTA ATGGTNCTGC TTNAATTGTT GGCCAACTGG TTCTTATTTT | 180 |
| | AAATATGTAA CTAGCTCTAC GGGTAGTTAC TAAACACATC CTGGTTT | 227 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1127: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 717 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1127: | |
| | CCAATGATAC CGTTATAGCA TGTTAATGTT TTTGTACGAA TATAATCTAA AACTTCGAGT | 60 |
| | TCATCACTTA ATTTCCACGT TTCTGCTTTG TTTAACCACA TTAAAGGAGT ATGAATGnCA | 120 |
| 45 | AAATCTTTGT CCATAGCTAG GCTTAATGTT ACGTTCATTG ATTTTATAAA ACTATCGCGA | 180 |
| | CAGTCTGGGT AGCCTGAAAA GTCTGTLTCA CATACGCCTG TAATAATATG CTTAGCCCCA | 240 |
| 50 | ATTTGATAAG CIAGAGCGCC TGCAAACGAC AAGAAAAGTA AATTTCTAGC TGGAACAAAT | 300 |
| | GTATTAGGTA TACCATCTTC ATTATTAGTA ATTTCCATAT CATGTTGTGT TAATGCGTTT | 360 |
| | GGAGTAAGTT GTGATAATAA TGACATATCT AAAACGTGAT GTTTCATTCC TTGATCTTGT | 420 |

| AGTTCAACTT CTTTGAAATG TTTTTTTGCA TAAAAGAGAC ATGTTGTACT GTCTTGACCA | 540 |
|---|---------------|
| CCACTAAAGA CAACGATGGC TTTTTCATTA TTTAATACAC TTTCCATTTT GTAATTGCTC | - 60 <u>0</u> |
| CTATCATTAA TAATATTAAT AAAGAGGTTA ATGGCATTGA TAAGCCCGTT TTTAATTTAT | 660 |
| AAAATAAAAA AAGCCMATCT CCATAAAAGA TAGACGAMAG AAATGGGTTG CTCCTAT | 717 |
| (2) INFORMATION FOR SEQ ID NO: 1128: | ÷ |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 595 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| (D) TOPOLOGY: linear | |
| | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1128: | |
| GATTATTGCA TTGACAACTT ATATCTATCT AACGTTAGTA GCATTTAATT TCATTTCCGG | 60 |
| GGTTCTAACT TTACCAGGAT TAGCGGCGTT GGTATTAGGT GTAGGTATGG CTGTAGATGC | 120 |
| CAATATTATC ATGTATGAGC GTATTAAGGA TGAACTTCGA ATAGGTAGAA CGATAAAGCA | 180 |
| AGCCTTTTCT AAAGCAAACA AAAGTTCATT CCTAACAATT TTTGATTCTA ACTTAACAAC | 240 |
| AGTTATCGCC GCAGCAGTAT TATTCTTCTT CGGTGAAAGT TCAGTTAAAG GTTTCGCGAC | 300 |
| AATGTTATTA TTAGGTATTC TAATGATCTT TGTTACAGCC GTGTTCTTAT CAAGATTCTT | 360 |
| ATTATCATTA CTTGTTTCAT CAAATATATT CAAAAATCAA TTTTGGTTAT nTGGTGTTAA | 420 |
| AAAGAATAAA CGACATGATA TTAATGAAGG TGTAGATGTT CATGACCTTA AAACTTCATT | 1 480 |
| CGAGAAATGG AATTTTGTTA AATTAGCTAA GCCATTAATT GGAGTAAGTA TTTTAATTGT | 540 |
| AGTGTCGGTT AGTTATTCNT TATATCTCAA GTAAACTTAG GANTGANTCT CAAGT | 595 |
| (2) INFORMATION FOR SEQ ID NO: 1129: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 371 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1129: | |
| ATTTTAACTT TCTAAGAACA AGTTGTCAAG ATTTTTTCTT AACATATCAT GTTCTGTTAC | 60 |
| AATATTAATA ATGAATACCG AAAGGACGAA TTGCAAATGA AAAGCGTTGG CTTAATCACA | 120 |
| CANDADATC COTTOATAA TGGGCATCAA TATCATATTA ATCAATCTAA AAAACTTACA | 180 |

| | ATCTATAATA AGTTACTCGT GCAAAATGGC TTTCCACCGC TGTTTAGTTT CGGACTACCA | 300 |
|----|---|-----|
| | GCAACTGCAG TTATCACTGG CGNCATTTGC GACTGCCGTT AAGCGCGGTT TTGGTGCGTA | 360 |
| 5 | CATGCnTGGn G | 371 |
| | (2) INFORMATION FOR SEQ ID NO: 1130: | 12 |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 200 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| 13 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1130: | |
| | ATGATGATGA GATTATGACT TTGCGAAAGA TATCGGTGCG CCTTATGAAT TTAAAACANA | 60 |
| 20 | nTAAAGACCA TGGTCGTTAC CGGTAGTTAA CTTTGCAGCT GGTGGCGTTG CGACTCCTCC | 120 |
| | AAGATGCTGC TTTAATGATG GAATTAGGTG CTGACGGTGT ATCCGTTGGA TCCGGGAATT | 180 |
| | TTAAAACCAG AAGATCCCGG | 200 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1131: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 203 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | - Andrews | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1131: | |
| | ATGAGCTAGT CGATTAAAGT TAATATTTGA AAATGAAGCA GGGCATTAAA TGCAATAAAT | 60 |
| | TAAATAAGTT GTCATTAAAG CATTAATAAT AGAAATGATT TTAACAGGAA AAAAGTGATG | 120 |
| 40 | AATATTTGGA AAAGATATAT ATCGTGCACT GTCCTGAGAG ATTAGATTTG GGAAACCAAT | 180 |
| | TTATCCnTGA ATCGAGATGT nGC | 203 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1132: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 182 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 50 | (D) TOPOLOGY: linear | |

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1132:

| | ATCTAACAGT ATTGAAATCT TTGTTAGCGT CAATCGACCA TGTATTTTTA AGTATTGTCT | 120 |
|----|---|-----|
| | | 180 |
| | CTAACAACTT AGCACGACGT CTTAACCCTT TAGTAAACAA TCCTTCTTTA GnTTTAGTAC | |
| 5 | GT | 182 |
| | (2) INFORMATION FOR SEQ ID NO: 1133: | |
| | (i) SEQUENCE CHARACTERISTICS: | , |
| 10 | (A) LENGTH: 485 base pairs | |
| 5 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1133: | |
| | CAAATTTAGC CAGGNATACA AATACATATA ATAAAACTGT TTGTAAGCTT ACGTTGACAA | 60 |
| | | 120 |
| 20 | TCTGGCGTAA TTGGAAAACT AATGAATTT CTCCAAGTAG GTTTTACCCT GTAAACMAAA | |
| • | TAACAATTCm AATAATATG: AATCACAAAG CGACTAGAAA TCCGGTAATA TGACTAATCA | 180 |
| | TATATTCAAT GTGTAATAAT TTTAACAGCA ATAAATAGAC AACATAATAA TTTAACGTAT | 240 |
| 25 | TAATGCCGCC AACAATGATA AATTTTAAAA TTTCAGCATG CGTTTGTGTT AGTTTCATAT | 300 |
| | GTGTACTCCT CAACATCANA ATATATGCAT AACTACGTTC TCGAACATAC TCGAATATGC | 360 |
| | GAGCCAATCC GCTTCACTTC AAATATGCTT ATTTCAATCT TTATACCCTT TCACAGCAAT | 420 |
| 30 | | 480 |
| | TTAGTCTCTT TnCCCTCATC CTTATAGGCC nTATATGTAA CCGATTATCG GGTGGACTCA | |
| | TTGGC | 485 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1134: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 213 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1134: | |
| 45 | CTTGTTTTAT CGACAGATGC TGAACACGCA GTCAAAATAA ATAAATTACA TAATAAAATT | 60 |
| | CCAATTAATC TTTTCATAAT ATCATCCTTT TGTTTTTCAA TTGATATTCA TTTTCAATTA | 120 |
| | | 180 |
| 50 | TAAAATATTA YAAGAATTAG TCAACGCCTG TGAGTAATAC ACATCAGTAA CATTICTATI | |
| | TTCATTTATG ATATTATCTA ATTATTAATT TAT | 213 |
| | (2) INFORMATION FOR SEQ ID NO: 1135: | |

| 5 | (A) LENGTH: 526 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1135: | |
| | TGTGACTCCA TGTATTCATG TATCATTGTA CATTTGTGAA TTGGTTGAAA ACTGATAGTG | 60 |
| 10 | CCCGTTTAAT TACAGGTACT GAGGATGCTT TCAGGACATG GATTTGTTCG AAAATATGAC | 120 |
| | AATATTTCAC TATGGCTCTT CACTTCTCTA GGGAAATTGC TATCTTGATT AATCCAATCA | 180 |
| 15 | ACCANTICAC CTANTGGTGT GTCATCACCA AGAAAACTTT GCATAAATTC GTAAAAGCTC | |
| 15 | | 240 |
| | AATACCTCAC CTCGATTAAT ATACTTGAGC CATTAATATA ATACCATAAA AGAATGTGTA | 300 |
| 20 | TTTTaCATAA AACTTTTTAT AAAGCAATTT TATAAATCTA AATTTATTGA ATGTTTAAGA | 360 |
| 20 | AGTTGTGTAT AATGAAATAA ACGTGTTGAA ATAGTTAGGA TGATGTTAGT GGATATCAAA | 420 |
| | CATATGAAAT ATTNTATTGA AGTCGTTAAG CANGGAGGCA TGACTAATGC TTCCAAATCA | 480 |
| 25 | TTATATATTG CACAACCTAC AATTAGGAAA GCNATTAAAG ATATTG | 526 |
| | (2) INFORMATION FOR SEQ ID NO: 1136: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 321 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1136: | |
| | AGCAAAAGCA ATGATGACAA AAGAACAAGC TATGTTAGCA GATGGAAGTA TTAAACAAGA | 60 |
| | TCAATATGAT AAACAACTGT TATCGANAAT CGGAAAATCA CAATTAGATG AATTGTCTTC | • |
| 40 | | 120 |
| | TAAAGATTTA CAAGTTTTAG CTATTTTTCC GAGAGATGAA TGCAGGAACA GTTTTAGATC | 180 |
| | CACAAATGAT AAAAnATGGA AGATGTTCAG TGCAAAAAGA GTATGGCAGC AGTTTTCTCC | 240 |
| 45 | AGCAACTTTT CCANATTTAC CCAGGTGTTT AACACGTCCT ATTGGATTTG GGCTTAGGAC | 300 |
| | AATTATTCCA TATGGGCGGA T | 321 |
| | (2) INFORMATION FOR SEQ ID NO: 1137: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 330 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1137: | |
|------|---|------|
| | ATARATCCTT ATARATCAT GAGTTGGACG ACTTATCCAC ACARTTATAC TTTTTCAGTT | 60 |
| 5 | CTCTATATGT CAAATACCTG TGAATATGTT GCTAAAAATA GTATAACTTT GTGTGTAATT | 120 |
| | TCTAATTATC CACAATTCTG AAAACTATAA ATGTGCATAA GTGGATAMCT TTCCTTCTAT | 180 |
| | AGAGTATCTG TTAGTGAGTG TATCAAAACA GTTTGGGAAA TAATTLATAA AGTNTGTATA | 240 |
| 10 | AGAICTGTAT AAGGTGTTCG AACATTGTAA ACACTCATGC TTCGGACCAA ACTCATGGTG | 300 |
| | ATGTTATGAA ATTTGATTGC TCGCATCGnG | 330 |
| | (2) INFORMATION FOR SEQ ID NO: 1138: | • |
| 15 | (i) SEQUENCE CHARACTERISTICS: | : |
| | (A) LENGTH: 459 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | * |
| 20 | (D) TOPOLOGY: linear | |
| • 0• | | , |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1138: | |
| 25 | CTTGATAAGG GAAGATTTGC CAGCACCATT CGGGCCCATG ATACCAATTA TTTCGCCGCG | 60. |
| | TACTGGTATC GATAAGGAAA TGTTTTTAAG TACATGCTTA TTACCTAAAA ACAGATTTAA | 120 |
| | ATCTTTGTT TCTAACAAAC GTTTATACCT CCTAATTAAA AGTTTAGGCT AACCTAATTA | 180 |
| 30 | ATTGTATAAT AAACTGAGAA TATTTATCAT GTCAAGTAAA TTCGTGATAT AATATAGACA | 240 |
| | ATGTATGTGA GGTGAAAGTA TGTTAACTGA AGAAAAAGAG GACTATTTAA AGGCAATCCT | 300 |
| 35 | TACGAATAAT GGCGATAAAA ACTTTGTGAC AAATAAAATC TTATCTCAAT TTTTAAATAT | 360 |
| 55 | TAAGCCTCCA TCTGTAAGTG AAATGGTAGG ACGTCTTGAA AAAGCAGGCT aTGTTGAAAC | 420 |
| | AAAACCATAC AAAGGTGTTA GATTAACAGA GGATGGTTT | 459 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1139: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| , | (A) LENGTH: 165 base pairs (B) TYPE: nucleic acid | |
| 45 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • .• |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1139: | |
| 50 | | 60 |
| | TARATACTCT CGCCGGTTAT TTCGCTTCCT CTATACGGAT TGGCGAAAGA TACGGTGCAT | 00 |

CGGTTTCAAC TAGCAAACGC TCCATTGACA CATGCTTAGC AACTTCTTTA GGCTGTTTAG

| | (2) INTOMERITOR FOR SEQ ID NO: 1140: | |
|----|---|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 214 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1140: | |
| | ACCTGAATGC CCATCAATGA CAGACTGGAT AAAGAAAATA TGGTACATAT aCACTATGGA | 60 |
| 15 | ATACTATGCA GCCAGAAAAA AATGAGGTCA TATCTTTTGT GGGACATAGA TGCAGCTGGA | 120 |
| | GGCCATTATA TTTAGTAAAC TAATGCAGGA ACAGAAAAAC AAATACTGCA TGTTCTCACA | 180 |
| | GCAGGAGCTG AATGATGACA ATTCATGAAC ATAA | 214 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1141: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 229 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1141: | • |
| | GTTTCTAGTT GTTTATAGTT ATCGCATCTC TTGATGTAAA ATCTAAGATG TTTATGCATT | 60 |
| | TCTAGATGTT AATTCTTCGC TGCTTAAGAA TTATCTTGAT GGTAAATCTA GTTGTGCCAT | 120 |
| 35 | GCATTTTCTC ATGATGAATC TAAGGTGTTA ATTCATTGAT GTGTGCTGTT TCTTGnnGCT | 180 |
| | TCATTATCTT GATGGTGAAT TTCGTTGTCT AATGCACTTT TTCAAATGA | 229 |
| | (2) INFORMATION FOR SEQ ID NO: 1142: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 311 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 45 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1142: | |
| 50 | TTATGAATCG TAAACACTAT TATGAAATTG CGAGAGTAGT ATGGACAATT AGAATGATGG | 60 |
| | TTTGAGATNA ATGAGTGTTA TTAACCAGTG CGTCATTTTC AAAATTAGAT GCCATTTGCT | 120 |
| | GTTTATATTA AGAAGATTTC ATAATTAACT ATGATAAGAA AAAATAATAA TCCCCTTAAAT | 100 |

| | GGTAAATGTG TGAATAGGAA TATCGTTAAA CTAGTTGTGT TCATGCTAAT TTTAGTTGTA | 300 |
|-----------|---|---------------|
| • | GCAGTAGCGG G | 311 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1143: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 403 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · · · · · · · |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1143: | |
| | GATCATGCTG CTTATGAATT ATTAAAAGAG CAATTAGAAG ATGTGCTTGA TACATTAACT | 60 |
| | GATAGAGYAG AAAATGTATT ACGATTAAGA TTTGGTCTTG ATGACGGCAG AACAAGAACA | 120 |
| 20 | CTTGAAGAAG TTGGTAAAGT TTTCGGTGTT ACACGTGAAC GTATTCGACA AATTGAAGCA | 180. |
| i. | AAAGCACTTA GAAAATTAAG ACATCCAAGT CGTAGTAAAC GTTTGAAAGA CTTTATGGAT | 240 |
| | TAATTTATAT CAATTTTAAT GATTGATACC AAGACATGAA TAAGCGCTTA TTTATTTTTA | 300 |
| 25 | GATTAAGATT TAACTTGAGT GAGGTTGGTA CATTGAATAA TGTTCAACCT CTTTTTTCAT | 360 |
| | AAAGGAGAAT AAAATGATTT CGTTAAATAA CCGATTAACG ACn | 403 |
| | (2) INFORMATION FOR SEQ ID NO: 1144: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 612 base pairs (B) TYPE: nucleic acid | |
| 35 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | e e e e e e e e e e e e e e e e e e e | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1144: | |
| 40 | NTTTTTATTG ACGAATNGAT TTGGATGCCA GTGGTTTGGT CCTAAATCTT GAATGGTAAT | 60 |
| | CGGTATTTTG AAGTTGTCAT GTGCTACACG GTAACCGATA CChATAAGTA CGAGTGCGAT | 120 |
| | GACAATGGTT GTTACGAGCA AGATGTATTG TAACCATTGC TTGAACACAA CAAGTTGTAT | 180 |
| 45 | ATAAGGCTTC ATTGACGATA CCTCCAAACC AATACAGCTA AATTAATTAT CAAAAGTGCG | 240 |
| | ATGAASCTAA GATAGAAACT AGGGTGCAGT TCTAAAATGT AGTTGTTTAA AATAATTTCT | 300 |
| | AACAATTGAT TTGTTACAAC TGCGAACGGT TGAATATTGA AAACACCATT TGCTATATGT | 360 |
| 50 | TGTAAAAAA TCGTAGGTAT TGTTAAACCA GATAACACCA GGATGACAAT AGCTAATATG | 420 |
| | ACTITACTAA TACTATICAA CAAGCCTGTT GTTAAAAGTT CGATGAGTAA TAACCACAGT | 480 |

| | AAGATATTCG GAATACTGAA CACAATCCAA ACTACACCAA CGATACTCCA TAACATAGTA | 600 |
|----------|---|-----|
| | TAAAACCATG In | 612 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1145: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 223 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1145: | |
| | GAATTAATTA CGCAATATCC GCATCTTAAA TCAGTAATCG AAAAATATGC TTTAAAATAA | 60 |
| | AAGTGATCAA TGAAGTGGTT TGAAGGTTGT NAATAAACCT TTGAGTCACT TCCATTTTTA | 120 |
| 20 | AAnGTATCCT GGATGGAACC AGAATAGATT TGAAGCTTCA GCGGTTTTTA ATGAAAATAG | 180 |
| | CCATTAAATG ATTTGGAAAC GGTAAGAGGG GGTATTTAAA ATG | 223 |
| - | (2) INFORMATION FOR SEQ ID NO: 1146: | • |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 598 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 30 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1146: | |
| 35 | CGCTACGGTT GTCACGTAGA GATTAAAGAC ATTCGTTTTA GCAGTCTTTT TTATTGAAGT | 60 |
| • | AGACAATGCA AGATTAAATG GTAGTGTCAT TTCATTTTAT TCAACTGCTA GTAATACAAT | 120 |
| | ACTCAGTGTT ATTTCTGAAG ACTGGTTGAT AATGAGACAT GCATATTTAC AAAACTGTGT | 180 |
| 40 . | ATATTGTGTA TATTGTATAT ATACAGAAGT TGATAGGGGG ACGTTGATGA AAATAATTTT | 240 |
| | AAAAAACAAT AGTGATTTTC CGATTTATGA ACAGATTAAG CAACAAGTAA AACAAAATAT | 300 |
| | TTTAAAGGGA CATGTTGCTC CTGGAGAGCA TTTGCCGTCA ATGAGAGAAC TTGCCAAAGA | 360 |
| 45 | TCTTCAAGTA AGTTTGATTA CTACCAAACG TGCTTATGAA GATTTAGAGA AAGACGGTTT | 420 |
| | TGTTACAACA ATTAGAGGAA AAGGGACCTT TGTTAAGGAG CAAGATAGTT CTATTTTAAA | 480 |
| 50 | AGAGAAACAA TTTTTTACCA TGAAAATTTG GGTTAAAGGA ATTGGGTTAA TTAAGCnCAA | 540 |
| | GCCCATCCGA ATTGCCACTT GAGGGANTTC CAGGATATTT NACCGTCATT TATTGAGG | 598 |
| | (2) INDODMATION FOR CEO ID NO. 1147. | |

| | (A) LENGTH: 400 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|------------|---|------|
| 5 . | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1147: | |
| | CAAATCCAAG TGCAACAGCT TTATCAACCG CTAAAGCTAA ATCCGTATCA GCTTTTTCAG | 60 |
| 10 | CTTGAACTGG TTTGATTTGT AACTGTTCTG TTAGAAGTTG GCGTTCTTCT TTACTGACTG | 120 |
| | AATCAAAGTC TCCCACTGAG AAAAAAGGGA TAATTTGATG CTTCAATAAA ATCAAAGCAC | 180 |
| 15 | CTCTATCAAC GCCGCCCCAT TTACCTTCAT TACTTTTGGC CCAAATATCT TGCGGCAAGT | 240 |
| • | GTCGATCAGA ACATAATAAA TTTATATGCA TATACACTCA ACCTTTCAAT GCTTGTGTGA | 300 |
| | CTTTTTAAAA TCCCCTGGTT AAAGGAAAAT GAACNGGTTA CCAGCATTGT AGGCACCATT | 360 |
| 20 | TCAACACCAA CTTCGGCGGA TCNGGATTAC GCCTCCATCC | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1148: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 352 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1148: | |
| | TTTTATGGGT CGTATTTTTT AAAGAACAGT CATCTCAATC AAAAGAATAG AATTATGATT | . 60 |
| 35 | AAAATTGATG TIGTGTAATT AAAGTAAGAA ATIIKAAATT TCCTAGATAC TAGATAAATC | 120 |
| | GTTCAATATT TTATTAATAA GGAGGCCAAT GAYTGTGAAT TATCTTAAAC ATAAGTTTTA | 180 |
| | TAACTTGTTA ACTACAATGA TTGTTCTCTT TATTTTTGTA CTTTCTGGTG CGATTTTTT | 240 |
| 40 | AACATTTCTA GGGTTTGGTT TATATGGATT AAGTAGAATA CTTATTTATT TTAGGTTGGG | 300 |
| | TGACTTTACA TATAATAGAA GTATGTACGA TAACCTATNA TATTATGGCA GT | 352 |
| | (2) INFORMATION FOR SEQ ID NO: 1149: | |
| 45 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 916 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1149: | |

| | GGCAAGTGTC GATCAGAACA TAATAAATTT ATATGCATAT ACACTCAACC TTTCAATGCT | 120 |
|-----------|---|------------|
| | TGTGTGACTT TTTTATAATC CTCTTGTTTA AAGAAAAATG AACCTGTTAC TAGCATTGTA | 180 |
| 5 | GCACCATTTT CAACACAAAC TTTCGCTGTA TCGGTATTTA CGCCTCCATC AACTTCAATA | 240 |
| | TCAAAGTTTA ATTGACGTTC CATTTTAATA GCATTAAGAC CCGCTATTTT TTCTACGCAT | 300 |
| | TGATCAATAA ATGATTGACC ACCAAACCCT GGGKTAACTG TCATCACTAG TACATAATCA | 360 |
| 10 | ACAATGTCTA AAATAGGKTC AATTTGTGAT ATKGGKGTAC CAGGATTAAT TACTACACCA | 420 |
| | GCTTTTTTAT CTAAATGTTT AATCATTTGA ATAGCACGAT GAATATGAGG CGTTGATTCG | 480 |
| 15 | ACATGAATTG AAATCATATC GGCACCATGT TCTGCAAATG ATGCAATATA CTTTTCTGGA | 540 |
| | TTTTCAATCA TCAAATGTAC GTCTATAGGT AATGTTGTGC CTTTTCTTAC TGCATCTAAT | 600 |
| | ATTGGTAAAC CAATAGATAT ATTAGGCACA AATTGACCAT CCATAACATC AAAATGAACT | 660 |
| 20 | CCGTCGACGC CTGCTTCTTC AAGTCGTTTT AATTCATGTT GTAAATCCAA AAAATCAACA | 720 |
| | GATAATAATG ATGGATATAG TTTTGTCATT TAATATCTAA CCTTTCTATT TGAAATTTCA | 780 |
| | TTAAATAGTT GTAAATAATG GTCGTATCTA AATTGCGCAA TATTCCCTAT CTCTAATTGA | 840 |
| 25 | TGCnTAACCA TTACCATTAG GGTCCTTGGn AAGGNTACCA ATCCCAAACC TTACCATGGT | aóo |
| | TCCCCCATAA CGGTTT | 916 |
| | (2) INFORMATION FOR SEQ ID NO: 1150: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 35 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1150: | |
| 40 | AATTGGTTGT GGCTTCATAA TGTGCAGTTG CTAGACTGAC AACAACATCG TTTTCTAAGC | 60 |
| | | |
| | CTACGATAAA GACATAATCG TTTTCGGTTT TGTTGTTTTC TAATGAGCGT TTGATGATAC | 120 |
| | • | 120 180 |
| 45 | • | |
| 45 | GTTTATCTTC AGTTAAAGAT AAATTTAACT TAGTATCGTA AAGTTTAAGT GCTTCGTTGT | 180 |
| 45 | GTTTATCTTC AGTTAAAGAT AAATTTAACT TAGTATCGTA AAGTTTAAGT GCTTCGTTGT AATGTGGATC TTTGACAGAT TGAATGGTTT TAAATTCCAT AAGAACACCT CCCCAATTTA | 180 240 |

55

(2) INFORMATION FOR SEQ ID NO: 1151:

| | (A) LENGTH: 156 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|----|---|-------|
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1151: | |
| 10 | CACCGTAGTT GCTACCGAAT ACCACCATGT CGCCAGGTTG TGCTAAGAAG TCCGGTGTAT | 60 |
| | TITGGTATAC AGTTAGCTAA TCCGTCGAAG TTGTTAGCGA CGGnATATCT TTTGACCTAA | 120 |
| | ACCTTTTAGA GTAATCCAAA CAAAACTTTC CAACCA | 156 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1152: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | , : . |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1152: | 60 |
| | TCAATATATT TATTTTCTAA TGTTAGCATT AGACTGTCAA TTAACTTGCT AAGTTGTTCT | |
| | TTITTAGTAA TTAAATAACG CATATAATCA TCTAAATTTT TCATTTTTTC ATCTAGCATT | 120 |
| 30 | AAAAGGTAGT GCTTGATATT ATTTCTACTG TTGCTCCAAA AACTGnTCAA ATATACGTCA | 180 |
| | CATAGTCATA CTACACCTTT ATATAGTTTA AATACCAATn GCATGACCTC GTG | 233 |
| | (2) INFORMATION FOR SEQ ID NO: 1153: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 339 base pairs | |
| į. | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1153: | |
| 45 | TATATTANCT ATCGTTTAGT GAATCGTTTT TTTAAAGTAA AGAGAATTTC ATATATTACT | 60 |
| 45 | GGTACAACTA CAAGTGTTAA TAAAGTTGAT GAAATTMAAC CACCAATAAC TGTAGCAGCT | 120 |
| | AATCCTTTCG AAATAAGAAT CGNGCTATCT TGACCAAATA ACANAGGAAC TAATGCACCA | 180 |
| 50 | ATTGTTGCAA TCGCCGTCAT TAATATCGGT CTAATTCTAG TACCGCCTGC TTCGATTAAT | |
| | GCTTCTTTCA TCTCCATGCC CTGTTGCTCA TTATTAATAA CACGGTCTAT TAACACAATG | 300 |
| | TAGCATACC AATTCAACAT TAGCATACC | 339 |

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 817 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1154: | |
|----|---|-------|
| 10 | GTCACCCGAG GAGATATHCA ACTATTACCA TCAAGATGHG AAAAATGGTG CCTTGGGCAA | 60 |
| | TTGGTTTTTT CATTTTAATC TTAATTATTA TATTGTTCTT TTTACTAAGA AACTTCAATT | 120 |
| 15 | CACCTGAAGC GCAAACTAAA ATATTAGTGA ATGCGATTGA GAATAATGAT AAACAAAAAG | 180 |
| | TAGCAACATT ATTAAGTACT AAAGATAATA AAGTAGATTC TGAAGAAGCA AAAGTATACA | 240 |
| | TTAACTATAT CAAAGATGAA GTTGGGCTTA AGCAATTTGT CAGCGACCTT AAAAATACGG | . 300 |
| 20 | TACATAAATT GAATAAGAGT AAGACCAGCG TAGCTTCTTA TATTCAAACC AGATCTGGTC | 360 |
| | AAAATATATT ACGTGTAAGT AAAAATGGCA CACGTTATAT CTTTTTCGAT AATATGAGCT | 420 |
| | TTACTGCACC TACCAAGCAA CCAATTGTTA AACCGAAAGA AAAAACAAAA TATGAGTTTA | 480 |
| 25 | AATCTGGTGG TAAGAAAAAG ATGGTTATAG CTGAAGCAAA TAAAGTGACG CCAATAGGTA | 540 |
| | ATTTTATACC GGGGACATAT AGAATTCCAG CTATGAAATC AACTGAGAAC GGTGATTTTG | 600 |
| 30 | CAGGCCATTT AAAATTTGAT TTTAGACAAA GTAATTCTGA AACGGTAGAT GTTACTGAAG | 660 |
| - | ATTTTGAAGA AGCAAATATA TCTGTAACTT TAAAAGGCGA TACAAAATTA AATGATAGTT | 720 |
| | CTAAAAAAGT AACTATAAAT GACCATGAAA TGGCATTTTC AAGTTCCAAA ACGTATGGTC | 780 |
| 35 | CATATCCACA AAATAAAGAT ATTACCATTT CCAGCTT | 817 |
| | (2) INFORMATION FOR SEQ ID NO: 1155: | • |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 322 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1155: | |
| 8 | ANAGAAAATC TACTCTTTTA TTTCACCGGT CCTTTCnTAT CTCTCATTTG GCATACTCCT | 60 |
| 50 | TTTTCCATAT TTTCCACTTT CANTACAGTG AATTTACATG TAATTTTACA AATACAATAG | 120 |
| | GAGTGCACAA TGGAATATAA CACTTATCTT TATAAAATTA TTTTATATAT TGaCGCACTT | 180 |
| | AAAACAATCT ACAAATAAAA TTATTATTTT TAGTTTTCAA TGAATAATTC ATTCTTATCT | 240 |
| | | |

ATTTAAAAAT ACATTTAACT GC

. 322

| | (2) INFORMATION FOR SEQ ID NO: 1156: | |
|-----------|---|---------------------------------------|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 777 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • • • • • • • • • • • • • • • • • • • |
| 10 | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1156: | |
| | GTTTCCAANG GAANGNGAAA AGCGTCAACC AATGTAACTA TTTAAAGTCA AAGTGTTTGA | 60 |
| 15 | CCAAATTTGA CTTAATATGT AAAATAATGA GTAACAGTTA TTACAAGGAG GAAATATAGA | 120 |
| | TGAATTTAAT TCCTACAGTT ATTGAAACAA CAAACCGCGG TGAACGTGCA TATGATATAT | 180 |
| | ACTCACGTTT ATTAAAAGAC CGTATTATTA TGTTAGGTTC ACAAATTGAT GACAACGTAG | 240 |
| 20 | CAAATTCAAT CGTATCACAG TTATTATTCT TACAAGCGCA AGACTCAGAG AAAGATATTT | 300_ |
| | ATTTATACAT TAATTCACCA GGTGGAAGTG TAACAGCTGG TTTTGCGATT TATGATACAA | 360 |
| 25 | TTCAACACAT TAAACCTGAT GTTCAAACAA TTTGTATCGG TATGGCTGCA TCAATGGGAT | 420 |
| | CATTCTTATT AGCAGCTGGT GCAAAAGGTA AACGTTTCGC GTTACCAAAT GCAGAAGTAA | 480 |
| | TGATTCACCA ACCATTAGGT GGTGCTCAAG GACAAGCAAC TGAAATCGAA ATTGCTGCAA | 540 |
| 30 | ATCACATTT AAAAACACGT GAAAAATTAA ACCGCATTTT ATCAGAGCGT ACTGGTCAAA | 600 |
| | GTATTGAAAA AATACAAAAA GACACAGATC GTGATAACTT CTTAACTGCA GAAGAAGCTA | 660 |
| | AAGAATATGG CTTAATTGAT GAAGTGATGG TACCTGAAAC AAAATAATTC AAAGTAAAGA | 720 |
| 35 | GTAGACTAAG CNGTCTGCNC TTTTTGTATG AGTAAACCAA GGTGTCAATA ATTTGTN | 777 |
| | (2) INFORMATION FOR SEQ ID NO: 1157: | i . |
| 40 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 155 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | • |
| | (D) TOPOLOGY: linear | . • |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1157: | |
| | TAATGTTGGT AAATGGGTTA AGGCTCAAGG TCGTATTGAA GAAGATACAT TTATTAGAGA | , 60 |
| 50 | TTTAGTTATG ATGATGTCTG ATATTGAAGA GATTAAAAAA GCGACAAAAA AAGATNAGGC | 120 |
| | TGAAGAAAGC GTGTAGAATT CCACTTGCAT ACTGC | 155 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|--|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1158: | • |
| 10 | GACTGGTAAA ATTTACTTGC AAGTAAAGCT AAAAGGTCAA ATAGATAAAG AACAACTTGT | 60 |
| | TTTTCAAAAT GACAAAAATG AAGAATTTCC TTTTGTTATA AAAGATGAAA AGGATGACAC | 120 |
| | AATAGTAAGA ATTTTAATTG AACAGCATAT GGATAAAATC AATATGCATG TTAAAACGTT | 180 |
| 15 | GGCTGAAAAG AAAAATCTAG ATAACAAAGA AATGGTGTAT TCTATTCATT TTAAAGAGAA | 240 |
| | AAAAGTACAA CATGATGATG CAAAAGAAGT GCCTTCAAAA CATCAAAATC AAGAAAATAA | 300 |
| 20 | TCAAGATCAG CTTAAAANAG ATATTGATGA CAAANAAGAT AGTCAAAAAT CAGATACTAA | 360 |
| • | GGGAAAGACG TACTAGCCTT TTTACTGGAA AAAGGGTTTA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1159: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 347 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1159: | |
| | GTTGGTACAG TGTTGAGTGG CTTTGAATAT CGAACACAAA AAGAAAAGTA TGACAATTTA | 60 |
| 35 | TATAAATTIT TCAAAGATAA TGAAGAGAAA TACCAATATA CAGGCTTTAC AAAAGAAGCA | 120 |
| | ATAAACAAGA CGCAAAATGT CGBATATAAA AATGAATATT TTTATATCAC TTACTCGTCA | 180 |
| 40 | AGAAGCTTAA AAGAATATCG TAAGTATTAC GAACCATTSA TTCATAAAAA TGATAAAGAA | 240 |
| | TTTAAAGAGG ATGGACCAGC CAGAAAGAGT GATTACGCGC TATCAGTCAG TACACATGTT | 300 |
| | AGTCCAGGAA TTTCTAGCAT CNGTGTGTGA ATGANGGGTA CTTTATN | 347 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1160: | |
| 50 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 203 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |

| | ATAGTTATTA ATTAGTAGAA TGAGGATATT TAAATATAAA GGATAGTGTT GAACTTATGG | 60 |
|----|---|-----|
| | ACATGAATTI CGATTATACA TGAACGGTGT TGTAGAACAA GCAAGGAATG AAATTGAATC | 120 |
| 5 | TGCGGGATAT GAGCAATTAA CTACTGCAGA AGATGTTGNA AAGTCCAAGA TGGNCACCTA | 180 |
| | GTTATGATCA TCTGTATGTG GTG | 203 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1161: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 203 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | e* |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1161: | |
| 20 | AATTTTCCNT TTCCATTGAC ATAACAATAT TTAATGGGGC CCAGTTACAG GAAATATCAG | 60 |
| | TTTAATTTCG TCTTCAATAC CATAGTCATA ATATTGAGTT TCTTGTGTTG GAAAATTTCC | 120 |
| 25 | TACATAGTTA CTCATTTTAA TTTGTnCAAT GTTTGAATTC GGAGGCACTC TGTTAGCATA | 180 |
| 20 | TCTTTAAACA TTAAATATGG ATA | 203 |
| | (2) INFORMATION FOR SEQ ID NO: 1162: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 220 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · |
| 35 | | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1162: | • |
| | GCCATTTTGT TGATAAAGGT ATACTAAAGG TTATCGTTTT GAAATTTTTA GTAACTAGGA | 60 |
| 40 | TATGTTTCGT GTTATAGGAC CGGAATTTGT GGTATACGGT AAAATTTTAA TGCTATTGGA | 120 |
| | ATTTTTAAAA ATGGAAAAAC ATGGACATTn AAATTGGAAT TTCATAATAT GTCCTAATTG | 180 |
| 45 | GACTTAACTT GTTGGGAGTT CATTTTACTA TTTnTATGGT | 220 |
| | (2) INFORMATION FOR SEQ ID NO: 1163: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 409 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | TTCACGTGCT TTGCCATCIT TTAAGAAAAA CACAGAAGGC TTTTGCATTT GATTGTAATT | 60 |
|----|---|-----|
| | GGATGCCATA GAGTAATGAT ATGCACCAGT TGATAATATA GCAAGATAGT CTCCACGTTT | 120 |
| 5 | GACTGGATGA AGGTAATTTA GCGTCTTTAA TAATGATATC ACCAGACTCA CATAATTTTC | 180 |
| | CAGCTATAGT TACACTGECA TCTGCTTCTT CATTTCTATT AACAAGCAAT GCTTGATACT | 240 |
| 40 | TTGCGTCATA AAGTGCAGTT CTGATATGAT CACTCATACC GCCATCGATT GAAACATATT | 300 |
| 10 | TATTATTCTC TGGAATTTCT TTAATGGTTC CAACTTCATA TAAAGTAACG CCAGCLTCAC | 360 |
| | CTACAATTGA TCGTCCCGGT TCAATACCTA TTTCTGGTGC ATCTATACC | 409 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1164: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1164: | |
| 25 | CTAAATAATT GTTTAAATTT TTCTTTACTA TTTAGACTCT TTCGTTTGCC ATGACTTTGT | 60 |
| | TGACTTGCAA TGATATGAAC TTAATTTTTG CGAAAAAAGG AATCTAGATT CATATATTCG | 120 |
| 30 | GTAAATCTAC CTTCTTCATC TTTTTGAACT TGTAATTCTA GCAATTCACG TTGTATCAAA | 180 |
| | TTTTGAATAA CCATTGTAAT ATCACGTGGT TGCATAGTTG AGCCCTTCTG AAGCAATTCA | 240 |
| | ATTGAAGGCG TTTATTTGAG TTTCGAAGCA TAAATCAATT TAAGCAAAAG ACTAAATCTG | 300 |
| 35 | CTCATCTAAA CCTAAGTCAC GTAAGGTCTA ATAATCDCTC GTATCACTAC GGTCTGCTTT | 360 |
| - | AATGATATTA nCCAGTnCGT GCCCCTTTAA ATTAACCAnA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1165: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 327 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1165: | |
| 50 | TCGTGATTAT TATTAACATT TTTTAGTAAT TGATAAAAAT CTTTTCTCGC TTCTGTAGGG | 60 |
| | CTAGTGATAA TCATATAAAC CCTCCTTTGT TTTCTGTTAC GCTAATTATA GCGTACGCAC | 120 |
| | TTGAGTACGT CATATTACCA ACGAGTTCAT CGTATACTTA ATACCTATAT GCTATCGTTC | 180 |

| • | GGACACACTA CCGTnCCCTA CCGCTTAACC ATTTTCGGGC TTAAATATTT TNAAAATTTT | 300 |
|----|---|-----|
| | GTGAGGATCC GCTTAAAAAA CCCCATA | |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1166: | 4 |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 148 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 10 | (C) STRANDEDNESS: COMDITE (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1166: | |
| | TTAGGATTTC AAAAATATGT CAGGTTTTCT AACATAAAGC TTAAAACATT GATATAACTG | 60 |
| ÷ | CGATTTCGAC TTCTAAAACG aCATTAAACA ATCTACAGCT AAAATATTTT TTCAATTTTT | 120 |
| 20 | AAAAATAATC nGATAAATCT CCGCAAAA | 148 |
| | (2) INFORMATION FOR SEQ ID NO: 1167: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 243 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1167: | |
| | NAAGGTTATC GCTCGTAAAG ATGTTGTTGA AGAAGTATTT GACGACAGAG ATGAAGTGGA | 60 |
| 35 | TTTAAGTACA GCGCTTGTTA AAACCCTGCA TATGAAATTG GTGTATTACG AGAAGAGTAC | 120 |
| | ACTAAAGTTT TGGTCGTGTA GGTCTCAGCA GCGAACAGCA GTATGCACGT CTnCGTGTGC | 180 |
| | TGACGTGAAT TTTATTTGAG GATTATAGAC AAGAGAGACA ACTTACTGGA TTTTGCCCTG | 240 |
| 40 | TTG | 243 |
| | (2) INFORMATION FOR SEQ ID NO: 1168: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 321 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1168: | |
| | TTATATACTA CTATAAAGTA ATCCAACTCT CAAGAAGGTA AATGGGCAAT CAAAAGCTAA | 60 |

| | CTACGATATG ACGCACAAAT GTTTAGGGTA GGTGTTGACA TGTGTACAAA AACCAGCAGA | 180 |
|----|---|-----|
| | AAATGGTTGT ATTCTTAGGG AAGCATTCAT CCTGTTTGTT TATGGATTCA TGTTACGTTA | 240 |
| 5 | CGCAATATGT TTTTATGTAG CACAGCGAAG TTACAAGTTT ATACGCTATA TATCCATTGA | 300 |
| | TnATAAGCAG ATGAAAnCGG C | 321 |
| | (2) INFORMATION FOR SEQ ID NO: 1169: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 191 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1169: | |
| 20 | TCTACATATA AAATTACTCT AAAAATATGT ATAGTCATAA ATTGTTGGTT GATTTAATTA | 60 |
| | AAAGTATGGA AATTAAGGGG CTCTTATGTA TATAAAAAAA TGAATTATGA TAAAATGTAA | 120 |
| | GANAATATTT AGGGTCGATT GGAGAGATAC CAGTGGTACC AATTAGAAGA CGACAGTTTA | 180 |
| 25 | ATGTTACCAT A | 191 |
| | (2) INFORMATION FOR SEQ ID NO: 1170: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 303 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1170: | |
| | AATGTGGCAA GGATGTGTGA TATGACTACA CATTTAATAT CATCCTACAT AATAATTTTG | 60 |
| 40 | CGCGCCAAAT TATCACACAT ACCACACCTA CGATAACAAC CAGCAAATAA GGAGATAGCT | 120 |
| | ACACGTATTT ATCGTCCAAC GCACTACTAT ATGTTGTTGn ATGGGCACAA GTTACAAGTG | 180 |
| | CTGCGCGATA NCAAAAGGTA TACCCCTAAA ACGTCCCAAA ANAATCGGTT GCCCTCTAAA | 240 |
| 45 | TTGTTTGTGT GCCATGATTA GTAAGCTCCT ATGTTAGAAA CAAATTTTTA ATATGTATAT | 300 |
| | TAG | 303 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1171: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 299 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 55 | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1171: | |
|-----|---|-----|
| 5 | AAAAAGGTGA GAAGACAATA ACGNACGCCA ACACTAAAAA ATCCATTAAC TGGAGAAATT | 60 |
| | ATTAGTAAAG GTGAATCGAA AGAAGAWATC ACAAAAGATC CAGTTAATGA ATTAACAGAA | 120 |
| 10 | TTCGGTGGCG AGAAAATACC GCAAGLCATA AAGATATCTT TGATCCAAAC TTACCAACAG | 180 |
| 10 | ATCAAACGGA AAAAGTACCA GGTAAACCAG GAATCAAGAA TCCAGACACA GGAAAAGTGA | 240 |
| | TCGAAGAGCC AGTGGATGAT GTGATTAAAC ACGGACCAAA AACGGGTACA CCAGAAACA | 299 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1172: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 821 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| - | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1172: | |
| 25 | CCATAGCACC ATACCCATAA CCAACCCGGA TCCACTAACA AATAAGTAAT AATTNACACG | 60 |
| | TAAAGAAGTA AATAGTTTGT TTAGTTTTTT ATCAACATTA TCAATGTTTT CCTCGACAGA | 120 |
| 30 | CACTGGAATT TTAACGATAG CTGTACCATT TGTAATTGAG TAGTTCGTTA TTTCACCCAT | 180 |
| | ACTACTATTT GGTAAAATTG TTAATTCTCC TGAAATTGTA TTGATTCGTG TTGAACGAAG | 240 |
| | TCCAATTGAT TTAACTGTTC CCTCTGCTAC AGTTGTACCA CCGTTATTTA TCTTAACATA | 300 |
| 35 | ATCACCTACA TCAAATTGGC TTTCAAATAT AATAAAGAAT CCTGTAAETA CGTCTTTAAC | 360 |
| • . | TATAGTTTGA GCACCAAAAC CTACTGCTAA GCCTACGACA CCAGCACTGG CAATTACCCC | |
| | TTCAACACTA ATGCCAAATT TACTTAAAAT CGTCGTAATA ACTATAAACC AAACGATATA | 480 |
| 40 | CTTCACTACA TTTTGAACAA GAGATATTAA AGTTTTAGAG CGCTTTTTGT TACTCTTTTT | 540 |
| | ACTITIATIT TGAATCTTAA ATCCCTGTTC AATCATTTTA TTCAGTATTT TAATAACTAT | 600 |
| 45 | GAGGGCTACG ATAATATAAA TAACAATCAT AGCGATTTTA GTTGCAATGT TTTCATATGT | 660 |
| , | TTCTATTTTT GTTAATGGCT CAAATAGAGA TGAAATAATA TTCATGACTT GATTCATGAT | 720 |
| | AAGCGTTACT CCCTTCTATA TGATATATCA ATATTGLATT CATATTTLGA TATACTTCCC | 780 |
| 50 | AACCTACGAA AGTCTCAATA TATCTAGAAT CAAATGGTCA C | 821 |
| | (2) INFORMATION FOR SEQ ID NO: 1173: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|---------|---|-----|
| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1173: | |
| | | |
| | CCCGAAATTA AAATAATAAT GTATGAATTT TTAAATATGA TTTAAACGTT TTCAGTTTTT | 60 |
| 10 | ATGAAAACGC ATGCATTTTA CAAATAAAAA TGGTACGATG GCACTGGTTA AAACGTTTTA | 120 |
| | CTAAAAACAA ATCATGAGGT GTATAACATG GCTGTCTCTT GATCAGATCT TGATCCCCTG | 180 |
| | CGCCATCAGA TCCTTGGCGG CAAGAAAGCC ATCCAGTTTA CTTTGCAGGG CTTCCCAACC | 240 |
| 15 | TTCCCAGAGG nCGCCCCAGC TGGnCAATTC CGGTTCGCTT GCTGTCCATA AAACCGCCCA | 300 |
| | GTCTAGCTAT CGCCATGT | 318 |
| | (2) INFORMATION FOR SEQ ID NO: 1174: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 206 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | - 4 |
| 25 | (b) Topologi: Timear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1174: | |
| 30 | GTTTTAAAGC GGTTATAAAG GTAAATATGC AATATTATAA ATATCTTCTT CAGAACTAAC | 60 |
| €. | CGAATCTCTT AAACTCATCT GTTTAGATAG CGTTTCAAAT TGATAAGTTT TAATTTTAAC | 120 |
| | CGTTACAGTT TTAGCTGACT GCTGTAATTT ATTTGACGTG CAGCTGTTTT CCTGACAATn | 180 |
| 35 | CCATACTGTC TTAAAnCTCT GCATCA | 206 |
| , . | (2) INFORMATION FOR SEQ ID NO: 1175: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 40 | (A) LENGTH: 653 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 45 | | , |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1175: | |
| | TCTGCATCAT GATATTTTAC ATCATCACTT ATAAGAACGT CACCTACATT TAAACTTTCA | 60 |
| 50 | TCTAAAGCTC CAGCAGAACC TGTATTAATA ATGACGTCCG GTTTAAACTT ATTAATTAAT | 120 |
| | AATGTCGTAG AAATTGCAGC ATTAACTTTT CCAATGCCAC TTTGGGTAAT CACTACTTCT | 180 |
| | CTATCTTTTA AAATGCCAGT ATAAAATTTA ACATGTGCAA CTGAAATTTC GCTTAATTGT | 240 |
| <i></i> | | |

| | TTTTGATTCA CCTCTTTTAA AAAATCCTAG CATTTGTTAT TTTATCACAT TTTAATCACT | 360 |
|-----------|---|-----|
| | ACAACGACAA GTATCATGAT TTTCATTACT GTATAAAACT TTTGCTTTAT TTTTATAAAA | 420 |
| 5 | AGCTCTTTCA ATAACTTGGT ATCATAAATA ATTATTTTTG AACTCATAAC AGTGAATTCG | 480 |
| | ATGCTTCTAA TTTGTCTATT TTTCAAAAAC TAATCATATC AATTACATCA ACCAATCGTG | 540 |
| | TCAAGAAACT TTATTAAATA ACAGGAAAAT GATATGTTTA AAATAATAAT GATGAAATAA | 600 |
| 10 | GAGGATTTTA CAATGGCTGA AAATAATCAA AATAGTCTCG TAACAAAGAT AGC | 653 |
| | (2) INFORMATION FOR SEQ ID NO: 1176: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 410 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1176: | |
| | ACATGGCCGT TnGnATCAAG ATCGTCAACG ATTGATTGGT ACAATTGAAG TGCCTATGAC | 60 |
| 25 | ATTGGCAACC GTTGGCGGTG GTACAAAAGT ATTACCAATT TGCTAAAGCT TCATTAGAGC | 120 |
| | TACTAAATGT AGAGTCAGCA CAAGAATTAG GTCATGTAGT TGCTGCCGTT GGTTTAGCGC | 180 |
| 30 | AAAACTTTGC AGCATGTCGC GCGCTTGTGT CAGAAGGTAT TCAACAAGGT CATATGAGTT | 240 |
| 30 | TACAATATAA ATCATTAGCT ATCGTTGTAG GGGCAAAAGG TGATGAAATT GCTAAAGLAG | 300 |
| | tGAAGCTTGA AAAAAGAACC CCGTGCAAAT ACACAAGCAG CGGAACATAT TTTACAAGAA | 360 |
| 35 | ATTAGACACA ATAGTAAAGG CGALAGCGAT TAAAGAAAGT TAAGTCAGTC | 410 |
| | (2) INFORMATION FOR SEQ ID NO: 1177: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 146 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| . • | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1177: | |
| | CATCAAGATA ACTACGGTTA TAATCCAAAC GACCCAACAT CATATAACTA TACTTACACT | 60 |
| | ATTGATGGCA CAAGGTAACT ACCATTACAC ATGGGAAAGG TAACTNGCAT CCAAGTCAAT | 120 |
| 50 | TAAACCAAGA TAATGGCTAC TACAGC | 146 |
| | (2) INFORMATION FOR SEO ID NO: 1178: | |

| 5 | (A) LENGTH: 225 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1178: | |
| 10 | TGTTCCTGGT GGAACTTTGG TTTCTTAATG TCATTCCAAA TTGCTGTATA TTCATTCATT | 60 |
| | GGTATTGAAC TTATAGGTGT ACTGCTGGTG AACGAAAGAT CTGAAAAAAC CTTACCGAAG | 120 |
| | CAATTAATAA TGTACTATCC GTATTTATAT CTATATCGTG GTNATATAAT ATGTCATCAA | 180 |
| 15 | CTGGATnTAC GTCAATAGAC CTTCGTAACC TTAATATCGC GACAT | 225 |
| | (2) INFORMATION FOR SEQ ID NO: 1179: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 319 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1179: | |
| | TGTACGCATA TGGTATCACT TGATGACCAA TTCACTTTGT CGAGAATAAC GTTATTTAAA | 60 |
| 30 | GACATTGATT TAAAGAATTG GTATTMCGTT AATTGTATTA GACTTTTCAC AGAAGTAGCG | 120 |
| | ACAACAATGA TTTCATCGTA ACACGTGCGC ATATNAAGCA TGGGAAAAGA CATGGNCTAT | 180 |
| | TGACCTGGCC TTTTGTGCAC TCGTACGATT GGTCAAACGT GGCTATATTG AAAGTTTGAA | 240 |
| 35 | ACAAGATGCG ACGGACACAC ATGCACGGGT GGGGATAGAT CTTGAGTCTT ATTGAGACGC | 300 |
| | TGTGACTGTG GCTGACATC | 319 |
| | (2) INFORMATION FOR SEQ ID NO: 1180: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 654 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 45 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1180: | |
| 50 | TITTATCTTG GTTTTGAACT AGATATGTGT AGTCAGGTAT AACATAATCA ATCCCTAATA | 60 |
| | AGTTATCATC AGGGAATTTG ATACCTGCAT CGATAATGAC AATTTCGTCT TTATACTCAA | 120 |
| | CTGCATAAGT ATTTTTACCG ATTTCACCTA GACCTCCAAG TGCATATACA CCTACTTCAT | 180 |

| | TTCGTAATCT AAATGTGCGC CCTCTAATTT AGTGATAAAT TCGATATTAA AATTACGATC | 300 |
|-----|---|---------------------------------------|
| | TTTCAAGTAA CGACGTACTT GTTCTTCTGT TTGAGCTTCA ACATAAAGTG ATTGTGTATT | 360 |
| 5 | TTCACGCACA ATTACCTCGT CTCTGTTATG TTGATAAAAA ACTTTAAATA CTGCCATGTT | 420 |
| | AAAAATTCCT CCTAAGAATG TTTGTYTAAT TTATTGTTAA CCCTAGLAAA ATCGTATTGG | 480 |
| | AGTATATATC GATAAATTCA TTCCAATCAT CTCTATAATG TAACTTAATA ACGATTTGGT | 540 |
| 10 | TAATAACTAG GTTCATCATG TCGTTCATTT TAAAAAATTA GTGAAATAAC ACTAAAATTT | 600 |
| | CAGTTAAATC TTATTTTACA TGATGAATGA TAATAAATAA AGCAGTTTAT CTCA | 654 |
| | (2) INFORMATION FOR SEQ ID NO: 1181: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 231 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ÷ |
| 20 | (b) Topologi: Timeat | · · · · · · · · · · · · · · · · · · · |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1181: | |
| .25 | CGGGTATATT ATAGACAACG TTTAAGGACT TCTTTTTAAC TAACTTGTTA AATGTTGCTG | . 60 |
| | TATTTTTGTA TTCAACACTG TAATATAGTT CTTCTGACGC TGATGCATTA CTCATTGTAA | 120 |
| | TAGATATTAA AAGACTCAAT ATTATTAAAC TAATAATAGC GCGCTTTATG ATTTTCATAT | 180 |
| 30 | TCTAATCTCA AATGAATTCC AGAACTTTAT ATGGTTCAGG TGCGACAACA T | 231 |
| | (2) INFORMATION FOR SEQ ID NO: 1182: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 245 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | 0.1 |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1182: | |
| | TAAGTTTATT AAGCTCTTGT CCGTTAGCAA TCACGCTACC GCTAGAAATT TGGTCAATTG | 60 |
| 45 | AACTTAGTAC ATTTAATAAG GTTGTCTTAC CTGATCCAGA AGGCCCCATA ATCGCACGAA | 120 |
| | TTCGCCTTTT TGTATGTCAA GTAATATCTT AGGCTGAATG GTGCTTTACG AGTTTGAACA | 180 |
| | GTGCCGAAAA CGCAAGCCCC TTGATATCTT AAATGTGGAG ACTACAACnC ATCAGTGnCA | 240 |
| 50 | CGGGA | 245 |

1868

(2) INFORMATION FOR SEQ ID NO: 1183:

| 5 | (A) LENGTH: 490 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|-------------|---|------|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1183: | |
| 10 | AGGTAAAGAT GATGGTGTAG AAGTTTATGT GCATTGCGAA GATCATGGCA TTGTATTTAA | 60 |
| | TGCAAGTCTA CCTTTGTACA AAGATGCCAT CCATCAAAAA GGATCAATGC GTAGTAATGA | 120 |
| | CAACGGTGAT GATATGAGTA TGATGGTGGG TACAGTGCTG AGTGGCTTTG AATATCGAGC | 180 |
| 15 | GCAAAAAGAA AAGTATGATA ATTTATATAA ATTTTTAAAA GAAAATGAAA AGCAATATCA | 240 |
| | ATATACAGGT TTTACTAAAG AAGCAATTAA CAAGACGCAA AACGTCGGGT ATCAAAATGA | 300 |
| | ATATTTTAT ATTACATATT TATCAAGAAA TTTAAAAGAA TATAGAAAAT ATTACGAACC | 360 |
| 20 | ATTGATACAT AArcAATGAT AAAGAGTTLA AAGAAGGTAT GCAACGAGCT AGAANAGAGC | 420 |
| ÷ | TAAACTATHC TGCTAATACA AATACTGTAG CAACGTTGTT TAGTACGAAT GATGAAAGGA | 480 |
| 25 | ATAGAAAGA | 490 |
| | (2) INFORMATION FOR SEQ ID NO: 1184: | |
| 30 . | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| • | (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1184: | |
| | CTCGCATTTT AATAAATCAT ACTCTTCTTT TCTTGCATAC GAATTAGAAT AACTCGCGAG | . 60 |
| 40 | ACCTATAAGT CTCTTTCCTC ACTAGATAGT TTATACTTTT GGTCnGTTGA AGTCAATAAT | 120 |
| 70 | TTTATCTAAA GCTATAAAAA ATCTTTTGAT AGC | 153 |
| | (2) INFORMATION FOR SEQ ID NO: 1185: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 164 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1185: | |
| | TCATTTATAT ACTGTATCAC GCTATCTTTA GTATGTGTGC ATMATCATTC GTTAGTGCGT | 6 |

| | AATGAACGTT ATATTTTAAT TCATGATTTA CTAAGACCAA CAAT | 164 |
|-----|---|---------------------------------------|
| | (2) INFORMATION FOR SEQ ID NO: 1186: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 143 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| * * | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1186: | · · · · · · · · · · · · · · · · · · · |
| 15 | CACAAGTGAC GTCATATTAT AAAAGTCACT CGGTTTGCGA TACGTTCTGT CTAAGAAATA | 60 |
| | GCGACGTGCA ATTTCATATT TTMTATAAAC ATCCGTTGAA AAAGGACATA AAACCATGCG | 120 |
| | TTGAACCAGG GTCTATACTT TCT | 143 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1187: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 209 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 25 | (D) TOPOLOGY: linear | 1 |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1187: | |
| 30 | CGTACAAGTT AAAACGTTTA TACGATTACG AAAAACCACC GAAGAGTGAG AAAGATCCAA | 60 |
| | TGGTTGTATA TGCAGTAAGT GCAGGATACA AATGGTTCTT TGCTTATCCA GATGAACATA | 120 |
| | TAGAGACTGT TAATACATTA nCAATCCCTA AAGATGTCTG TTTATTAGCT CAGCATGANC | 180 |
| 35 | ATACAGTTCG GTCACATAGT GTCAATTCA | 209 |
| | (2) INFORMATION FOR SEQ ID NO: 1188: | , |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 243 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | (D) TOPOLOGI. TIMELE | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1188: | о Э |
| | TTGGAATCGC TGTCGACGGA TAGCAACCTG GATTGTAAAA ATAATGTTGG CTTTAAAAAT | 60 |
| 50 | ACCGTGGCAA TATTAAATGA ATAATCGCTG CTGAATATAC ACCCAATGCA CATTGAACTA | 120 |
| | ACATAAnCCC ATTTGACTCA TCTACGCCCA CTATTGGCTT TATAGTCACT GAACTAAGCT | 180 |

| | TAT | 243 |
|------|---|------|
| | (2) INFORMATION FOR SEQ ID NO: 1189: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | (b) Torobodi: Illiedi | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1189: | |
| 15 | CACCAGGCAT TACCATACCA GCACTCATAC CACCAATCAC KCTCGATAAC ATCAATACCG | 60 |
| 15 | AAAAATTGTG GCCAACTGCA AACATAAATT CTGACACTGA AAACAAAATT AATCCTATAC | 120 |
| | ATATAATTAA TITCTTCCCT AATTTGTCAG CTAGCGTACC ACCAAACGGC GATATAATCA | 180 |
| 20 · | TTTGAGATAA CGCAAAAGCA GCAACTAGTA ATCCTAAATC ACTACCAGTT AATCCCAAAT | 240 |
| | CTTTTAAATA AACAGGCAAG ACTGGTATTA CTAAACCGaT ACCTAAAAAA ATCAAGAAAA | 300 |
| | TATTAAAATA TAAGACAAAA ATCTGTTTAT TCATATGCTC ACCTCTTTTT TCTCCATGTC | 360 |
| 25 | ATGCTTAAAG CTGTTATTCT TCTTTTCCAC GACAGATTGC AATTCATGCT AAATATTCGT | 420 |
| | AAAAAGTTTC TATATTGTAT TACAACATTG CTACATTTGA CAATATTTTE TCTTTGTAAT | 480 |
| | TATCACTATN TTCCATTTAA TTGTATAATT AATGACATAT TNNAATA | 527 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1190: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 889 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1190: | |
| 40 | AAAACGTGGC AGTAATTCAG TGTATGTTCA ATATGATGAT ATTATGTTTT TTGAATCATC | 60 |
| | AACAAAATCT CACAGACTCA TTGCCCATTT AGATAACCGT CAAATTGAAT TTTATGGTAA | 120 |
| 45 | TTTAAAAGAA CTGAGTCAAT TAGATGATCG TTTCTTTAGA TGTCATAATA GCTTTGTCGT | 180 |
| | CAATCGCCAT AATATTGAAT CTATAGATTC GAAAGAGCGA ATTGTCTATT TTÄAÄAATAA | 240 |
| | AGAACACTGC TATGCATCGG TGaGAAACGT TAAAAAAATA TAATAAGATA ATAAAGTCAG | .300 |
| 50 | TTAACGGCGT ATTCAATTGT AAATCTTGTT GGATTTTAAC AAGATAACTA GCAAATGCAC | 360 |
| | TGTATAGCTG GCTTTTAAT TTTATTAACA AAATTAAATA TGACGCGTGA ATTAAAAAAT | 420 |
| | | |

| | CTCTACAATC CTATGGCGCA ATTTTTAACA AAATATACTA AATETGAAAT TGACAGTTTC | 54 O |
|----|---|-------|
| | CATAAATAAA ATGCTATAAT TTCCTACTCC GTGAATCTTA TTTTGTTTTA AAAAACAGTG | 600 |
| 5 | TAGCACAAGm TTCAACTTGT TTCCTACACT GTTTTATAAA TGAATTATTT AAAATGCTTG | 660 |
| | TTCAACCTCT TGTAATGTTG GCAAACTATT AATAGCACCA TACTTCGTTG TCACTATTGC | 720 |
| | AGCAACGCGA TTGCTAAACG CTAAAATTTC CTCACCTTCA TTTTCAAATA ACTGAGTTAA | 780 |
| 10 | ATTTAACACA TCGGTTGCTA AAATCCTGCT AATAACTGCA CCAATAAATG CATCCCCTGC | 840 |
| | CCCAGTTGTA TCAACAGGTT TTACCTTATA GCCACTATGA TAATGATTA | 889 |
| | (2) INFORMATION FOR SEQ ID NO: 1191: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 254 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ě |
| ., | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1191: | |
| 25 | AGTTAAAGGC GTTGAATTAA TGGCCTTCCC ACACATGACA TATAAACAAG CGTGCGCCTA | , 60 |
| , | TGGTCTGATA ACCAGATACA CGTTTGAATG GATTAATTGC GTTCTCAATT AGGCGTGATA | 120 |
| | TGGCTTTAAA GATTTNAGTC TGTTGAAATG ATGGTGAATT AAAGCATTGC GCTAAAGGTG | - 180 |
| 30 | CACTGACAAT ATCTCGTAAA GATATGGTGC TTTAACAGAT TTGTAACATC TATGGTCTAA | 240 |
| | ngatacggg TTAA | 254 |
| | (2) INFORMATION FOR SEQ ID NO: 1192: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 189 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1192: | |
| 45 | GGCTCATAAG TTACACCTAA TGCATCTTCA TCTGGAAGCT GTGGTTTATC ATCTTCTAAA | 60 |
| • | TCAGCAGTTG GCGTTTTTC ATATAATTCC TTTGGCGCAC CAAGATACGC TAATAATTGA | 120 |
| | GCTGTGTATn CTAGGCATCC ATACCGTATT CGTTAAACCA GTATATTTCA GCTGAATGAT | 180 |
| 50 | CTGTCCTAC | 189 |

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(2) INFORMATION FOR SEQ ID NO: 1193:

| | (A) LENGTH: 215 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|-----|---|-----|
| 5 | | 1 |
| - | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1193: | |
| 10 | TTGATATTGA TCGATGACCG GTGATGTGAA ACTGAAACTG ACCAATGAAT GAAAAAATGG | 60 |
| . • | GCAATGTTTT TGACAACAAT GGTCATTTAC CAAATAAAAA TATTGnCACC ATTAATACCT | 120 |
| | GNCAAACGTG TTTGTTCCTA AACCTAAAAT GATAAATCCT ATTGAGATTA TGGACTTGGT | 180 |
| 15 | AAGCTGCAAT CTTTTTAATA TCTTTATAAG CAATG | 215 |
| | (2) INFORMATION FOR SEQ ID NO: 1194: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 158 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1194: | |
| | AGAATTTGCn ACTGGTTTAC CAACGCATCT ATGTTCGGTC GCTATACCGC ATACAGATGT | 60 |
| 30 | CGAACATATT AACCATAGAA CGTAGGTGTG GTGTTCTAGA AAAAGAAGTG CCGTTATTGA | 120 |
| | AATGGGACAC TTGATCAACA GCCGAGTGAA ATCGTTTT | 158 |
| ÷ | (2) INFORMATION FOR SEQ ID NO: 1195: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 180 base pairs (B) TYPE: nucleic acid | |
| 40 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear |);- |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1195: | |
| 45 | ACTGATTGCC GTGTCTGTGG TTGATCATTG ACTAATTGTT GGCCATCATT GGnTTCTTGG | 60 |
| | TCTAATAGTC CTCTTGCTCC TGCGTCGTAA CATTGATGCC AATCATGCAC CACAGCCTTT | 120 |
| | CGGTTCATCA TAACATTTCT GCCAATGTCT CTACATGACA CGGGCTCATA TTTCTTTCTG | 180 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1196: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 274 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1196: | |
|------|--|-----|
| | GTTAAAGCGA ATTATTCACA ATATAAAAAA TCATCTGATC AAGTCGTATT AGAATTAGGT | 60 |
| 5 | ACAAATGGCG ACTITACTGT CAAACAGCTC GACGATTTAC TTAATCAATT TGGAAAAGCC | 120 |
| · | AAGATTTATT TAGTTAATAC ACGTGTTCCA AGAATTTmTG AGGGCAAATG TAAATCGATT | 180 |
| 10 | ATTAGCTGAC GCGGGCGAAA CGGAAGTCCC AATGGTCACA TTAATTGGAT TGGGTATTAG | 240 |
| v. · | GCGCTTCACA AGGGACCTTG GTGGAATATT TTTG | 274 |
| | (2) INFORMATION FOR SEQ ID NO: 1197: | |
| 15 | ALL ADDRESS OF THE PROPERTY OF | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 154 base pairs | |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| -00 | (D) TOPOLOGY: linear | |
| 20 | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1197: | |
| 25 | ACGTAACCTA TATTCATCTC TGTTCCCAAT AATAATAACA ATACATAACT GATATTAGCT | 60 |
| | GTCTTTCATC TCTAATTAAT ATGCGTCATG AGCTAATATC GGTTATTTTT TTGTGTCAAA | 120 |
| • . | NAATTTTAT TTTATCTCTC CATCGCATTA ATTG | 154 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1198: | • |
| | (i) SEQUENCE CHARACTERISTICS: | * |
| | (A) LENGTH: 249 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 35 | (D) TOPOLOGY: linear | |
| | | |
| | | 4 |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1198: | |
| | AATCCTCACC CGTAATAAAC TCGTTTTGAA TGCGTTGTTC GAACTCACGG TATATTAAAG | 60 |
| • | CAATATCCTC TAACTTATTT TTAGTTCGAG TTTGCATATT TTTATCAGCA ATAAAGTGTT | 120 |
| 45 | CTAAATGTTC AGGCGTTACT GCATATTTTT TAAAATCTTG AATTTGTTCT GTTAATTTTT | 180 |
| | CACTAAACCC ATAATATTTT GCTTGTGATT GATAAAGTTT TAAATACTTT TGTTGTTCnT | 240 |
| | GAACAATGn | 249 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1199: | |
| | (i) SEQUENCE CHARACTERISTICS: | |

| ÷ | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1199: | |
| | TTGGTAAAAA TCGACATCAA ATACTAAATC TGATCCATCT GAATCCCATG TTTAAAACCG | 60 |
| 10 | AACTTGTGCA TTAATTGTAA AGTTCAAACT CTTCATCTTC ATAGATCGCG ATGCGTCTTT | 120 |
| | TAATTCTTTA GGTGATACTT TGTAGATCTA TAACAAAATT AnCTA | 165 |
| | (2) INFORMATION FOR SEQ ID NO: 1200: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 236 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1200: | |
| 05 | TTATTAGCGA TTAAAAATAT GTCCTTTTT AATAAAGGAG ATATATGTTT AATTGGATGT | 60 |
| 25 | CAACATCGGA GTCATTGGCG AAAAATAGGG CTGCGGTCGA TGGAGTTCAA AACTATTTTA | 120 |
| | ATGCATTACA TGTTGTGAGT NAAGAGCAGG CGTACTTTTC TTTTCAAGGA TGTGACATAT | 180 |
| 30 | CACAGAGCGT ACAATAGAAA CTCAGATACC ATTACATGGA nAGTCCGCGT CCAATG | 236 |
| | (2) INFORMATION FOR SEQ ID NO: 1201: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 146 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1201: | |
| | TAATGCTAAA CAGTATTATG GAGATAATGG CTTAGTTCAA ATTTCTGATG NAAGTCAACA | 60 |
| 45 | CTTCTAAAAT TTGTAAATGA AGCATTAGAC AATAACGAAC AATCAGTTGA AGATTACAAA | 120 |
| | AATGGTAAAG GCAAAGCTAT GGGCTT | 146 |
| | (2) INFORMATION FOR SEQ ID NO: 1202: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TODOLOGY, linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1202: | |
|------------|---|-------|
| | ATTGATGATA GTATTGATGG TAATACCATA AACATACAGC ATTATCACAA GTAAAAGTAA | 60 |
| 5 | GCCTAAATGT CCATAAAATC TACTTGTCAC AATATATGTC GGTATTATCG TAACGGGAAG | 120 |
| | TCATTTCGTA CTTGATTAAA CTTTTGTGTA ATTGCTTTAG TACCTTCTAA ATACCTGGTT | 180 |
| | GATGAGACCA CATACTGATA CCACCATAAC CATAAACAAA AGGTACACCA GAATTGGGCA | 240 |
| 10 | TACTTCTTAT TCCATCCAAA CCTCCGTAAC CTAATTGCTA CGGGTAATAT TCCAGCACAC | 300 |
| for er | TAATAGTATT GATGTAATTA ACTGAACGGC CGCTnGATAA TAAGTCTTAC AGTCTTAAAC | 360 |
| | GTCCATGCGC ATCnTnACCC ATTCA | 3,85 |
| 1 5 | (2) INFORMATION FOR SEQ ID NO: 1203: | |
| | A CONTRACT CHARD COURT COTTCC. | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 580 base pairs | |
| 20 | (B) TYPE: nucleic acid | |
| 20 | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1203: | |
| | ACATTGAACG AGTACAGAAA ACTTATTGNA AATAAAGGCT GTTAAAGATA AAGAAGAAGA | 60 |
| | TACTTACAGA GGTAAGTATT TTGCGGAAGA AAGAAAAAC GAAAAATTGG AAAAAGAAAA | 120 |
| 30 | TATAAAACTA AAAAACAAAA TTTATGAATT ACAAAACGAA GAAGATAACG AGGAGGACGA | 180 |
| | AGAAGACAAG GAGGACGAGA ACGATGTATT ACAAAATTGG TGAGATAAAA AACAAAATTA | 240 |
| 35 | TAAGCTTTAA CGGGTTTGAA TTTAAAGTGT CTGTGATGAA GAGACATGAC GGTATCAGTA | 300 |
| 33 | TACAAATCAA GGATATGAAT AATGTTCCAC TTAAATCGTT TCATGTCATA GATTTAAGCG | 1 360 |
| | AACTATATAT TGCGACGGAT GCAATGCGTG AYGTTATAAA CGAATGGATT GAAAATAACA | 420 |
| 40 | CAGATGAACA GGACAAACTA ATTAACTTAG TCATGAAATG GTAGGAGGTA TGANAAGTGA | 480 |
| | ATGATTTACA AGAGAGAGA TTAGAAACAT TCGAACAAGA CGACCGATTC AAAGTAACTG | 540 |
| | ATCTAGACAG TGCTAACTGG GTTTTTTNAG AAACTNGGAT | 580 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1204: | • |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 139 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | ATCGTATGGT TGAGGCGAAT TTAACTGAAA AATTAGACAA CGAATCTTGA TGAAAAGANA | 60 |
|----|--|-----|
| | ATGATTGGCT AAAATAGCAG CTAATCAAAT CAACGATAAT GAATGCTTAT TTATCGTGCT | 120 |
| 5 | GGTTCATCTA CATTGGAGC | 139 |
| | (2) INFORMATION FOR SEQ ID NO: 1205: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 229 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1205: | |
| ٠. | AGGAGGATAT CAGACTTACA PACTATTCTT TATCATACTG PAATTCAAAT AGACACCTTA | 60 |
| 20 | ATTGAAGAAG GCGTTGACGC GCTACTTTTC rAAACGTATT ACGACCTNGG AAGNGTTAAC | 120 |
| | AAATGTCATT TCCACGGAAC GGGGAAAGGA AATACGGCGT TGCCAATCCA TTGCTCCAAT | 180 |
| | TGAACCGGTT GCAAACACAA ATTGACTTGG TTGAAGGGGC AGGCATGCA | 229 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1206: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | • |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1206: | |
| | TCGACAAGTT TTTAACAGTT CGTTATTATA TGAATGTAAG TAAAAATTTC TTAGCTACAA | 60 |
| | CTTACATATT ATAAATGCAT AAATTAAACA AAAAGGGGCG AAAAAAGTTG ACTCATTTAT | 120 |
| 40 | CAGATTTAGA TATTGCGAAT CAATCAACAC TACAACCAAT TAAGGATATT GCTGCATCAG | 180 |
| | TAGGTATITC AGAGGATGCA TTAGAACCTT ATGGTCATTA CAAAGCTAAA ATCGACATTA | 240 |
| | ATTAAAATTA CGCCAAGAGA AAACAAAGGG AAGTTGTTTT AGTTAACTGC GATGAGCCCA | 300 |
| 45 | ACACCAGCTG GTGAAGGLAA tCMACGGTTA CAGTTGGLTT AGCTGaTGCA TTCCmTGaGT | 360 |
| | TaATGAAAAC GTTATGGTTG ccTTaGGGGG CCTGCCTTT | 399 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1207: | |
| 50 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 138 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1207: | |
|----|---|-------|
| | ATAAACAATA CGATTTGTAT GCTACTTGTC TGAAGACAAC ATAAAACAAT ATGTTAACTG | 60. |
| 5 | ATATTGAGGA TATGGGCTTT CAAAATCCAN TTCAAAAAAG GTTATGTTGA AATATGACGC | 120 |
| | GGTTGTTGAA AGAGACCC | 138 |
| | (2) INFORMATION FOR SEQ ID NO: 1208: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 655 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1208: | |
| 20 | AGTCGCCTAA CTTTTATTAT CAGTCCAATC AGTTTCATCA AGTATAAATG TTATTGCTTA | 60 |
| , | TTTTTGTATT CTTGGCGTAT TTTTTGTTCT TCTGCATAGC GCTCTGGATT TTTCTTATAA | 120 |
| | AAATCTTGGT GATAGTCTTC GGCTTTGTAA AATTGTGACG CTGGTALTAT TTTTGTTGCA | 180 |
| 25 | ATTGCCTTAT CAGCATTAAT CGTATTTTTA AGCTGCTCGA TATAAGTCTC AGCGAGTTCT | 240 |
| | TTTTGATGAT CATTAGTGTA GAAAATAGCT GTTThATATT GAGGACCACG GTCTTGATAT | 300 |
| | TGACCACCTG TATCTAATGG GTCAATGACT GAGAAAAATA TTTCTAATAA CTTATTGTAT | 360 |
| 30 | GAGAATAATG CAACATCATA TTGAATTTCA ACAGTTTCTA AATGACCACT CGTACCTGAT | 420 |
| - | TTTACTTGTT CGTAAGTAGG ATTTTCAATA TGTCCGCCCA TATATCCAGA AGTTACTTTT | 480 |
| | TCTATGCCGT CAAAGGTGTC AAATGGTTTC GTCATACACC AAAAGCAACC TCCGGCAAAA | 540 |
| 35 | TAAGCTGTAT TAATATTCAT TTTTGACATC CTTTCCATTA GACCTTAGTA CGATTTATTA | : 600 |
| | AGAAATCACT TGCTTTTTGA ATTGTTTTTA TATAACGTTA ATANGNGATT ATNAT | 655 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1209: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 213 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1209: | |
| 50 | CCGnCCCCAA TGGAAATTAC CTTTGGTnCC CCATTTTAAT TGTTAAATTA TTGGAGTGTT | 60 |

| | AATCTCACTA TCTTCAAATA AGCTTGTGTA TAGTTTAACA GCTTCTTCAG CTTGGTTATT | 180 |
|------------|---|-----------|
| | AAACATTAAA AATGTCGTGA TTTTTGGAAT ATC | 213 |
| . 5 | (2) INFORMATION FOR SEQ ID NO: 1210: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 149 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1210: | |
| | TTGATTGCAA CTTTGATAGT GAAAACATTT ACATGATGTT GTCACTGGTG CACGGGCGTC | . 60 |
| | GAGAACAATC ATTGCGTTAT TGACGGTGCT GCCCTGCTGT CTCAGTTTGT TGATGCAAGC | 120 |
| 20 | ACTACACGAA ACCCAATAGC nTCACCAGG | 149 |
| | (2) INFORMATION FOR SEQ ID NO: 1211: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 142 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1211: | |
| | AATGTTTCTC CTAATTTTAA ATGTTTAGGA ATATTAACTA GGATAATAAA TCCAGCGACA | 60 |
| 35 | TCCCAAATGG GATTCATATA AGAATGTTGG ATGATAATnT TGGCCGTTAA TATACATATT | 120 |
| | TTCTATTATA AAATTGGGCA AA | 142 |
| | (2) INFORMATION FOR SEQ ID NO: 1212: | - |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 163 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212: | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212: TTTAAATTTA GTCACTTCAC CTTTTAAAGC ATGTTCATAA AATGTTTGCA TCATCAATGC | 60 |
| 50 | | 60 120 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 765 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|------|
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1213: | |
| | GTCACCTTC ACGTCTGAA GAAAAAGGCT ATATAAGAAG AGATCCAACG AAACCACGTG | 60 |
| | CTATAGAAAT TGTAAGTGAT CAAACAAATG ATAATATTAA TATGGAAGAA ACGATTCATG | 120 |
| 15 | TGCCAGTTAT TGGTAAAGTC ACAGCAGGTG TTCCTATTAC CGCAGTAGAA AATATTGAAG | 180 |
| | AATATITICC ATTACCIGAA CACTTAACAT CGACACAA TAGCGACATA TICATATTAA | 240 |
| | ACGTCGTAGG CGACAGTATG ATTGAGGCTG GTATATTAGA CGGAGACAAA GTAATTGTnC | 300 |
| 20 | GCAGTCAAAC CATAGCAGAA AATGGAGACA TTATTGTTGC TATGACTGAG GAAGATGAAG | 360 |
| | CAACTGTCAA ACGCTTCTAT AAAGAAAAA ATCGTTATCG ATTACAACCT GAAAATAGTA | 420 |
| | CAATGGAGCC AATTTACCTA GACAATGTTG CTGTAATTGG GAAAGTAATT GGTTTGTACC | 480 |
| 25 | GCGAAATGTA ATATTTTAAA CCGTTATATA TTATCGTAAT TGTTAAGCCC TCATTTTAT | 540 |
| | AAATTTTGGG nCTCTTGAAA AAGTTACGTT TTCAAGAGGT TTTATTTATT CTAATCTAAA | 600 |
| | TTCAGTTCAA ACAGAAATTG CGAATTGTTA GATAATCTCA TTCTTTArTA TAAATnTTGA | 660 |
| 30 | ATTACAGATT TCTGCAAAAT GTTACACAAA TTAAAACTCG CCCCCGTAAT AATTTACAGG | 720 |
| | AGCGAGCCAT TATTATTTT TTCnTTCTTT TTTATTAAGT ATATC | 765 |
| | (2) INFORMATION FOR SEQ ID NO: 1214: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 495 base pairs (B) TYPE: nucleic acid | |
| 40 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1214: | |
| 45 | AGTTGCCATC AAAAATACAG AACCTAATnA TNACCTTTTA TGATTTTTTG TGAATTCAAA | . 60 |
| | GTCACTTCT TTTTnAAGCT TTAAATTTCT CCCCATTTTT TTAGCCCCCT ATAAGGATTG | 120 |
| | AATATCAATG CCTTCTTTCA TTAAAATTTC TCTAATTTTC GAAACAAATA ATAATGCATG | 18 |
| 50 | | 24 |
| | TTCTCCATCA CCATGCACAC AAATTGTATC TGCTTGTAAC GTTACTTCCT TATTGTTTTT | 30 |
| | TGAAATAACT TTATYYYCCL TCACCATCTT TAAAACCTGC TTAAGTGCTT CGTCAGTATC | 20 |

| | ATCAGCAAAC ACTTCAGAAG CTGTAATTAA TCCGACATTC TTTGCTTCTG AAATTAGATA | 420 |
|----|---|-----|
| | TGAATTTGCT AATCCTACTA ACACTAGTGA TGGATCAAAG TCATAAACAG CTTGTGCTAT | 480 |
| 5 | AACGTTTGCn ATTnC | 495 |
| | (2) INFORMATION FOR SEQ ID NO: 1215: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 243 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1215: | |
| | Antgtccagg tacccgtggt ccaaaattcg atgtacgtag accattgnct cgtatttgtc | 60 |
| 20 | AGATTGTGTT AATGATTGTC TCTGTATTAG GAAGTTTATT CTCCATTTTA ACAATTAGAA | 120 |
| | AAATAGATCC GTTAAAGGCG ATTGGGTAGG AGGTGTGCAA ATGTTGAAAT TGAAATGTAC | 180 |
| | AAGTCATTAA GTGGATCTAC ATGAGCGTAA GGTCATTGGA ATAGGTTTGC TGTGACTCGC | 240 |
| 25 | CGA | 243 |
| | (2) INFORMATION FOR SEQ ID NO: 1216: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1216: | |
| | GGGCTTCTTT CTAAAATAAC TAAGTGAATT ATCTATATAT GAAGAGGTCT CCAATACTTT | 60 |
| 40 | TTATATAATT CGTGATTACA TTCTATACTT TTAATTGTAT TTTCTGCGTA GGAAAGTGGT | 120 |
| | TTTATTAATT CGATTAGTTC GAACTACAnT CAAGAAAAGG TAAAATTTGT GCATGAGCAA | 180 |
| | GAGAAACATA CCTGAACCAA AGGCACCCGA ACAGTACCTA GGCCTAAGCG GCTAATTATA | 240 |
| 45 | AATGCTCAAG CGCAnG | 256 |
| | (2) INFORMATION FOR SEQ ID NO: 1217: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1217: | |
|----|---|------|
| | TITATTITTT CTTCTAAACG AAACATTGCT TCTTTTTGTG ATTGTTTTGT ATTCTTGTTC | 60 |
| 5 | AACACAACAC TTACGCGCTT CCATTTATCT GTGTATGGAT CTTTATACTT CTCGTAGTAT | 120 |
| | CTGTATTTAG TTTCGTTATT TTTGTTTTTA AATTTTTCAA TCCACATGTT TATACCTCCT | 180 |
| | GAGAGAACGT ACGTTCTGTA AATTTGTAAA AAATAATAAG GGTAGGTGGG CTACCCAAAA | 240 |
| 0 | TITAGTACTA GGTACTAAAT ATGTTATAAT AAAATAAAA GTAGGTGATA AGATGACTCA | 300 |
| | ATTTCTAGGG GCGCTTCTTC TTACAGGAGT TTTAGGTTAC ATACCATATA AATATCTAAC | 360 |
| | | 400 |
| 15 | AATGATAGGT TTAGTTAGTG AAAAAAACAA GATTATCAAT | 51 2 |
| | (2) INFORMATION FOR SEQ ID NO: 1218: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs | |
| 20 | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | • |
| | (D) TOPOLOGY: linear | • |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1218: | |
| | | |
| * | CCAAGTGTCA ATTTTAGATG ATTTTTTTGT TGACCTATCG CCTTAACTGA AGAAACTGAT | 60 |
| 30 | AAATCATCCA TTTCAAAAAT AGGTCTAGAA AAATCTGTTC CGAAGGCCTT AAACGATTCA | 120 |
| | TATCACGAAT ATTTTTAATC GTTATATCAT TTTCTGTTAA TAATACATCT ACTTGCTTTA | 180 |
| | CGGGATCTAA CGAAGTTGTT TTAGATAATT CTTTCATCCA TTTATTTAAA CCTTCAGCTA | 240 |
| 35 | ACGATTCTAT ATTTTCAATA TCCATCGTCA TACCTGCAGC CATATGATGG CCGCCAAATT | 300 |
| | TAGCGATTAA CTCTTGATGT GCTGATAGTA TTTCAAACAT CGACACTTGA TCAATTGATC | 360 |
| | TGGCGGAGCT TTTGCATGAT TTTGCTCCCT ATCAATATTT | 400 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1219: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| .s | (A) LENGTH: 458 base pairs | |
| 45 | (B) TYPE: nucleic acid | . " |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1219: | |
| | AAGATATTAG ACATAAAATC TAAAAACAGC AGTAAGATGA TTTATGATTA GAAACTATCT | 60 |
| | TACTCCTCTT CACTTTTTAT AATACTTCTG AATGTCTTCA CTTATACTTC TAGTCACAGA | 120 |

| | GCATTCATTT CTTGTcTAGC AACGTTCTAC TCTAGCGGAA nTAALTAGCT ACCATCCTCG | 240 |
|----|---|-----|
| 5 | CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGcTCTCGC | 300 |
| 5 | TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG | 360 |
| | TITTCACTIC GCCAAGCCAT TITTCTITGT GTTTACTTTT TATTTTGACG TTTTAGACAT | 420 |
| 10 | AAAAAAAGAG ACCTCACGGT CTCAACTTGG CCTGGGCA | 458 |
| | (2) INFORMATION FOR SEQ ID NO: 1220: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 494 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1220: | |
| | CAAAATTTAT TTCTTGTAAA GTACAATATA AGTTAAATGT TGTTGTTAGG ATTGATTCTT | 60 |
| 25 | TCATCTGAGC ATTTAATTGT AAGTCGCTAT ATTTAATTTG TTCAGTATTT AMAAATAAAT | 120 |
| | TGAAAAATTC AACTGATAAT AAAGGTGTTC TAATCATACA AATACTTGAC GGTTCGTAAA | 180 |
| | TAGTGTTCAT TTGTAAGCAC CTCACATATT TGAATAGACA AATAGAGCCC TTTCAGGCTC | 240 |
| 30 | TATTTGCTGT AATCTTAACA GCAGAAGCTA TTAAAACTAC CAGTCTTAGC ACAACCAGGA | 300 |
| * | GTACATAAAC TATGACTTGT AATACGTTCG TCACCTGCTG AATCATTTGA GTDATTGTTT | 360 |
| | GCTTTAACTT GCACGTCTAA ATCAAGAACT TTTTCCATAG ATAAAACCTC CTATTATTAG | 420 |
| 35 | TTGAAGTTAA GGCCTACTTC AATTGTCATA TTATCCCTTT TCACACAACA AATCAATAAA | 480 |
| | TTATATAATT ATAT | 494 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1221: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 148 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1221: | |
| | ACTATTATTT TAATAGTGAC GACAGTTTTA ATTTTATTAA GTATTGCTTT AATTACCTTT | 60 |
| | ATGCAATACT ATTTCACACA AGANACCGAA AATGCCATAA GAGAAGATGC TAGACGTATA | 120 |
| | AGTTCACTGG TCGAACAATC ACATAATA | 148 |

| 5 . | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 401 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|------------|---|-------|
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1222: | |
| | TCGCTTTTAC ATCAAATAAA TTATCTTTAT ACAATTTCGT ATGAATTACT TCTTTATAAT | 60 |
| | TATAAAAATG AGGAATITTT TGATTGTTTA ATTCACTTGC TAATTGATTA GCTTTTTGTT | 120 |
| 15 | GGTCTTTAAT TGTAACGTCG TGTGGTGCAG TATATTTTAT TTCACTTGAT AAGGACGCTC | 180 |
| | TACTTATAGC AGCAAAGCAA AGAACTGAAA CAGTAATCGC TGAAATGATT GCCATGACCG | 240 |
| | TAAGTGAAAA AGCATTTTC TTAATACGAT ACATAATAGA TGATGAGAAC ATGACATCAT | 300 |
| 20 | TLACACTTAT AACACCTTKT CTAAACLTCT TCACCATTTT AAAAACTAGA GAYACAGAGC | 360 |
| - | TTTTAAAAAA TAAGNGTGCC CCAATCACAG TTGACAANAA A | 401 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1223: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 176 base pairs | |
| .7 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 30 | (C) STRANDEDNESS: GOUDTE (D) TOPOLOGY: linear | |
| | | · . • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1223: | |
| 35 | CTTGACCAAA TCCATTTTTT AACAAAAGTG GTCAAGTGAA ATCCCATCTT TCCAAATCAA | 60 |
| | AAAAGAGCTA AAGCAAAATG CTCTAGCCCT TGaTATTACT GATTTCCCAT CATTGTnTAG | 120 |
| | CGTATTAATA TTGCTTCATG TACTGATCTC TTTCCCATTC AGAGACTTGA GTTCTG | 176 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1224: | |
| ÷ | (i) SEQUENCE CHARACTERISTICS: | |
| 45 | (A) LENGTH: 283 base pairs (B) TYPE: nucleic acid | |
| 43 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 50 · | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1224: | |
| | AATACTTTTA CGATAATTAT AAAGGTTCAT TCAAATCTTA GGGCAAAATG TATAATATTT | . 60 |
| | TTATGCAAAT TTAAAACANT AACACTTATT TCAAGGTTCA ATATTTTGAG AATAAGGAGT | 120 |

| | AATGCCAATC AAACTCGCTC GAAATAGGGG GAAACGAGGC HAICAIIIII GACAATGA | 4G1 240 |
|-----------|---|---------|
| 5 | GTCAATAGGG AAGAATAACA ATTAGGAATG ACTCATAGGA GGA | 283 |
| 3 | (2) INFORMATION FOR SEQ ID NO: 1225: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 217 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1225: | |
| | AAAAGAAGAG AAGAAGTTG AAGAACCTCA AGCACCTAAA GTTGATAACC AACAAGAC | GT 60 |
| | TAAAACTACG GCTGGTAAAG CTGAAGAAAC AACACAACCA GTTGCACAAC CATTAGTA | 120° |
| 20 | ATTCCACAGG CCATTACAGG AATTTAAGTC GGATACCACG TGAATNACGT CAGGATG | rCn 180 |
| | GCCGTTCACA TGACACGCTC TACATATTCA CCACTCG | 217 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1226: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1226: | |
| 35 | TGGGTACTAT TTATTACGTA AAACTTTTCG TTAGCGATGC CGGCATTGCA AGAGCAAC | GT 60 |
| | TTACAAAAGC GGACTAGGTT TGCACTTTCT GCTGTTCCAT CGCATATGGA TTAGTAAC | GGT 120 |
| 40 | CTTTATGGGn ACTGTAAGTG ATCCGAGCAA TGTCGGATAA TCTAGGTCTT GGATAG | 176 |
| | (2) INFORMATION FOR SEQ ID NO: 1227: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . • |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1227: | |
| | AATGAAAATA AAGAAGATGA TTTTGTTGCA TATGGGTCTC CAGAACATAA TTATCAA | PTT 60 |
| <i>55</i> | GGTGGAAGTT TAATCAAAAG TAAAAATTTA AGCACGTTAT TAAAACCAGT ACATCAAA | ACC 120 |
| | | |

| | GCGGCCGTTT TAATTTTGTT TTCAAGTTAA TCATACTTAC ATATAAAAAT GAAAAGTTGA | 240 |
|-------|--|-----|
| 1 2 - | ATTITTAGTA CAATTICCAC IGTATTIATC IGTTAACCAC ITTATACCCG CAATATITCG | 300 |
| 5 | TTGATCTTAT ATAAACACTT TTGGCTGCTT TTCCTTGACC TAGATTAAAA TTATAGATTT | 360 |
| | TCCTTGTAAG AGTGTGTTTG TAGTATCATA AATATGTAAA | 400 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1228: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| 15 | (D) TOPOLOGY: linear | |
| | and the control of th | ¥ , |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1228: | |
| 20 | ATCTAGCATG CTTTTGGAAA ACGATAAGAA TTTGGTGTTT GAATTTCATA ACCAACACCA | 60 |
| | GCAGTTTCAA CAACTACGTG TGTAGGATAT AAATGTGTTA CTTGACCTTT GACATACGCG | 120 |
| 25 | TACATTATAG GCACATCCTT ACATACTCAN | 150 |
| | (2) INFORMATION FOR SEQ ID NO: 1229: | · · |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 138 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1229: | - |
| | TCGGTACAGT GCATTTGGTG CGTCATGGTT TACAAGGNAA AAATAAGTGA TCACTATTTA | 60 |
| | TCAGTATGGG AAAAAGCAAC GACGTATCAA ATGTACCATG GCTTAGCATT ATTAATTATA | 120 |
| 40 | GGTGTAATTA GTGGTACA | 138 |
| | (2) INFORMATION FOR SEQ ID NO: 1230: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: | |
| 40 | (A) LENGTH: 182 base pairs (B) TYPE: nucleic acid | |
| .* | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | - |
| 60 | | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1230: | |
| | THE THE COTTON OF THE | 60 |

| | CCTTGATTAT NCTAAGAAAA GTAAAAGCAC ACGGAGTATC CTATCAGAAA ACCAGTATAC | 180 |
|----|---|-----|
| | CA | 182 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1231: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1231: | |
| | TCTCTTTAAA TTGTACACAA TTCTGGATAA CTATCCCCAT TTCTGTGGAT AAACACCTTG | 60 |
| | ATGTCTTATT ACTTATCCTC GTTTTTATAT CCCATATTTA TCAACGGKTA TCGCTTTTTT | 120 |
| 20 | TCATAAAAA aCACTACCGT ACCYCTTATT TAAGAAATAC AGTAGTATTA TTTTCAATAT | 180 |
| | ATTTTAGCTA GCnTTTCTAC GTCGTACAGT CGCGATTAAA CCTATACCTG CTA | 233 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1232: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid | |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1232: | |
| 35 | GTTTTTGGTA AAAGTACTAA TATTAACCAA GTATTGAGTC ATATGTTAAA ACAAGATGCG | 60 |
| | AATGATATTG GCTTTGCTAA ATTACTACAA AATGAGAATA ATCGTATGAG TTATAACGAG | 120 |
| 40 | TTAATGAGTG AATGGCAATC ACATCAACGT GCATTTTTAG AAGAGTTGAG GCATGTTGAA | 180 |
| | ATGTTAAAAG AAGAATCTAT TAGAGCATAT GATGTTTATA AAAATTGTGA GTCTTTCTCT | 240 |
| | AAGATTGAAC AGGTTATTAA TAGTGAAAAA ACAAGTATTG AAGAACAGGT ATATCATTTA | 300 |
| 45 | GATAATGAAA CGTTACGAGA CAATAAAGAA ATAGAAGTTT GGGATAATCG ATTTAATTAn | 360 |
| | ATTGnTAGCC CAATGGnCCC TTTAA | 385 |
| | (2) INFORMATION FOR SEQ ID NO: 1233: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 180 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1233: | |
|-----|---|------|
| | CTGAAAAGAT TCAACTAATC TGAGTCAGGT TACAATCTCA TGATAACCGC TCGCACCTCG | 60 |
| 5 | GAGAAAGACG CTCAAACAGT ACAGAGCTCG ACCGCAGGAT ATTTTTTGTG AAAATGAACG | 120 |
| | TATGAGCTGT TCAGANGGCA CTTTATTGCG CAATAAAACG GTAAAAATCC TGAAGTGAAG | 180 |
| | (2) INFORMATION FOR SEQ ID NO: 1234: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: | |
| 9 . | (A) LENGTH: 453 base pairs | • |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 15 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1234: | |
| 20 | ACCATTTTAA TTTnCnTTAT GACCTTGTAT GCCATTATCA aCAGTTATGA TTAATGTTAT | 60 |
| | GCYTTCATCA TGAGCATTTC TAAATGCTAG TTCGTTTGGT CCATATCTTC GGTAAAGCGG | 120 |
| | TTAGGAATAT GCCATCCTAC TTGTGCACCT AAAAGTTGTA ATGTTATCAC TAAAATTGTA | 180 |
| 25 | GTTGCGGTAA CACCGTCGGC ATCGTAATCA CCATAAACTA GGATTTTCTC ATCATTCGCT | 240 |
| | ATCGCTCTTT TAATTCTTTC AATAGTCTTA GTCATATCGC TCAATTGNAG TGCATCATGA | 30,0 |
| 30 | TTGATATCTG TATCTGAAAT GATGGATTCT ATTGCTTGTn CATCAATAAT CGATTTACTT | 360 |
| 30 | NCTAATATTT TTTTTACGAT TGGCGTTAAC TTTAATTTTG ATGTTAATTC ATCACTTATG | 420 |
| | TATTCAGCTG GTTTAGTTAA TTTCCACTTA TAC | 453 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1235: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 163 base pairs (B) TYPE: nucleic acid | |
| 40 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (b) Torobodi. 11Md1 | |
| | 000 TD NO 1235 | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1235: | 60 |
| | CGTGATTAAG TTGGATACTA AAATTTGGGA TGTTAGAGAA TGTGATGAAG ATTThCAGCA | |
| | ATGTCCTGAA ATTAATGAAA TAAGAGACAT TGTTTTAAAG CGGTGGTTTG ATAGGTTTAC | 120 |
| 50 | CAACTGAAGC AGTTTATGGA CTTGCAGCGA ATGCGGCAGA TGA | 163 |
| | (2) INFORMATION FOR SEQ ID NO: 1236: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs | |
| E E | (N) DERIOTI. 133 SOUP PORT | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----------|---|-----|
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1236: | |
| | GTTAACACAT CGCTTATAAC GTGTAAATAT AAACACTGTT TTATAAAAAC TTTTTATACC | 60 |
| 10 | ATTACCGGCA CCGATAAATG TGTACTATGG AGCACAACAA TAACTGGAAT ACTTHGATTT | 120 |
| | AATCCCGCTA TAACATTTCC TAAT | 144 |
| | (2) INFORMATION FOR SEQ ID NO: 1237: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 204 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1237: | |
| 25 | ATAGTTTAAG GTGATATTCA AACAATATTA GGTTTGATTT AACTATCAAG CATCTACTTT | 60 |
| • | GTCATGTTTA ATACCAGCAA ATAATAAAAT CCATGTCACG ATAATAAATG GCATGTTAAT | 120 |
| | GCAGGGTAAG CCCAACCGGT CCAGCCATGG TGGTGGTACC CTAnTTGGCC nCCACCTACC | 180 |
| 30 | GGTTAATTAA CCACCCCAA AAAA | 204 |
| | (2) INFORMATION FOR SEQ ID NO: 1238: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1238: | |
| | CGGTCATTTT GGTTATTMAA CAACTATACC TGAGGGGTGG TGGGTAATTC GTATTGCCGA | 60 |
| 45 | TTCAGTTTTG TTAATATGCT GACCACCTGC ACCAGAAGCT CTGAATGTAT CAACTGTGAA | 120 |
| | TAGCATCCGG ATTGGTTTCA ATCTGCTATG GCATCAT | 157 |
| | (2) INFORMATION FOR SEQ ID NO: 1239: | , |
| 50 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 164 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| ب | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1239: | |
|----|--|-------|
| - | TTAAAGCATG TTCATAAATG TTTGCATCAT CATGCACGTT CTGGACCGAG CCTTCANCAC | 60 |
| 5 | AAGGTAATTT GTACAGCATA CCGGCTCTAA CTCTTCGTTG CGTATGCCTG CAATTTCTTA | 120 |
| | CCTCGATACT TAAGTCAATT TTCCGGGCAT AAGGGTGTTC ATTT | 164 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1240: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 239 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ·2 . |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1240: | |
| 20 | TTGAAAAACT GAAAACGGTG AAGTTTTACA AACAACTAAA ACAGATAAAG ATGGTAAATA | 60 |
| | TCAATTTACT GGATTAGAAA ATGGAACTTA TAAAGTTGAA TTGAAACACC ATCAGTTACA | 120 |
| 25 | CACCACACAA GTAGTTCAGA ACTATAAGTT GATCAATGTC TCACACAGTG CATAATAGAA | 180 |
| 25 | CAACATGCCG GTCTCAACAC TCACTAGGCA GAGGATCATA ACGGTCGTnG TAAGCTCGG | 239 |
| | (2) INFORMATION FOR SEQ ID NO: 1241: | |
| 30 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 152 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | • • • |
| | (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1241: | |
| 40 | TGATAAATAA TAGCGCCATC ATAAGTTGCA GGGTGGTAAT CATAATTTCT ACCATGAGTC | 60 |
| | TTTGCCTTGA AAGACCGTGC ACCACTTTCT TTTAAATCGG TAAACGATAA TGnCAAGTTT | 120 |
| | AAAATAATTT GGCGTGTTGG CATTTGAGTA TC | 152 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1242: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 148 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1242:

| | ATCTTTACCT TTCACTGTTC ACTTATGTAC CATAATACTT CTGACAGTTA CTAATTAACA | 120 |
|----|---|-----|
| _ | GCAACTCTAA CTCATTTATA TTTAACTA | 148 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1243: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 588 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1243: | |
| | GGTACCAATC GATCGTTACA AACGTTTCGT TAAAGACGAT AAAAAAGTAC CAACAGGCAA | 60 |
| | TGAATATCGT GAATTAGTAT TAAAAGCAAT TCACATGATT ATGCTTGGTT TCTTGTATAA | 120 |
| 20 | ATATATTGTT GCTTACTTTA TTAACACATA TGCAATCATG CCGTTACAAT TAGACTTACA | 180 |
| | TGGCTTTGTC AATTTGTGGT TATATATGTA CGCATACAGC TTATATTTAT TCTTTGACTT | 240 |
| 25 | TGCAGGTTAT AGTTTATTTG CGATAGCATT TAGTTATTTA TTCGGTATTA AAACACCACC | 300 |
| | AAACTTCGAT AAACCTTTCA AAGCGAAAAA TATTAAAGAT TTCTGGAATA GATGGCATAT | 360 |
| | GACATTATCA TTCTGGTTCA GAGATTGTAT TTACATGAGA TCTTTATTCT ACATGTCTCG | 420 |
| 30 | TAAAAAATTA TTGAAGAGTC AATTTGCAAT GTCCAACGTG GCATTCTTAA TCAACTTCTT | 480 |
| | CATAATGGGG ATTTGGGCAT GGGAACGAAG TGTAATACCA TTGGTTTAAG GGGTTAAACC | 540 |
| | ATGGCCAGCC TTGGTTAAAG GGTANGGNCC AATAAGGACG GTGGGCGG | 588 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1244: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 376 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | • |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1244: | |
| | ATTGCTGGAG AAAGGCAAGG CTTTGCAGGC GGATTGAACT CGACATTCAC TAGTATGGGT | 60 |
| * | AATTTCATAG GTCCTTTAAT CGCAGGTGCG TTATTTGATG TACACATTGA AGCACCAATT | 120 |
| 50 | TATATGGCTA TAGGTGTTTC ATTAGCAGGT GTTGTTATTG TTTTAATTGA AAAGCAACAT | 180 |
| | AGAGCAAAAT TGAAAGAACA AAATATGTAG CATAAGTATT TTGGTGTATA TTGATATAAA | 240 |
| 55 | GTAAAGCGTA ATATTATGAA TGATTAGCAT CGTTTTTCTT ATGAATTTTA TTAAGAAAAT | 300 |

| | GTTATATGTn ACAAAA | 376 |
|------------|---|------|
| | (2) INFORMATION FOR SEQ ID NO: 1245: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 288 base pairs (B) TYPE: nucleic acid | |
| 10 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | Orang karang at taun an | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1245: | |
| 15 | CAATTTGTTC TAAAGCAAAT TCTTTACATT TCTCACGGAA TTCAGCTGTT GACATTTCT | 60 |
| | TTCGGTCAAC ACCTTTTTC GTTAATGGCT TGTTCAATTG GGTAAACCAT GTGGTTATCC | 120 |
| | CCCAACCTGG GTACCGTATG GGGTGGCCAT TAGGAAACCC CTTGGCAATA GGTTTTTTAA | 180 |
| 20 | TAAACCGGTA nCAAATTAAA AGGTCCTTTT TTAAAAAATT TTTGGTTTCC AAAGGGGCCA | 240 |
| | ATGGITCCCC CAATTAATGG TTAAAGGTTT TAACCCCAAT TTTCCGGC | 288 |
| | (2) INFORMATION FOR SEQ ID NO: 1246: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 161 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . 11 |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1246: | |
| 35 | CATCATCAAT AGAACGGTAT TCGCAACGTC GTAGAAATCC CTTAAACGAC GAGAACAAAG | 60 |
| | CAAGTCGACA TCAGTAAAAC ATTAAAGATA TTATGGCTGA AGCAGAGAAC TTAATAACTT | 120 |
| - | TTTATAAATC TATACCNTCC AAAATGTAAA ACTACCAAAA T | 161 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1247: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 421 base pairs (B) TYPE: nucleic acid | |
| 4 5 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | * |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1247: | |
| | TCACTACGTT GTTTAATTGT GGTAATTGCA GTTTTACAGG CTTGTCTAGT GAAGATTTAA | 60 |
| | AACTTAATTC AAGTGTTTTA GTCATGAATA TGTCCTCCTG ATTAAATTGA TAAAGATTTG | 120 |

| | TTAATTTGGT CGTTTGATGC ATCAGGGTTA ATGTTAGCGA ATCGACGCTT | AAATTCTGTT | 240 |
|------------|---|-------------------|------------|
| _ | TGTTTGCCGT TAGCGTCtAC TTTAGTAAAT GaTAATACAA TAGTGATGTG | GTTTATTTLA | 300 |
| 5 | CTCATATTTT AAAACCTCCT TTCACACTAT ATATCGAAAC AAAATAATAA | AATGGCTAAT | 360 |
| | TTTATTTTCT ATGTTTAAAA TCTATAAAAN AGGCAATAGA TATGTGTAAC | TAAAATATAn | 420 |
| 10 | G | | 421 |
| | (2) INFORMATION FOR SEQ ID NO: 1248: | | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 409 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| 20 | (with appropriate percentage of the Mo. 1249). | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1248: | | c 0 |
| | ATAAGCTGCT GTTGATAATC CAAGTGCTAA AGTTAAATAT AATATAGTGC | | 60 |
| 25 | ATTCTTCTAT AAAAACACCT CTTCATATTT AATCCATATC TCTTTTTCGT | | 120 |
| | GAATTTTCTG AAAATAGTCA AGGTTAATTT ATTTGCTGCA AATTTCAACC | | 180 |
| | AAATGGACAT CAAAGTATAA TTGTATTATT ATTAAATTGT GCAGTGTATA | | 240 |
| 3 0 | ATGCAGGAAC ATGTCGCCTA TTGAGCCCGT TAAAAAGACG GTGACTAAAT | GAGATTTCT | 300 |
| | TTAACCATCA TTCGTTGTCA AAGTTTGGAA ATGATGGTTG TTTTTTATTG | TTTAAATTAA | 360 |
| | TCATTGCGAC TTCTATATCA ATGAAAGTTA TCTTAATATA TGAACTTCA | | 409 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1249: | · | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 217 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1249: | | |
| 45 | | A A TEMPTA CICA A | 60 |
| | CTTTCAATTA CGAACAAATC ATTACTAGTT TATTTAATGA TAATGACTGN | | |
| | AAAACGTAAC ATGATCATTT AGCTTGAATT GGTAAAACTG TTTATCCAAC | | 120 |
| 50 | CAAATCACAC CGGTAAAACG TCAAAATATA TTGTnTCTAT GCCCGTTTTT | ACCAGTTATC | 180 |
| | TCATTGCAGG TATATTGATG AATTCACAAG TTGGTAT | | 217 |

(2) INFORMATION FOR SEQ ID NO: 1250:

| 5 | (A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 380 |
|-------|---|---------------|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1250: | |
| | | 60 |
| 10 | CAGAACGTGC GGATCGTTTT TATGCAACCT AAACCAGGTA CGGATTTAGC GTGGTTAAGT | |
| ** *4 | GGCAGTGCAC TAAGTATATT CATTGATCCT GCATTTACAC GATGAAAGCA TTTATTGCAT | 120 |
| .* | GAGTGGGTAG ATGCATTTTG CTGGAATGAT TCACAAATGC ATTAGAGNAC ATTTAC | 176 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1251: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 212 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ** |
| | (b) TOPOLOGI: Tilleat | > |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1251: | |
| | TTTCAACTTT CTAAATTATA ATATATCTTT TTAAAATAAG CTAGAATTTC TATATAATAA | 60 |
| | ATGTTAATAA CGAAAAGGGA TGATGCATAG TGATCGCAAG CACGCCAGAG GCCGATTTGA | 120 |
| 30 | TATTGCGAGT TAGTTTATAT GGTTTGGGAT GATATGGATA GAATTGGTAA ACATCTCCTA | 180 |
| | AAGCATGGTA TAGTGCAATT NAAAANCTGT GT | 212 |
| | (2) INFORMATION FOR SEQ ID NO: 1252: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 131 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| * | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1252: | |
| 45 | CAGTAAGTCA ATTGAAATGG CTAATTTATT AAATCTATAA AAGCATAGAG CACTGTTGTG | 60 |
| | AGTTCATAAT CAAAGATTTA TAAATGTNTC AGACTGCCAA TATAACATTT AGGACCTAGA | 120 |
| | ACATTGATTA T | 131 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1253: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | • 01 |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253: | |
|----|---|------|
| | TTAGTAGTCA TCGGTATTGG TGGTTCTTAC TTAGGTGCAC GTGCAGCAAT CGAMATGTTA | 60 |
| 5 | ACGTCATCAT TTAGAAACAG CAATGAATAC CCTGAMATTG TATTTGTTGG TAATCACTTA | 120 |
| | TCATCAACAT ATACGAAAGA GTTAGTTGAT TATTTAGCAG ACAAAGATTT CTCTGTAAAC | 180 |
| 10 | GTTATTTCTA AATCTGGTAC AACTACAGAA CCAGCAGTTG CATTTAGATT GTTCAAACAA | 240 |
| ,, | TTAGTTGAAG AAAGATACGG TAAAGAAGAA GCACAAAAAC GTATATTTGC AACAACGGAT | 300 |
| | AAAGAAAAG GNGCTTTAAA ACAGTTGGCT ACAAACGAAG GTTATGAAAC GTTTATCGTA | 360 |
| 15 | CCTGATGATG TAGGTGGAAG ATATTCTGTT TTAACAGCAG TAGGATTATT ACCAATTGCA | 420 |
| | ACAGCTGGAA TTAACATCGA AGCTATGATG ATTGGTGCTG CA | 462 |
| | (2) INFORMATION FOR SEQ ID NO: 1254: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | (B) 10102001. 2211022 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254: | |
| | ACTCATAAGT GAATGGTTGA TTACCACTAG TTAAAACTTC ATATACTATA GTTTCTTTTT | . 60 |
| 30 | TTATTTTGCA ATTAGTTATT TTCATTATAA ACTTCCTTTC AAACACTGCT GAAATAGACG | 120 |
| | TCTTTTTCAA ATAAGCATGA TTAATACTTC AATTCTTTAA TCCACATATA TTTAAAAGTG | 180 |
| 35 | AGGTAGTAGG TAATAAATAT AAGACTTAAA GTTAAGATTG CTTTTTCAT GTTTCATAAT | 240 |
| | TAAAACCTCT GTAAATTTAA GGTTAGTATT ATGAAATAAT GGATTGGTTT ATTCTTTAGT | 300 |
| | ACTARCTICG TAGTARATTA TATAGTICGC TARATTGTAT TTATCTACTA TATTTITGGA | 360 |
| 40 | ATAAACAATT TCCTTTCTT TCTTCAGTAA ATTATAAAAA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1255: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 137 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1255: | |

•

| | NAATCTATGT ATGGGGGCAT CCAAAGATTT CATAGACTAC TTATTTGTTG ATGAAGCCGG | 120 |
|-----------|---|-----|
| | ACAAGCAATC CTCAAGC | 137 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1256: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 139 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . * |
| | | |
| ·. | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256: | |
| 15 | TGAAATGTAG AAATTGAATT AGAAATGAAG ATTAAAAATC DACACGTATC GTTCAAGTGG | 60 |
| | TGCAGGTGGT CAGCCGTAAA CACAACTGAC TCTGCGTACG TATTACCATT TCCACTGGTG | 120 |
| 20 | | 139 |
| | TCATTGCAAC ATCTTCTGA (2) INFORMATION FOR SEQ ID NO: 1257: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257: | * - |
| | TTACCANTTA TITTAACACC ATGTTTAGAC CAATTTGATC TGACTAAATT AATCGCTGTT | 60 |
| 35 | TGTACCTCCA AATTGTTACA ACGTACACCT TTAGTTTTTC TAAATTAATG TATATTCATC | 120 |
| | ACATCTTCTT CAGTTAAGGG TCAAAGTATA ATTTGTCGAA ATTGTGAAGT CGTTGTA | 177 |
| | (2) INFORMATION FOR SEQ ID NO: 1258: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 250 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | .* |
| 45 | (b) TopoLogi: Timear | |
| - | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258: | |
| | AAGACCAACC GAAATGAATA TCGACATGGA TTAAGCCTAT ATTCAGATGT AAACGGCGAT | 60 |
| 50 | TATATTAAAA AGCCAATTAC AGAATGTAGT GGTTAATGAA ATATGCCCAA GAATGGGCTG | 120 |
| | TATCACTTAG GTGTATCAAA CTGACCAAAA ATTGGAAGGA CTTTAGGCCA AAAACCATGC | 180 |

| | TTAATTTTC | 250 |
|----|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1259: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 170 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259: | |
| 15 | ACATTTACGG GACATTTCAT TACATCACCC TGCTTTATTT TGGATTATGG CCTAATTTAT | 60 |
| | ACTGATAAAT CTAGGAGGTG GAAAAAAGAA TGCCCTGCAA TTTAATTnCA TTTAACCAAA | 120 |
| | TAATGAAACA ATAAAAAACA TTATATCGTT ACTTATTAAG TAATTTGGCA | 170 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1260: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 313 base pairs (B) TYPE: nucleic acid | |
| 25 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260: | |
| 30 | TTTGTACTCC GATACGTTGT ATTCAGGTTG ATGACACTAG GAATTTGTAA TGATCAATTT | 60 |
| | CTCTAATTCT TTACAATTGA TAGAATTCTT CGATTTGTGG ATAGACATTC ATATCATTGT | 120 |
| 35 | CTAATGATTT TTGGTGATTC ATAAATTGTG ACTAAAGCTT GGATGCTTTA GGATTGTAGC | 180 |
| | TGAGACACAT GTTGCGTGAC TGNGGATTTA TCANATAATC TCAATCACGT GATCCNATCA | 240 |
| | CATTCATCAG CTCACTAAAT CAAGATGATC GTCGTTTATG GGCGATTAAT GGCGTACCGC | 300 |
| 40 | CAGTGTCCGC ACG | 313 |
| | (2) INFORMATION FOR SEQ ID NO: 1261: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 206 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261: | |
| | TAGCGATCAT TTAATCAAGG TTAGATTATT TAATGTCAGC ATTACGTTTG ACAATGAACT | 60 |

| | GTTTGAGGTT ATCACAATGC CATTTAACAC TATGCGCACA TGGCTGAACT AATNAGCGAC | 180 |
|-----------------|---|------|
| | GAGATGACTT CAAACCTTGA TTAGGT | 206 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1262: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262: | |
| *. | AAGTGTGTAC ACGATAGCTA AACTCAAATA TCACAGAACA ACAAATGTCT TAGTACTTTG | . 60 |
| | TGCCGGTGGT GGTACAAGTG GATTATTAGC CAATGCACTA ATAAAGCAGC TGAAGAATAT | 120 |
| 20 | CATHTGCCAG TGAAAGCGGC ACTG | 144 |
| | (2) INFORMATION FOR SEQ ID NO: 1263: | - |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263: | 1 |
|) | ATAACGACAC CTAATGCAAT TTGAATAAAG CAGTAGAATT TGTGGGAATC GATTATTGAT | 60 |
| 35 | AACCGAACTA ATAATCACAG CAAAAATAAA ATTAAAAATG CTCTAATAGT GCCTACATAC | 120 |
| | TCCTCAAATT TT | 132 |
| | (2) INFORMATION FOR SEQ ID NO: 1264: | |
| 40 ⁻ | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 159 base pairs (B) TYPE: nucleic acid | * |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264: | |
| 50 | TATGTCAATT TCGTAGAATT GGTTTTANGC GCTATTTAGA ATAGCCATCA GATAAAATCA | 60 |
| | TTATTTAAAC GTATAATAGG TCAAAATATA GAGAGTTACT ATACAAATTT CTAACTTTCA | 120 |
| | CTTAAAATAA AATATATATA ATTAAAGTGG AGGAGAAGG | 159 |

(i) SEQUENCE CHARACTERISTICS:

| 5 | (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265: | |
| 10 | ATAGCTCAAG CAATCATTAT GTTTATAATG ATTGTATGGT TCTTTATAGA TGCTTTATTG | 60 |
| | ATTAATTAAT AAAAAGCTTA TTGCAAAATA TGTTTTTCGG TAACTGTAAT TTAGTGATTT | 120 |
| 15 | TATCATTAAC AG | 132 |
| | (2) INFORMATION FOR SEQ ID NO: 1266: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 405 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266: | |
| | CATGGATTTA TCTTAGCGAT TGGTCTAATT TTACCTTTAG GTGCACAAAA TGTATTTATT | 60 |
| | TTTAACCAAG GAGCTAATCA ACCAAAATAT AGATATGTAT TGCCTGCAAT AATTACAGCC | 120 |
| 30 | GGGTTGTCAG ACAGCTTACT TATTATTATT GCAGTGGTAG GAGTWTCTAT CATTATTATG | 180 |
| | TCTTTACCTG TACTTCAWGC AWTTATTTAT ATAGTTGGTT TAATTTTCTT GATGTATATG | 240 |
| 35 | GCTTGGACCA TTTGGCATGA TAAACCCTCA ACAGATGGAG AAACTCAAAT TATGTCTCCA | 300 |
| | ATGAAACAAG TAAGTTTTGC TTTATCAGTT LCATTACTCA ATCCACATGC TATTTLAGAT | 360 |
| | ACAATTGGAT TAATTGGLAG TAGTGCTGCA TTATATAGTG GCnGC | 405 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1267: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267: | |
| | TCTTTATATT GCAGTACAAA ATTCGCGTGG AGGTTTAACA CAAGTAGACC GCACAAGATT | 60 |
| | TACCCTOTCA ACCTATTACT GTGTAATGCA TTCGCACCTG GNTATCGTTC AAACACCAAT | 120 |

| | (2) INFORMATION FOR SEQ ID NO: 1268: | |
|----|---|------|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 247 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268: | 0.0 |
| | TITGCCCAAG TGACGTAAAG TACCCAATGT CCATTTGTAC TTGTATCGCC ATCAACAGTA | . 60 |
| | ATCATATTAA ATGTATGGTC AGTCGAAGAT TTTAATAATT GATGAAGTGT ATTCGATTCA | 120 |
| 15 | ATCGATGCAT CGTGTTATAA AAGCAAGCAT GTAGCCAATT GGGAATCAAC CCGANCTTGG | 180 |
| | | 240 |
| | CACACATGTA CGTTACACAT TAGAACNCAA GTGACCGACG GTAATCCTAC CCGCTCAACA | 247 |
| 20 | CAAGCGC | |
| | (2) INFORMATION FOR SEQ ID NO: 1269: | - |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 215 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | , |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269: | |
| | TCATTGTATA TGAGCAGATT GGCTAGGCGG TGGCTGGACT GACGGAATCG ACACCCGGCT | 60 |
| 35 | GGGGTTGGGA AAAGTACAAG ACGCAACATG CTATGATTTT CCTATGTGGT TATCGTCCGA | 120 |
| | TITAAAGTGA GCAGCGCACG GTCAGTCATC TCTCACAGNA CCTAAAAAGA ACAGTAAGCN | 180 |
| | CAACCTAAAG CAGTGGAACT TAAAATCATC AAGGT | 215 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1270: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270: | |
| | ACAATAAAGA CTATTAAAAG AGATATAGGT TAGATATTAC ACTTTTAGAG CAAGACGGTA | 60 |
| | TARATGCAAG TARATTCGTG TATTTATCAA TACAGCAGGT NGAGTGAAAG GCCCAGCAG | 119 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 223 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| | | - 0 |
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271: | |
| | CGTGGCACGT TAAGCGTTTA ACCATAGCAT TAAGATGATT GTCTAGCAGA GGCGATTTGC | 60 |
| | GGGCTCACTA CAGTGCATGA TGAACTTAAT GCTTCAAATG TAACATTAAA AATAAAAGCA | 120 |
| 15 | ACGATGICAC TICTIACTIC TACATCIGCC ATHITCGIGA TITCGIATCT ATCCCGCATC | 180 |
| | TCATCTTGAA CGTACGAGCC TAATCGCCCn GCGCGATCCT GCC | 223 |
| | (2) INFORMATION FOR SEQ ID NO: 1272: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 120 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 25 | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272: | |
| 30 | TAGTTACAAT ATCTGTCAAT TTCTGGAGAA CCACTAAAGC TATGCATAAT CCCGCCTACC | 60 |
| | TCTTCAGCAT GCTCCTCCAA TAAGATATCG GTACAGTCTT GAGnTGCTTC ACGGTTATGA | 120 |
| | (2) 'INFORMATION FOR SEQ ID NO: 1273: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 126 base pairs | |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (0, 101000000000000000000000000000000000 | |
| | | |
| * | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273: | • |
| 45 | TTGCGCGGCA GTAAAATTCA AACTATTGGC GTCATTTTGC CTAGCTTAAC AAATCCGnTT | 60 |
| | TTCTCAGCAC TGATGCAAAG TATTCATGAC CATAAACCAT CTGATGTTGA TTTATGCTGG | 120 |
| | TTAACA | 126 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1274: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 131 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 12/4: | |
|----------|---|------|
| | GATTCTGAAG GATCAATACh ACATGTACAA TTTTGGCGTA GGTGCAAAGG CATCAGGTTT | 60 |
| 5 | GCTTGCTAAT CTACATCGAA GCGGCTACCT AAATTAATGA GAAATCACAC TCAGTTAATG | 120 |
| | CATGTACTAG C | 131 |
| | (2) INFORMATION FOR SEQ ID NO: 1275: | |
| 10 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 159 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275: | |
| 20 | TGGAGTATTA CCTCAAGTGA ATACAACATA CCTGTTGGAA GATTTTTCAA AACTTTAATT | . 60 |
| | GGACCAAGTG ATGCCATTGA TGAGTTAAAT CCTAATAGAT TCAGGTTACC TCGGATGATT | 120 |
| | GATACTAATT TGGCCTGGCG CACGCTTTAG TANTAGTGG | 159 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1276: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 577 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276: | - |
| | GAAGTAAATA ATATATAGAA TATAACAGGA AATAAAATAG ATAATATTAA TGTTGTTTTT | 60 |
| | TTACGCATTA TAACTTTAAA TTCGATTTTC AAGTAACTTA GTATCATAAT TAGATCCCCT | 120 |
| 40 | TTGCTTTTTA TTGnTGAAGT ATGAATCAAC AATTGAGACT LTTTGTATTT CAATATCATC | 180 |
| | CAAATTAATA TGAAGTTGTT GAAGATATAA AATCGTATCA TTTACATTTG AAGTAATAAT | 240 |
| | TITSATAGIG CCATTATGAT TITTYYCIGAA TAACTAAATC ATCTTTATCI AGITTITAACI | 300 |
| 45 | TTCTTATATA TTCATCGGAT AACGTAATCT GAGATTGCTG ATTGGTTCTA ATATGTGACG | 360 |
| | TTGAATCATT AAGTATTATT TCTCCATTTT CAATGAGAAT AATTTTGTCT GACATACGTT | 420 |
| 50 | CGACTTCTTC AATATAGTGC GATGTATAGA GTATCGTTCG ATTATCTTCT TTTAAATTTT | 480 |
| 50 | CAATAATTGA CCAAAAATAT TCTCTAATTT CTATATCCAT AGTCGATGTT GGTTCATCTA | 540 |

| | (2) INFORMATION FOR SEQ ID NO: 12//: | |
|----|---|------|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 131 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277: | |
| | CTAAAnTAAG GTAATAGTTA CCAAGTACCA TATCTTGTGG ATGGTGTACT ACAGGTTTAC | . 60 |
| 15 | CATCTTTAGG TTCAAGATGT TTTGATGACT GCTAACATCA ACATTCTTGC TTCAGCTTGT | 120 |
| | GCCTCTTTG A | 131 |
| | (2) INFORMATION FOR SEQ ID NO: 1278: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 166 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 25 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278: | |
| 30 | GTTTGCGATA TTTTAGGCAG ACAACCTAAC TTTACAGAAA CAGGTATCTT TTCTGTTATG | 60 |
| | TGGAGTGAAC ATTGCTCTTA TAAACATTCT AAACCGTTTT TAAAGAATTT CCTACGCAGG | 120 |
| | TGCCATGGTT TGGGCTGGAG TCAGGTGCGT TGTGTATAGC TGATNA | 166 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1279: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 418 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279: | * |
| 45 | CATAATTATG AAAATGATAT GATTTTTATT AGACCATTTA AAAAAGCATA ATTTAAATCG | 60 |
| | AAGGCAGGAC ATTGAAATAT GAAATTTTCA ACTTTAAGTG AAGAAGAATT TACCAACTAC | 120 |
| 50 | ACCAAAAAGC ACTTCAAACA TTATACGCAG TCTATAGAAT TATATAATTA TAGAAATAAA | 180 |
| 50 | ATAAATCATG AAGCACATAT TGTGGGAGTG AAGAATGATA AAAATGAAGT TATAGCTGCA | 240 |
| | TGTTTATTAA CAGAGGCACG AATTTTTAAA TTCTACAAAT ATTTCTACTC TCATAGAGGT | 300 |
| 55 | | |

| | ATTATTAT MAMAATAGAG GAGTATTAT TCTTGTT&T | |
|----|---|-------|
| | (2) INFORMATION FOR SEQ ID NO: 1280: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 449 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | (D) TOPOLOGY: Timear | . * |
| | to the control of the second of the control of the | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280: | : .* |
| 15 | GACATATCAT AAATTACATG GTGATAAAAT ThTCGGCTAC GATACTAACG GATTCCCGAT | 60 |
| | TACCTGGTTT TATCCATTAG GTGAAAAGAA AGTTGAACGT AAGGCACCAA AATTAGAAAA | 120 |
| | ATAATTAAAT AAAACAGCTT AATGATGTAA TGAAATTAGT GAGTTAATCA CTGACTTCTA | 180 |
| 20 | CGTCATTGAG CTGTTTTTT GTGCTTTGTT ACAAAGCATT ATTGAATTTA TTTTACGTGT | 240 |
| • | TCATATTTTG AAACATCAAA GCCGTCTTGT TTAGCTTTGT TGATAATGTC TTTGATTGAA | 300 |
| | TGTAGTCCTT TATCGGCGAA GTATGATCTT AAGTTGTCTT TTGTAGCTTG GTCAGCATTC | 360 |
| 25 | TTATCTAATA ACACATCAAT ATAACTTAAT TCATGTTCTA AGAAGTTTGC ATCATCATGT | 420 |
| | AGTACGAGTC CATTTTGAGA ATAAACTTT | . 449 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1281: | • |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 289 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · . |
| 35 | (b) Toronogi. Timedi | , |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281: | |
| 40 | TATTTATATG TACTGATGAT GAAGTTTATT ATCTATCAAG TGGATCAAAT CCGAAATATA | 60 |
| | ATCAGTATAT GGGTGCATAT CATCTACAAT GGCATATGAT AAAATATGCA AAATCACATA | 120 |
| | ATATTAATAG GTATAATTTT TATGGAATAA CAGGCGTCTT TAGTAATGAG GCGGATGATT | 180 |
| 45 | TTGGTGTTCA ACAATTTAAA AAGGGTTTTA ATGCACATGT TGAAGAATTA ATTGGTGATT | 240 |
| | TCATCCAACC AGTAAAACCC ATTCCAATAT TAATnTGCCA AACCTnAAT | 289 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1282: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 402 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282: | |
|-----------------|---|-----|
| | ATTCAGGTCG AGGTGGCCCG GCTCCATGCA CCGCGACGCA ACGGGGGAGG CAGACAAGGT | 60 |
| 5 | ATAGGGCGGC GCCTACAATC CATGCCAACC CGTTCCATGT GCTCGCCGAG GCGGCATAAA | 120 |
| | TCGCCGTGAC GATCAGCGGT CCAATGATCG AAGTTAGGCT GGTAAGAGCC GCGAGCGATC | 180 |
| 10 | CTTGAAGCTG TCCCTGATGG TCGTCATCTA CCTGCCTGGA CAGCATGGCC TGCAACGCGG | 240 |
| | GCATCCCGAT GCCGCCGGAA GCGAGAAGAA CTAATTGATA CAACACTTTC TCAACCTGAT | 300 |
| | CTTCTTTACC TTCTACATAG CGCGTGAGCA GAACCATCTT GATGGCACAG CTAAATAATG | 360 |
| 15 | CaATgGGAAT GATGTATGAC ATTCGGGGTG CATAATTTCT CT | 402 |
| | (2) INFORMATION FOR SEQ ID NO: 1283: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 20 | (A) LENGTH: 224 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | • |
| | (D) TOPOLOGY: linear | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283: | |
| | TATTGACAAC CAGAGTACAA ACAGCAGCTA TATTATAGAC TTAGGTCTGA AGTGGTAGTG | 60 |
| 30 · | GCGGTGGACT ATTGTTGCGA CTGGACACCC GAGATATTGC TCAGCANAGC ATCATATACA | 120 |
| * | GGAAGTATTA AAAGAGACTT GnCGAGTAAC AAATACTGAA GTAATAAGAT TAAAAGAGTG | 180 |
| | AGGTGTATAA TTATCCTCGT TCTTTTATAT TAGTATGATA GAGA | 224 |
| 35 · | (2) INFORMATION FOR SEQ ID NO: 1284: | |
| - | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 146 base pairs (B) TYPE: nucleic acid | |
| 40 _. | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284: | |
| 45 | CGTGGGAGAT TGTGCATATT GATTATGCAA GGAAGNACGC CATAAAAGTG GATGGCCAGA | 60 |
| | CATCATTAAT ATTATTGATA CCACATCAGA AGGTATTCAA AGTGAATCGG TGATAAGTGA | 120 |
| 5 <i>0</i> | ATCAATTAAG TCTGCCAAAG AAAAGA | 146 |
| | (a) Typopyamioy for CD IR No. 1005 | |

| 5 | (A) LENGTH: 137 base pairs (B) TYPE: nucl ic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|---|---------|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285: | o ** '. |
| 10 | ATTTCGCGTG ACTGGACTTG GATCCGCAAC TTGGTAATTT AAGGAATTCT TGTCATTATA | 60 |
| * | AGCCCTCCAT TTCATGATTT GATTTGCCAC TCGGTAACCA TTGGGGTTAC AGCTTCACTA | 120 |
| | GGGGANATAC GAACCTC | 137 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1286: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 594 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 20 | (D) TOPOLOGY: linear | - |
| • • | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286: | |
| 25 | GCTATTGATT ATGGTTAGCm TGTTGTTCwC TTTACTCATT GTTCCTTGGt TAAGCTCrAA | 60 |
| - | AAAAGCACGT ACTTTAAAGA AACATGCAGC TAATGAACAG GCCCGATTTT TAAATCATTT | 120 |
| 30 | TTATGATTAT AAAGCTGGTA TGGATGAACT ACGTCGATTT AATCAAATTA ATCATTATCG | 180 |
| | AGATAATTTG ATGGCTAAAT TAAATCATTT TGATAAATTA CAACTTAAAG AGCAACGCTT | 240 |
| | TTTAACGATT TATGATTTTA TATTAAATAT TATTGCTATG CTTTCGATTT TTGGTAGTTT AGTTCTAGGA TTAATTCAAA TTAATGCAGG CCAACTAAAT ATTATTTATA TGACGAGTAT | 360 |
| 35 | AGTTCTAGGA TTAATTCAAA TTAATGCAGG CCAACTAAAT ATTATTATA TCGCGTATTA AGTTTTAATG GTCTTAACTT TATTTGAACA AGCTGTACCA ATGACAAATG TCGCGTATTA | 420 |
| | TARAGCGGAT ACTGACCAAG CATTGCACGA TATTAATGAA GTGATATCTG TACCTTCTAC | 480 |
| 40 | TAATGGAAAA AAACGTCTTA ATGATAAGTA TGATGCAACG AACATTTATG AAGTTAAGGA | 540 |
| | TGCTAGTTTT AAGTATTGGA ATCAGCAAAC GTATGTnTTG TCGGATATTn ATTT | 59 |
| | (2) INFORMATION FOR SEQ ID NO: 1287: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | · ' |
| 50 | (D) TOPOLOGY: linear | |
| | | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287:

| | TGAAGTAGTA ATAAACCCGG AACCCTAAAA CTGGATGGAG GATGAAACCA | AAAAGGAACC | 120 |
|----|---|------------|-----|
| 5 | AGCCAAGCCA AATTGGGGAA ACCAGGACGG CCCAATGGAG GTCCAACCAA | TCCAAACCCC | 180 |
| | ATTCCGCTAA TGnCTATGGG TCCCAATTAG GAATCCAATG GATGGATGGA | TTn | 233 |
| | (2) INFORMATION FOR SEQ ID NO: 1288: | | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| 15 | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288: | | |
| | AATCCCTGTA CGTTCGTAÄA GCTAGCTGGn TAATAAAAA GAGTCTGGAA | AGTAGGCAAC | 60 |
| 20 | AATCAATGAC AATGAGCAGA TCCAATCGCA GTATGCTTAC TCGTGTAAGA | AACGCAAACA | 120 |
| | TGGTGCGTCA CG | | 132 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1289: | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 154 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | |
| 30 | (D) TOPOLOGY: linear | | |
| | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289: | | |
| 35 | TATCTGATAA TTCTGTACCC AGGCGTTTTA ATATGTTTAT CTGGTGTCAT | GATACATAAA | 60 |
| | CATTGTACCT TTAGGTCATA CGATGTCGCA AATAACTGCT CTTGCCGTTA | CAACACCATT | 120 |
| • | ACGGTTATAC ACTTHTAGCC AATCATTATC TGGG | • | 154 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1290: | ÷ | |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 145 base pairs(B) TYPE: nucleic acid | | |
| 45 | <pre>(C) STRANDEDNESS: double (D) TOPOLOGY: linear</pre> | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290: | | |
| | AAAAGTGGCA CATGCGGCTG TAAAGTCCTC TGTTTCTGAT AAATCATAAC | CTATATACAT | 60 |
| | GTCTACCTTC CAACTCATCT AAGAAATAAG TCATATTTTT TTGAATGTTG | GATAATCAAT | 120 |
| | | | |

(2) INFORMATION FOR SEQ ID NO: 1291:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 360 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----------|--|------|
| 10 | | |
| 4 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291: | |
| | CTTAATGCTA TATATTCTTT GTTTTTGATA CCATTTCATC GTCTTCTCTT GATTTCTAAA | 60 |
| 15 | CAATTTAGAA AATAAAAGAA TATACGCTTC AGACTTATTA AAACCCGCTA TATCATCTTG | 120 |
| | ATATTGTATT AACAATTGAG TAAAGCTGTG TATTAAGTCA TCTTTCTTCG ATGCAATGGT | 180 |
| | AGTTAATGAT TTTACACGAT AAGCATATTT ATCTGTAAAT AACTTAGCAA CTACCCCACC | 240. |
| 20 | TAAATCATGT CCTAGAATAT GTGCCTCATG AATATTTAAC TTCTCCATTA GAATTTTTAA | 300 |
| | ATCCTCAACG TGATCGTTTA AATCGTATGA TTCACTTTTA GAAGACTTGC CATGACCTCT | 360 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1292: | |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 164 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| 30 | (D) TOPOLOGY: linear | |
| | en and the second of the secon | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292: | |
| 35 | TGTGTTAGTT GTTTATGTTG TTGATATATA CTGCTCGTGC ACATGGTACC CAGACGATTC | 60 |
| | AACGNTGAGT ACACAAAATA CAAAATCTAC GGCACATGGT ACCGTTTATA AAAGATGTGG | 120 |
| 40 | AACCTTACTA GCATTTGTTG AGAACGCTAC ACGTTTAAAT CAAG | 164 |
| | (2) INFORMATION FOR SEQ ID NO: 1293: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293: | |
| | TTAATITTCT ATATATTCT TAGGTTATAT TGGTATCTAT GCCAGTAAGT GACATGACGT | 60 |
| | TAGATCATTG AATCCAAGAT CGANACATTG GGACATATTT ATTAACGACA TGGCTTCAAC | 120 |

| | (2) INFORMATION FOR SEQ ID NO: 1294: | |
|----|---|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 213 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294: | |
| | GTCATGCNTA ACAGGTGAAT ACCTAGTAAT TCAGATATTA TCATTTATAT ACCCTCTTAT | 60 |
| 15 | ATTTTAGTGC ATTATCTCGA AATCGAGATA CTTAATGTAA ATTTTTAGTG CAGCCTACAC | 120 |
| | TTCGTGATTG GGCAnTAGTT CTTAAACGCT GTGGTAAGAT GTTAATTCAT CCTTGGTTAA | 180 |
| | CACACAAACG CTTGGTTAAT GCTCAGCAGC TAG | 213 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1295: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 163 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295: | • |
| | AAGAAGTTTG AAGTCTATGA AAACAATCAA AAATTGCCAG TGAGACTTGT ATCATATAGT | 60 |
| | CCTGTACCAG AAGACCATGC CTATATTCGA TTCCCAGTTT CAGATGGCAC ACAGATGAAA | 120 |
| 35 | TGTTTCTCGn CCAATGAGAG GGAGAACATA GTATCAATAG ATG | 163 |
| | (2) INFORMATION FOR SEQ ID NO: 1296: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 207 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296: | |
| | TAGCTTTAAT ACATTCTGAT TTTTAAACGC TTCGAAATGT TTTCAGTAAC TAATTTTGCC | 60 |
| 50 | ATAATCCCAA AAACTCCTTG ATTATTAACT GCnTTTTGAT TGGCTACATT AAGGCTTTAT | 120 |
| | ACACATCAGC TCACCATGCC CATATCTACT AATGGTTATA TCCCTAGAGT CCCAGCGATA | 180 |
| | | 207 |

| | , | |
|----------|---|--------|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297: | |
| 10 | ATGGCATCGG TTGGTTATGA AAAGnCAAGC CATGGGGAGG CCATATTTGG GGTGGAATCA | 60 |
| | TACCTGGAAC CTTTGGTGCC TACCACCAAT TGGTAACGGT TTTACCATCG GATTTTTAGT | 120 |
| 15 | GATACAGCGA TATGTTTTGT ACAGG | 145 |
| | (2) INFORMATION FOR SEQ ID NO: 1298: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 139 base pairs | -)(-** |
| 20 | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | · - |
| | (b) 10102000 000000 | |
| | | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298: | |
| | TCCAAAAGTT AAAGGTCAAT TGAAACAGAN AAAGCTTATT ATGTCTGGAA AAGTATTAAA | 60 |
| 30 | AGTAATGGTA TCAAATGACA TTGAACGTAA TCATTTTGAT AAGGCATGTA ATGAAGTCTT | 120 |
| | TCAAGCGTTG AATTGTGGT | 139 |
| - | (2) INFORMATION FOR SEQ ID NO: 1299: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299: | |
| | GATATTGGCA ACCTTCAGCC GATGACCTCA TGGCAAATGA TTGGGAAGTT ATAAACCCAA | 60 |
| 45 | CTAGAGACCA GGAATTATTG AAGCAATTAT AGAAATGCTA TCAATGATAC TTTTTAAATT | 120 |
| | GTTTTTAAAC TCATTTTCAA AGTAAACAAC AGTCTTGTCT GAAATTGTTA CATGATAAAT | 180 |
| 50 | AGTGTTACTA GCATACACGC CGTTTAGGAA CCCAGAGTTT TTAAGTTTAT TTAAATCGTA | 240 |
| | TTTTACATCT TCGAAATGTA GTTTTTGAAA ATACTTTGTA TGTATATCTT TAGCACTTCC | 300 |
| | AAAATTTATT GGCAGGTTAA TTTAATCGAA CCTAACTTTA CACATTCTAA ATAATCTTTG | 360 |

(2) INFORMATION FOR SEQ ID NO: 1300:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 693 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300: | |
| | CTACAGTGCA ATTTAACCAT GAAGTTGTTG ATTTTGAACA ATTATCAAAT GGTCAATGGG | 60 |
| 15 | AAGTTACTGT TAAAAATCGC CTAACTGGTG AGAAATTCAA ACAAGTAACT GACTACGTAT | 120 |
| | TCATCGGTGC TGGCGGTGGA GCAATTCCAT TATTACAAAA AACAGGTATC CCTGAAAGTA | 180 |
| | AACATTTGGG TGGATTCCCT ATCAGTGGTC AATTCTTAGC TTGTACAAAC CCACAAGTTA | 240 |
| 20 | TTGAACAACA CGATGCCAAA GTTTATGGTA AAGAGCCACC TGGTACACCA CCAATGACTG | 300 |
| | TACCTCATTT AGATACGCGT TACATTGATG GTCAAAGAAC ATTATTATTT GGACCATTTG | 360 |
| 25 | CTAATGTTGG ACCTAAATTC TTGAAAAATG GTTCTAACTT AGATTTATTC AAGTCTGTTA | 420 |
| 25 | AAACATACAA CATTACAACT TTATTAGCAG CAGCAGTNAA AAACTTACCT TTAATTAAAT | 480 |
| | ACTCATTTGA CCAAGTAATT ATGACAAAAG AAGGTTGTAT GAACCACTTA CGTACTTTCT | 540 |
| 30 | ATCCAĞAAGC ACGTAATGAA GATTGGCAAT TATACACTGC TGGTAAACGT GTACAAGTTA | 600 |
| | TCAAAGATAC ACCTGAACAC GGTAAAGGAT TCATCCAATT CGGTACAGAA GTGGTTAACT | 660 |
| | CACAAGACCA CACTGMAATT GCATTATTAG GTG | 693 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1301: | : |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 471 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (with appropriate production, and the No. 1201. | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301: | 60 |
| | CATACTTGGG TAATGCTGCC CATGGNACGC TGGNACAAGG TAAAGTTGCA CGTTTAATTT | |
| | GTGnATGTAT ATAAAACAGA TGGGAACACC ATTTGAAGGG GATCCTCGTG CAAACTTAAA | 120 |
| 50 | ACGTGTATTA AAAGAAATGG AAGATTTAGG CTTCACAGAC TTTAACCTAG GACCTGAACC | 180 |
| | AGAATTCTTC TTGTTTAAGT TGGATGAAAA AGGGGAACCA ACTTTAGAAC TTAATGATGA | 240 |
| 55 | TGGTGGATAT TTCGATTTAG CACCTACAGA TTTAGGTGAA AACTGTCGTC GTGATATTGT | 300 |

| | TCAACATGAA ALTGACTTAA ATATGCAGAT GCTGTTACAG CATGTGATAA TATCCAAACA | 420 |
|----|---|-----|
| | TTTAAATTGG TTGTTAAAAC AATCGCACGT AAACATAATT TACACGCAAC A | 471 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1302: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302: | |
| | CATGTGATTA AGAACGTTCA CTGATGAATT TTTGATGATC GTTCGGTTTT TGTTTGGATT | 60 |
| | TTAATGATTA TTTATACAAA AACAGCCGTA TTTCAAGCCG TACATTTTAA ATTTAACTAA | 120 |
| 20 | ATTTGCATCT AGTTAATAAT TGCATTTATC AAATTTGTCT TATTGATCCA ATCTAATTTG | 180 |
| | TACTCACAAA CTAGTTTYAA ATTCTAACTT TATCTCTCAG TTCGTTATCA ATCATCAGAC | 240 |
| | ATAAACCAAT GAAGCAATCA GAAAACACTC TAATTTTCTa TTAGAAATTT GnTTTAATAT | 300 |
| 25 | AAAAAAACAG GCTTACTTCA TATAATTTAT GAAATAAACC CGTCAATTTT TGTTTAATAT | 360 |
| | GCTTGGTGAT CTnTTATTCT GCGTAATAAT GCTAAACCTG | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1303: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 35 | (D) TOPOLOGY: linear | - T |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303: | |
| 40 | AAAAGCTTAG TTGAACTTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC | 60 |
| | AAAAGACTGG GGTAAACTnC GCCTAGCTTA TGAAATCAAT GGATTTCAAA GATGGGCTCT | 120 |
| • | ACAACATC | 128 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1304: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | TCCTTCGGAT TCTAAATGGC ATTGGACAGT GTTTACAAGC TCGCATTTCT CCACTTTTTG | 60 |
|-------------|---|-----|
| | CAATTTCTTT TACAATTTCT AAAGCTTCAT CAAAGTTTCC TTCAATAGNA AACGATTTCT | 120 |
| 5 | GCACCATACA TTACTGACTT G | 141 |
| | (2) INFORMATION FOR SEQ ID NO: 1305: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 162 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305: | |
| | GACTGGTAAA CACTAAGTGA ATTAGCTGGA CAATGAAAAA TATCCACAAT CATTAATTAA | 60 |
| 20 | CGTACGCGTA ACAGATAATA TCGGTTGAAG AAATGTTGAC GTTAAGAGTT ATGACTAANT | 120 |
| | AGAGTAGAAT GATGGTGAGG TCGATTTTAG TAGACTCTGG AC | 162 |
| 25 ′ | (2) INFORMATION FOR SEQ ID NO: 1306: | • |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 282 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306: | |
| 35 | TTCTTAGTTG CTCGAACTAA TAATTTGCTT AATAATGATS TAGCTGTTAT TGTGTCATAT | 60 |
| | TCTAAAGGTG CCATAAATTT AAAAACTATA GTAGTTGTTT TAAATTTAGT TGTTGGTGAA | 120 |
| | ACTITGATAT GTATATITGG TIGAGATIGT CTACTCAAAT ATATAGCCTC CTCTATATCT | 180 |
| 40 | TCTTACATCT ATATTTTCT AGTGATTTTA AATTGAACTA AGCTATTTTT CATATAATTT | 240 |
| | AATGAATACA AAATAGGTTC ATCTGATTCA TTATAGTGCG TA | 282 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1307: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | A LUCATION DECORPTION (SEC. ID. NO. 1207 | |

| | AAGGAAAAA CCCTTGGCCT TTGGAAAAAA CCCAAAAGGA AAGGGGTTTA AAAAAAAAAA | 120 |
|----|--|-----|
| | AAGTTTAACC CGGTTGGCCC CAATTCCCGC CCGGGGAACC CAAAAGGAnT TTTAAAAAAG | 180 |
| | GAAACCCAAT TCCCGGCCGG AAAAGGGTTT TTAAGCCCAA CCGGATTTTA AGGAAAACCA | 240 |
| | TTTTAAGATT ACCTGGGAAA AAAAACCGTT TAGGAA | 276 |
| | (2) INFORMATION FOR SEQ ID NO: 1308: | |
| 9 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 692 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 5 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308: | |
| 0 | TGTATTTAAT GCTCGTACAC ACAATTACAA AACTGCAAGA GAAAAAGCAT TGAGTAATAA | 60 |
| | TCATATTCCA GAAAATGTAT ATGACAATCT AGTAAAAACT GTACATAAAT ATTTACCATT | 120 |
| | GCTACATAGA TATACTGAAT TGCGCAAAGA ATTGCTAGGT TTAGATGACT TGAAAATGTA | 180 |
| 5 | TGATTTATAT ACACCATTAA TTAAAGATAT TAAGTTTGAA ATGCCTTATG AAGAAGCTAA | 240 |
| | AGAGTGGATG TTAAAAGCAT TAGAACCAAT GGGTGAAGAA TATTTAAATG TAGTTAAAGA | 300 |
| | AGGCTTAYAC AATCGTTGGG TCGATGTCTA TGAGAATAAA GGTAAACGTT CAGGTGGCTA | 360 |
| 30 | TTCATCAGGT GCACATTTAA CTAATCCATT TATTCTACTT AACTGGTCTA ATACTATTTC | 420 |
| | AGACTTATAC ACATTAGTTC ATGAATTTGG GCATTCAGCA CATAGTTACT TCAGTAGAAA | 480 |
| | ATTCCAACCG TCAAATTCtA GTGACTACAC TATTTTTGTC GCTGAAGTTG CATCAACTTG | 540 |
| 35 | TAACGAAGCA CTTTTAAGTG ATTATATGGA TAAACATCTT GATGATGAAA AACGCTTATT | 600 |
| | ATTATTAAAC CAAGAATTAG ANCGTTTCAG AGCTACATTA TTCCGACAAA CAATGTTCGC | 660 |
| 40 | AGAATTTGAG CATAANATTC ATGCAATTGA AG | 692 |
| | (2) INFORMATION FOR SEQ ID NO: 1309: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 45 | (A) LENGTH: 151 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309: | |
| | GGACTATTCG ATGATAGCTT TTTTGACTGG ATTTACTAAA ATGAAAGCAA GTACTATATA | 60 |

| | atCGAGTAAT ATCTATATAT GACATTTTAA A | 151 |
|-----------|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1310: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 10 | (D) TOPOLOGY: linear | , |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310: | (8) |
| 15 | TGTGCATTTG ATAATATTCA CTATGATTCG TGGTCATTCA CATCGTCTAC GCTCACCGGT | 60 |
| | CTARACGTAC CTARCCCARC ATGTARTGAR CARATGCGAT ATTARCACCT TTATT | 115 |
| | (2) INFORMATION FOR SEQ ID NO: 1311: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 164 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | - |
| 25 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311: | |
| 30 | CACCCAACTG ACCTCAATGG TATAATGCAT TTGTGAATAC CGAATATCAT TGGAATATCT | 60 |
| | CCTATCATAG GAATATAATA TGTATATATC TTCGTAATCn TGTTCATTTT TAAGAAAATC | 120 |
| | AATAGAAGTG TATCGATTAA AACTACATTT GAACCATTAC TTTG | 164 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1312: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312: | |
| | GAGGAAAATC GAAGTGAAAT TATTAAAATA TGGCGATGGT GGAATACGAA TAGATGGTGG | 60 |
| | TTTAATAGGC GGCTTTATTC GGGTGTTATT GTATGTAAAG TGAAAAATTT AAnCCCATTT | 120 |
| 50 | CAAATTGGTG ATATCGTTGC G | 141 |
| | (2) INFORMATION FOR SEQ ID NO: 1313: | |
| <i>EE</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-------------|---|-------|
| 5 | | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313: | |
| | AATTGGTATT ATGCATAGTG CAATGGATGC TGGTATTAAA nTCCAGAGGA TTACAATTAT | 60 |
| 10 | TAGTTTCAAT AATCACGATT AGTTGAGATG GTTAGCCACA ACTTTCTAGT GTATCACCAT | 120 |
| 1 - 1 - 1 W | TATATGTATC GGT | . 133 |
| | (2) INFORMATION FOR SEQ ID NO: 1314: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 629 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314: | |
| 25 | TTGCAATTAG AATGCTGTTT CACCCCTTTA AACCATACTA TATATTTAAA TTTAGAGTCC | 60 |
| | CATTTACACC AGGTTTAATA CCGAAAAGAC GCGAAGAAAT TGCAACTAAA ATTGGCCAAG | 120 |
| | TGATTGAAGA GCATTTGCTT ACAGAAACTT TAATTAATGA AAAATTGAAA 10000000000000000000000000000000000 | 180 |
| 30 | CACAGCAAGC AATAGAATCT ATGATTCAAC AGCAGTTACA AAAGTTGACG AAAGATCAAT | 240 |
| | TGTCAATAAA ACAAATTACT TCTCAAATCG LATTGATTTA GAACAAGTAT TACAAACTAA | 360 |
| | TGGAAATCAA TATATTGAAT CACAATTGAA TAATTATTAT aCAAAGCATC AAAACCAAAC | 420 |
| 35 | AATAGCATCT TTATTGCCAA ATCAACTTGT AACATTTTTA AATCAGCATG TAGATAACGC | 480 |
| | AACAGACTTA TTATGTGATC GTGCAAGGAA TTATTTATCA TCTGCAAAAG GCACACAAGA | 540 |
| 40 | TATTAATGAT ATGTTGGATA CTTTTTCAA TGAGAAAGGT AAGTTAATTG GTATGTTGCA | 600 |
| 40 | AATGTTTATG ACAAAAGAGA GTATTGCAGA TCGCATTCAA CAAGAACTTA TACGTTTAAC | 629 |
| | ATCTCATCCT AAAGCAAGAA CAATTGTGA | 623 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1315: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

1916 :

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 1315:

| | ATACAGGTAC GTTCGTTATC AATGGTGCAG AACGTGTAAT CGTATCTCAA TTAGTTCGTT | 120 |
|------------|---|-----|
| | CACCATCCGT TTATTTCAAT GAAAAAATCG ACAAAAATGG TCGTGAAAAC TATGATGCAA | 180 |
| 5 | CAATTATTCC AAACCGTGGT GCATGGTTAG AATATGAAAC AGATGCTAAA GATGTTGTAT | 240 |
| | ACGTACGTAT TGATAGAACA CGTAAACTAC CATTAACAGT ATTGTTACGT GCATTAGGGT | 300 |
| 10 | TCTCAAGCGA CCCAAGAAAT TGnTGACCTT TAAGGGGACC AATGGAATAT nTACCGTAAT | 360 |
| 10 | ACCTTTAGGA GGAAAGACCG GCACCTGAAA CCACTGGAA | 399 |
| | (2) INFORMATION FOR SEQ ID NO: 1316: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 778 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316: | |
| | ATAAACATTT TAANATGTAA TINAGAAATT TTTTTAGTAC AAAATCTTTC TTAATAATGA | 60 |
| 25 | TTAAGGAGGT CAGTAATGAT TGAAATTAAA ACATTAACGA ATAATGATTT TAATGAGTAT | 120 |
| | AAGAGACTTG TTTCGACAGT CAATGAAGAA TTCACTCAAG ATTCACATTA TAGTCAAACA | 180 |
| 30 | ATGACEGACA CCTTAATACA TGACATTTTA AATCAAGGTT CACCGAAATG TATTGTATTT | 240 |
| | GGCTGTTATG AAAACGAAAC ACTTATCGCA ACAGCTGCCT TAGAACAAAT TCGATACGTT | 300 |
| 3 | GGAAAAGAAC ATAAATCATT AATTAAATAC AACTTTGTTA CTAATAACGA TAAATCGATT | 360 |
| 35 | AATAGCGAGC TCATTAATTT CATTATTAAT TATGCACGGC AGAACAATTA CGAATCTTTA | 420 |
| | CTTACATCAA TTGTGTCAAA CAACATAGnn GCTAAAGTTT TCTATAGTGC ACTAGGATTC | 480 |
| | GACATTCTTG GTTTTGAGAA AAATGCAATT AAAATCGGAA ATACCTATTT CGATGAACAT | 540 |
| 10 | TGGCTTTTT ATGATTTGAT TAATAAGTAA TACAGTTTTA TATATTCTAC rTTTCTCATA | 600 |
| | AATTCAAATC ATATAGGTTC TATTTTTCAT ACAACTACTC TACTATTGAG TAGTTGTTTT | 660 |
| | TTATTTGATA TGATAACAAT AAGTTTTTTT CAGAATATTC TATGTTTTAG GGGTGTCAAA | 720 |
| 15 | ACTTAATGGG TAACCGCAAT TATTCATGGA nTTATCnTAA GCGATTGGGT CCTAANTT | 778 |
| | (2) INFORMATION FOR SEQ ID NO: 1317: | |
| 5 0 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 465 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317: | |
|----|--|------|
| | TGCACAAGGT GGTGCAGCAA TTGCAGCGTT CTTTATTATT AAACAAAATA AGAAGTTAAA | 60 |
| 5 | AGGTGTGGCA TCTGCCGCAG TATTTTCAGC ATTACTTGGT ATTACAGAAC CGGCTATGTT | 120 |
| | TGGTGTTACT TAAAACTAAG ATATCCATTT ATTGGCGCTA TCGTTGGATC AGGTATTGGT | 180 |
| | TCAGCATATA TTGCTTTCTT CAAGGTTAAA GCAATCGCAT TAGGAACTGC TGGATTGCCA | 240 |
| 10 | GGATTLATTT CAATCAATCC AGTACATGCA GGATGGTTAC ACTACTTTGT TGGTATGACA | 300 |
| | ATATCATTCA TCATTGCTAT AACAGTTACT TTAALTTTAT CLAABAGAAB AGCAAATAAA | 360 |
| 15 | GAAGTTGTAG AATAAAAAA GAGGTATGAC AGTAATCAAA GTATCAGTCA TTGCAAATGC | 420 |
| | AATAGGATGA AACTTTAAGC TGTCATACCT TTNAATTTAG TTATA | 465 |
| | (2) INFORMATION FOR SEQ ID NO: 1318: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150-base pairs | |
| - | (E) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318: | |
| | GACTTAATAT AACTGATCTT TTGCTATTAT TGAAACATAT TTATAAAGAA AATAGCATTG | . 60 |
| 30 | CATAATACCC AAGCAATAAA TACTATAATA TTTTGGAAGT AACTAATCAA ACATCTAAGA | 120 |
| | CATGATTGAT AnCACCACAG AAAAATAAGA | 150 |
| - | (2) INFORMATION FOR SEQ ID NO: 1319: | • |
| 35 | (i) SEQUENCE CHARACTERISTICS: | |
| • | (A) LENGTH: 131 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | |
| | | |
| • | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319: | |
| 45 | CCACCTTTTA ACGTACGTAT CCATGAATCA TATGATTAAT TTAATATCAT TATTACTTAT | 60 |
| | TTCTTATCTT TATTNTCTTT TTTTCTTCTG AAAAGTAGTA ATGAACCTAT TGATGCTAAT | 120 |
| | AATCCCCAAA T | 131 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1320: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 140 base pairs | |

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320: | |
|----------|---|------|
| | (XI) SECONICE DESCRIPTION: SEC ID NO: 1320: | |
| | TAGTGTCCAA ATGAAAGTGT GGCTACCTAT AGCTGGTCCA TGAAGCTTTA TTTTTAACTG | 60 |
| 10 | GTTTGTACAA TATTTAAATA TCAAAATCTT CTCGCGnTTT GGACAGTTTT TTTGGTATTA | 120 |
| , | ACCATTAATA AACGGAAAGA | 140 |
| | (2) INFORMATION FOR SEQ ID NO: 1321: | |
| 15 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 140 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321: | |
| 25 | CTTATTATAT AATTCTAATC CTAGTACATT ATACATTTTA TCAAATAGTC AACTGGATAA | . 60 |
| | CTTTGAAAGT GAATGATnCT TTTAAAATAA AGAAGATAAT ATAAAGTGCT TGATAATGGA | 120 |
| • | TTTGTAGTTG ATGATTTAAA | 140 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1322: | |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 185 base pairs(B) TYPE: nucleic acid | |
| 35 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322: | |
| 40 | TCGTTGCAAC ACAGGCACTA TTTTACCTTT ATATGTTGTA ATAGTTTGAT TGCTGCCATT | 60 |
| | TAAACAACCA CCTTTCTTAC TCCACAAATT TACCATGAAT AGCGCGCGCG CCATAGCGGG | 120 |
| 45 | ATACTAAAGT GTTCTGCACC TTGCCTGTCT CCTTCAAnTT TCGATTACTG TAGAGCACAA | 180 |
| | GTACG | 185 |
| | (2) INFORMATION FOR SEQ ID NO: 1323: | |
| 50 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 148 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| J-J | | |

| | (XI) SEQUENCE DESCRIPTION: SEQ ID NO. 1010 | |
|-----------|---|---------|
| | ACCTGCAATT TTCGTTATTC AAAACAATAA CTATGCAATT TCAACACCAC GGAGCAAGCA | 60 |
| 5 | AACTGCTGCT GAAACATTAG CTCAAAAAGC AATTGCTGTA GGTATTCCTG GGTATCCCAA | 120 |
| | GTTGGTGGTA TGGTGCGGTA nTTGGTTT | 148 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1324: | • |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid | |
| 15 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324: | • • • • |
| 20 | GAAAGCATTG ATGGACAAAG ATGAACCACC AAATGAATGG CGATTAGATT CCAATTGATA | 60 |
| | TGGCTCACGG AAAATTTATG CTACAATTGC GTCCAGTAAA CAGTGGCACT AATAGTCCAC | 120 |
| 25 | TTANGCTCCC TAGTGGATGA A | 141 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1325: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 204 base pairs | |
| 30 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325: | |
| | TTATACTATC GTGAAGGGTT TATTACTCAA TTAATGCCTA AAAAGGATAA AAGTTATTTA | 60 |
| | GTTATTGATA ATTTTAATCG TATAGATACA GACATTTTCC AAACGTATAT TAATGTGTTA | 120 |
| 40 | GAAGGCTATG AAGTAACATT ACCACGTTAT AATAAAGACG GTAATATGAT TAAATGGTCA | 180 |
| | CGACAAAAG ATTCTTTCTA TTAT | 204 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1326: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 147 base pairs | • |
| <i>50</i> | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1326: | • |

| | THE THE STATE OF T | 120 |
|----|--|-----|
| _ | AGCAGCTTTT TCTTTATTAA CAGCTGT | 147 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1327: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 530 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327: | |
| | CATTNAATGA AGAAACTGAA CCCNGAACTA TACGACGCAG AAGGCAATTT AATTAATAAT | 60 |
| | AGTAAAACAT CCAGCTTAAT CCATTGATGT GTTATAAAAG TGAAAAGCTC CAATCAAAGT | 120 |
| 20 | TGACGCTCAA ATAGTTTAAC TTTGATCGGA GCTTTTTTAT AATGTATACC GAAAGGTTCA | 180 |
| | AATATTATAT AATGGTAGAA TTGAAAGAGA ATATAAAAAA GTGAGGATAT AAAATGAAAG | 240 |
| 25 | TTAATCCTAA TAATATAGAA TTAATCATTA GTGCAGTAAA AGAAGAACAA TATCCAGAAA | 300 |
| 20 | CAGAATTGTC TGAAGTGCAC TGAGCGGTCG ATCTAATGTA GGTAAGTCTA CATTTATCCA | 360 |
| | ATAGTATGAT TGGCAGAAAA AATATGGCAC GTACATCACA GCAACCCGGC AAAACGCAAA | 420 |
| 30 | CGTTAAATTT TTATAATATA GATGAACAAC TTATTTTTGT GGATGTTCCA GGGTATGGAT | 480 |
| | ATGCTAAAGT AAGTAAAACA CAACGTGAAA AATTTGGGAA AATGATTGAG | 530 |
| | (2) INFORMATION FOR SEQ ID NO: 1328: | , |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328: | |
| 45 | AAGAAAGTTT GATCTAGGCC AACCTTTCTA ACAACGATAC GACAGTTTAA TAATGTCTCA | 60 |
| | TATCTTGACT TCCCATGATG ATATGGTCGT TAATCACATC AATGACTTAA ATCTGGATNA | 120 |
| | ATAGATGCGA ATGGATCTTG AAAAATCATT GTA | 153 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1329: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329: | |
|----|---|-------------|
| | TGTAGTTCGT TTGTGCTCTA ATTAAACGGT CGAAACCATG GATTAGACCT GCGATTACAA | 60 |
| 5 | CTGCAATGAT ACCTGAAGCA TGAACTTCTT CTGnTAAAAA GTATACGACA AAAGG | 115 |
| | (2) INFORMATION FOR SEQ ID NO: 1330: | • |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | *** |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330: | |
| | AACAAGTTAT CTACATCTGC TGATAGGCAT ACTATTACTA ATAAATAATG CATCTTTTTG | 60 |
| 20 | CCAGATGTTT TCTTAATCAA TTGCACCAAC GAATGGCACT CTCATCTGTA Gn | 112 |
| | (2) INFORMATION FOR SEQ ID NO: 1331: | e i gapere |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 203 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331: | |
| | TTCATTGCAG ACANTTGGTG AACCATGTGG ACGAACTAGT CCTAGATTAA GATAAGAGAT | 60 |
| 35 | TAGTGANCAT TGCCACCACT GCAATTAAAC ATTCTTGGAA AAATTAACTT AAGTTAGAAT | 120 |
| • | CTTAATGCAT ACAGATACGG CGAAGATGAT GCCAAAGAAC GTCACGACTT TATGATGATG | 180 |
| | ACTGAACCCA GTTTTTACGG AAG | 203 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1332: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 269 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | : : : |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332: | |
| | ATGATGTACT AATATCTAAT AAGCTTGCTA AGTCTTGAGA CCTCATTTTA ATCACCTTTT | 60 |

| | GACIATORA TICIGITAGI ACGITIGACA TATTAATCAC TCCACYTTAA CGCAATAWAW | 180 |
|----------|---|-----|
| | TTTAWTAGCG TTGGCTATTG TTGTTTAACG CGATGGNATT TACAACTTGT AACGTAAGAG | 240 |
| 5 | AATGAAAAAT AAGCTGnATA TGTTGTTTG | 269 |
| | (2) INFORMATION FOR SEQ ID NO: 1333: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 142 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333: | |
| | TAGCTTTTGC CCAATATGGT GAATCATGCG CCGTTCTGTA ATAATCTTCA CTTGGCATTC | 60 |
| 20 | TTGGAATTTG AACAACATCC TGTTCATTTT TATAGAnTGC TTAAATGGTA CAGCTGAAAA | 120 |
| | ATCAAAGTAA TGTCCTTTTC TG | 142 |
| | (2) INFORMATION FOR SEQ ID NO: 1334: | * |
| 25 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 211 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334: | |
| 35 | ACTGATGCCC AATATGCATC TTGnCAATTG CAGGTGTGCA TGACTAAACA CATGACAAAT | 60 |
| | CTGCCTGACT TTTTGCTGAC CCATAAATAA TTGGnCTAAC TTTTTGCATC TTGATCTTGC | 120 |
| | ATCCTTGCCT TCCTATTTAA AATGCTACAA ATAAATTTGC CGGCGAGTGA ATTTTAATGT | 180 |
| 40 | TTTACAACGC TGTTCAATAC CTGGGAATAA G | 211 |
| | (2) INFORMATION FOR SEQ ID NO: 1335: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335: | • |
| | CTTGAATCTC TTGTGCCTCT GTGATGTATC ATCAAATTAT TTGCACTGCT TCTTCTTTTA | 60 |

| | TCCGCTCGC | | | 129 |
|----|--|--------------|---------------------------------------|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1336: | | () | |
| 5 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 633 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | | | |
| 10 | (D) TOPOLOGY: linear | • | | |
| | was a second of | | · · · · · · · · · · · · · · · · · · · | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: | 1336: | | |
| 15 | CATGATGGCn TCTTACCAAA GGCGATTTTA AGAGCAATGA | TACCAAGATA | TTTTTAATAC | 60 |
| | TGATCAAAGT TCAGGTGGTA GCACAATTAC ACAACAACT | GTTAAAAATC | AAGTTCTTAC | 120 |
| | CAACGAAAAA ACATATAGTA GAAAAGCAAA TGAATnCGCC | TAGCAATTAG | ATTAGAACAC | 180 |
| 20 | CTACTCTCAA AAGATGAAAT TATATATACA TATTTAAAT | A TAGTTCCLTC | GGTAGAGATT | 240 |
| | ATAATGGCGC TAATATTTCC GGAATTGCAT CCGCTTCAT | A TAGTCTATTI | GGTATTCCAC | 300 |
| - | CAAAAGATTT ATCAATTGCA CAATCTGCAT ACCTTATCG | 3 TTTGTTGCAA | AGCCCATATG | 360 |
| 25 | GCTATACACC CTACGAAAAA GATGGAACGT TAAAATCGG | A TAAAGATTTG | AAATATAGTA | 420 |
| | TTCAAAGACA ACATTATGTA TTAAAGCGTA TGTTAATCG | A AGATCAAATC | ACTGAAAAAG | 480 |
| | AATACAACGA CGCATTAAAA TATGATATTA AATCACATT | T GTTAAATCGA | AAAAAGCGTT | 540 |
| 30 | AATTGATGCT CACTTTTTAA AGTAACCACA ACAATGAAT | C CAAATATTA | AAACAGCAGT | 600 |
| | AAGATTATTT TCAATTAGAA AATTTCTCAC TGC | | | 633 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1337: | | | |
| | (i) SEQUENCE CHARACTERISTICS: | | • | |
| | (A) LENGTH: 317 base pairs(B) TYPE: nucleic acid | | | . • |
| 40 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | • | |
| | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: | 1337: | , <u></u> | |
| 45 | ATCAATATTT AGCAGTTATC ATTATGCTTG AACGGGTGC | | G AAGTCATCCA | 60 |
| | CTTTTCCTA TACTACAAGG ACCTTTACTT TAAAACAAG | | | 120 |
| | | | | |
| 50 | TAATTTCTTT TCTGTCACAT CGCTCATTCT AACTACTAC | | | |
| | ATTTAAACTC AATCAACTnT CAATTAATGA TGCATAAT | | | |
| | ACTICAAATA TOTTAGAAAT GTOOTGTACT ATATOTOT | TT TATTCTCAR | A AGTCATAGGT | 300 |

| | (2) INFORMATION FOR SEQ ID NO: 1338: | |
|----|---|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338: | |
| | TACGGCATAT ACCTCGTTCA TCAATGTTCG TAAACATTAT TTAAAACATC TCTTACATCT | 60 |
| 15 | TGCGTTGGAA GTTCTTCATA GTCGAATTTC ATTGTmTTAT CAAAGTTTTC CATTTGCGAC | 120 |
| | ACTCC | 125 |
| | (2) INFORMATION FOR SEQ ID NO: 1339: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339: | |
| | GAGCTTCGTT CCATTGTTAT CAAACGATTG CCATTCTGAA ATGCTGTAAA TAGCATGCTT | 60 |
| 30 | CAAATCATCT TGTGCCTGCA GCAGTTTCTT TGNAATATGC TTCATATCAT T | 111 |
| | (2) INFORMATION FOR SEQ ID NO: 1340: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 158 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340: | |
| | TCACACGTTT AGTTTTCTAT GAATACCAAT ATTTTAACAC CATGTTTAGC CAATTTGTCT | 60 |
| 45 | GCTAAATTAA TCGTGTTTGT CCTCCAAATT GACACGCACC TTTAGTTTTT CTAAATAATG | 120 |
| | ATATCATCAC ATCTCTCAGT TAAAGGTCAA ANATATTG | 158 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1341: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341: | |
|----|---|------|
| | GCTTCAGGTC AATTAAAACG TTCAAGAGCT TTCACATCTC ACTTATTCGC AAACAAGAGC | 60 |
| 5 | ACTANACANA NACGICANTI ACGINANGCI AGATTAGIGI CINAGAGCGA TAIGANACGI | 120 |
| | GTAAAACAAT TATTAGCATA CAAAAAATAA GAACAAATAC AGAAATCGGT AGGAATTACC | 180 |
| 10 | TAAGGAGGAA TTTTTTATGC CACGAGTTAA AGGTGGAACA GTAACAAGAG CGCGTCGTAA | 240 |
| | AAAAACGATT AAATTAGCTA AAGGTTACTT CGGTTCAAAA CATACATTAT ACAAAGTAGC | 300 |
| | TAAGCAACAA GTAATGAAAT CAGGTCAATA TGCTTTCCGT GACCGTCGTC AACGTAAACG | 360 |
| 15 | TGACTTCCGT AAATTATGGA TTACACGTAT CAACGCAGCA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1342: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 20 | (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | ···· |
| | (D) TOPOLOGY: linear | |
| | | |
| 25 | (/) CRANDOR PROGREDATION, CRO ID NO. 1242. | |
| *. | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342: | |
| | GTTGAACAAG GGCAACAAAA ATTTCGAGCG AAACAGATTT TTGAATGGTT ATATCAAAAA | 60 |
| 30 | AGAGTAGATT CGATTGATGA AATGACGAAC TTATCGAAAG ACTTACGACA GCTTTTAAAA | 120 |
| | GATAACTTTA CTGTTACAAC TTTAACAACT GTAGTAAAAC AAGAAAGTAA AGACGGTACA | 180 |
| | ATTAAATTCT TATTTGAATT ACAAGATGGC TATACAATTG AAACTGTTTT AATGAGACAT | 240 |
| 35 | GATTATGGAA ATTCAGTATG TGTAACGACA CAAGTAGGTT GTCGCATCGG ATGTACGTTT | 300 |
| | TGTGCTTCTA CACTTGGCGG CTTAAAAAGA AACCTTGAAG CTGGCGAAAT TGTTTCACAA | 360 |
| | GTTTTAACAG TTCAAAAAGC CCTTGATGCT ACAGAAGAGC | 400 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1343: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid | - |
| 45 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (b) Toronogi. Timear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343: | |
| | GAAAATTTCA TCAGGTGTTG GCGTGGAACG TACATTCCCA TTACACACAC CAAAAATTGA | 60 |

| | TITACGTGGT AAAGCTGCTA GAATCCAAGA AATTCGTTAA TCAGCATTTA AACAAAGCTA | 180 |
|----------|---|------|
| | TGTATGAGTC AAATTCGACT CAAACAATAA AGCCATCTAG GTCACTTTTA TGGAGTGATA | 240 |
| <i>5</i> | TAGATGGCTT TTTTTGCTGT TTAGTTAATG TAAAGTTGAT AATGTAATTG TTTATTCCTT | 300 |
| | CTCTATTCAT AACGTGTTTG CTCAAAATGG TTATATAAAC AAAAATCTAC TAAGTGCCAT | 360 |
| 10 | TGAAAAGGAC TTAGTAGATT TATTAAATAT ATGCGTANA | 399 |
| ,,, | (2) INFORMATION FOR SEQ ID NO: 1344: | • |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 134 base pairs (B) TYPE: nucleic acid | |
| 15 | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344: | |
| | AACTTACAAC ACCAGGTAAT AACAGCAATA AAGGCACCAG TTAGTGCGGT AATGCCAnTA | . 60 |
| | TCTAGGCCTT TAGGTTGCCA TAGTACGAGA TGTAGAGGTA CTAGAGGAAT GAGTGTCGCT | 120 |
| 25 | AAAGTTGTCG TCGT | 134 |
| | (2) INFORMATION FOR SEQ ID NO: 1345: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 30 | (A) LENGTH: 109 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 35 | are well | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345: | |
| | TCATAATAAA CAAGTTCACA TGAATCACAA CATCTGAAGA CAATGTTCAA AATGAGGCTG | 60 |
| 40 | GCACAATAGA TGATCGCAAG TCGnATCATC ACACAGTACT GAAGCAAGA | 109 |
| | (2) INFORMATION FOR SEQ ID NO: 1346: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 45 | (A) LENGTH: 113 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346: | |
| | CCATATCTGG nACGACCGAC ACCTTTACCA CCAACGATTG GTGCCATTTG TTTGCATAAG | 60 |
| | • | |

| | (2) INFORMATION FOR SEQ ID NO. 1347. | |
|-------------|--|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347: | |
| , | CAATTGAAAG GTGAATTTTA TAGGTCCATG ACAAACTAAG GCTTGTTAAA GCTTATTAAC | 60 |
| 15 | ACAGTTTCAT CAAATAGTTA AATTAGTTTT TGTTTTGCAA TAAATTGGGT ATAGATTACA | 120 |
| | Antg | 124 |
| | (2) INFORMATION FOR SEQ ID NO: 1348: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 337 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348: | |
| | CATCAGTGGC CTGATCACCC CAACATTTGA CATCAATGCA TACCAGTTGA TTTGAACAAT | 60 |
| 30 . | GATTGCATTG AGCTATCATC AAGTTTGTCT TTAAGCTACT AAACCCACGA ACCATGTTAA | 120 |
| | CCCCGTGGTC ACCATCACCA ATTGCTCGAT CTAATTCAGT TAATTCAGAT TCATGTTTTT | 180 |
| • | | 240 |
| 35 | TAAACGTTTC TTCTAAATTT AATAAACGTG CTTTCATATC ATCALTTCAT TGTGCaCtaT | |
| | AAATGLATAT TATTCATATT CACTTCTnAT TTAAAGTATG ACTTGTTGTT GGTGCTAAAA | 300 |
| | ATGCTTCCAA ATATTCTGGT TTATTAGGCA CGATAGT | 337 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1349: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 162 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349: | |
| 50 | CAGCACGTAA ATACAACAAA GCGATCCCCA GCTTGTGGCA CATCATTAAT ACCTGTAATT | 60 |
| | TO THE PARTY OF TH | 120 |

(2) INFORMATION FOR SEQ ID NO: 1350:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|---|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350: | |
| | CAATTTACT TTGAATTCT TTTTTATCTT TTCTAGTTTT ATCGTCCCAC TCTTCAATCC | 60 |
| | APTITTIAGC TITATCTCA TTATTAGTCA ACTTGCCTAT TTCTTTTAAT ATTCTTTATG | 120 |
| 15 | ATTGTATTTA TTGTATGTAT ATGGGATTGT TGGCGCTATT TTTTGGTATT TTTTTATATT | 180 |
| | | 240 |
| | TTTATCCATA GCATCTACAA CAATTAAATC TGGTTTtGCT TTAGCAACTC TTTCAACATC | |
| 20 | ATTITCTCCA ATATAATCAA CCCCTTTTAA ATAAGGTTTT AAAATTGAAG AATCTTTAGT | 300 |
| | TATATCTGAA ACAGCAATTG GTTTGATTCC TAACTTTATA AAATCACCAA CATAAAATCC | 360 |
| | AGTTAATACA GCAACTCTTT TAAGGTTCTC NGGGACTTT | 399 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1351: | |
| <i>30</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351: | |
| 35 | TAAAACTTAG GCGGTTTTGC ATGATTATAG CGCTCAACAC GTTTGAAATT ATAGGTCATC | 60 |
| | TCTGGTATTC TTGTACGATT CTTTTTCCAA TCTAAATCAA AGTTTTCAAT TTCTTCTTTT | 120 |
| 40 | GAGTTTAGAC TTAATCGATC ACGTTCATGT TCTTTAAAAG ATGGAATAAC TTGTTTAAGT | 180 |
| 70 | GACCCTTCCA TTCTTAATTG ACCATGTGAA AACCAAGCTA TGTAGTTACT CACTTGTGAA | 240 |
| | ATTITATCAA TATCATCACC AATTGACACA ATCGTTAAAT TATTITCAAT ATAATCATTT | 300 |
| 45 | GTTAATTCAA TCGCACGTTC CATAAATTGT GGTGTTAAAT AGTCAATAAC ATGATTTAAA | 360 |
| • * | ATAATAATAT TTGATTTTGA TGAGCGTGCA ATACTTAATA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1352: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352: | |
|-------------|---|-----|
| 5 | AAGGGAACAA AAGCTGGAGC TCCACCGCGG TGCGGCCGCT CTAGAACTAG TGGATCCCCC | 60 |
| - | GGGCTGCAGG AATTCGGCAC GAGCATATCT AGTATTTTAG GACGGAGGNA GTACATT | 117 |
| | (2) INFORMATION FOR SEQ ID NO: 1353: | 1 |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ; |
| 15 | (b) Topologi: linear | *** |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353: | |
| | AGTTCAGGAG AGTTATAAAT ATTAGGGTGG TACATGCCCG AAATCATTGG AATTGTTAAA | 60 |
| 20 | GTAGATTTTA CAGTTTAGAG ATAACAGACA TGTCTATATG AAGGGCTGTC TACCCTCGTA | 120 |
| • | AGGTTATATC CTACAGNTGA ACGTATCAAG CTT | 153 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1354: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 159 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| <i>30</i> _ | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354: | |
| 35 | TGTTGTAACA GCTCTCTATG TTTACGTTGG AAGTATGGTT TATTTTTCAT CTTCACATTT | 60 |
| | AGTTCCTTAT TTAAAAGTGA TAGAGCAATT GCACTCGTAG GTCAAGAAGC GGGATGCCAA | 120 |
| | CACAAAGTTC ACAAGAnAAT ACACTTTTGA AAATATTGG | 159 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1355: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | * 8 |
| | (C) STRANDEDNESS: GOUDIE (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355: | |
| | CONCETTOTT CARCONTIGE AGAAGTTGTC TCATATACTT ACTACGGCTT GCTAATACTC | 60 |

| CAAATTATAG ATGTCAACAT GTTTCTTCGA CACCTACAAA AGATGCACAA (2) INFORMATION FOR SEQ ID NO: 1357: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357: TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGN GCCTCACTAT CATTT. ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCAT GTTGAAGATA TCG (2) INFORMATION FOR SEQ ID NO: 1358: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACAATCAAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCAGG ATAAAAGATGA AATAAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTCAGAA | (: | INFORMATION FOR SEQ ID NO: 1356: | |
|---|-----|--|-----|
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356: GGATTCATTG GTGCTTATTT ATTTACATTC AATAATGAGA NCTTTACACA ACCAM CAAATTATAG ATGTCAACAT GTTTCTTCGA CACCTACAAA AGATGCACAA (2) INFORMATION FOR SEQ ID NO: 1357: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357: TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGN GCCTCACTAT CATTT. 30 ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCAT GTTGAAGATA TCG (2) INFORMATION FOR SEQ ID NO: 1358: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: 45 GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCAG 66 ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTC | | (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356: GGATTCATTG GTGCTTATTT ATTTACATTC AATAATGAGA NCTTTACACA ACCAM CAAATTATAG ATGTCAACAT GTTTCTTCGA CACCTACAAA AGATGCACAA (2) INFORMATION FOR SEQ ID NO: 1357: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357: TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGN GCCTCACTAT CATTT. 30 ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCAT GTTGAAGATA TCG (2) INFORMATION FOR SEQ ID NO: 1358: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: 45 GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCAG 66 ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTC | | | |
| CAAATTATAG ATGTCAACAT GTTTCTTCGA CACCTACAAA AGATGCACAA (2) INFORMATION FOR SEQ ID NO: 1357: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357: TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGN GCCTCACTAT CATTT. ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCAT GTTGAAGATA TCG (2) INFORMATION FOR SEQ ID NO: 1358: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACAATCAAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCAGG ATAAAAGATGA AATAAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTCAGAA | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356: | |
| (2) INFORMATION FOR SEQ ID NO: 1357: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357: TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGA GCCTCACTAT CATTTAGTACAGAGATA TCG (2) INFORMATION FOR SEQ ID NO: 1358: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: GTGTCGGTAA GTCCACTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACAATTATATCAAA ATCATTAAAT CGAGGAAAGCA ATACTACAAG ACATGTCGAA CTATTGGTCAAAACGG TTATATTGCA GACACACCTG GATTCAGAG ACATGTCGAA CATGTC ATAAAAGATGA AATAAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTC | GC | ATTCATTG GTGCTTATTT ATTTACATTC AATAATGAGA NCTTTACACA ACCAATTGGT | 60 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357: TAATGGTGGG GTATATTAT ATTAGTACCG AATTTTAGGGG GCCTCACTAT CATTT. 30 ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCATGTGAAGATA TCG (2) INFORMATION FOR SEQ ID NO: 1358: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: 45 GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACGATTATATCAAA ATCATTAAAT CGAGGAAAGCA ATACTACAAG ACATGTCGAA CTATTGGTCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCACAGA ACTAAAAGGT TATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCACAGA ACATGAGTGAA CATGTCGAA CATGTCGAA ACATGATCAAAAAAGGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTC | C. | NATTATAG ATGTCAACAT GTTTCTTCGA CACCTACAAA AGATGCACAA | 110 |
| (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357: TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGN GCCTCACTAT CATTT ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCAT GTTGAAGATA TCG (2) INFORMATION FOR SEQ ID NO: 1358: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACA ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTG GTCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCAT GTCAAAAGGT AATAAAAGGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTC | (2 | INFORMATION FOR SEQ ID NO: 1357: | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357: TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGM GCCTCACTAT CATTT. ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCATGGTGAAGATA TCG (2) INFORMATION FOR SEQ ID NO: 1358: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACCACACACACACACACACACACACACACACACACA | | (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357: TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGN GCCTCACTAT CATTT. 30 ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCAT GTTGAAGATA TCG (2) INFORMATION FOR SEQ ID NO: 1358: 35 | | (D) TOPOLOGY: linear | |
| 30 ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCAT GTTGAAGATA TCG (2) INFORMATION FOR SEQ ID NO: 1358: 35 (i) SEQUENCE CHARACTERISTICS: | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357: | |
| GTTGAAGATA TCG (2) INFORMATION FOR SEQ ID NO: 1358: 35 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACA ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTAC GTCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCAA 50 ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTA | TA | TGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGn GCCTCACTAT CATTTATCAA | 60 |
| (2) INFORMATION FOR SEQ ID NO: 1358: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACA ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTC GTCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCAA ATAAAGATGA AATAAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTC | A7 | ATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCATTAGTC | 120 |
| (a) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACA ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTC GTCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCAA ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTC | G | GAAGATA TCG | 133 |
| (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACA ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTC GTCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCAA 50 ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTA | ~(2 | INFORMATION FOR SEQ ID NO: 1358: | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACA ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTC GTCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCAA ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTA | | (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: GTGTCGGTAA GTCCACTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACA ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTC GTCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCAA 50 ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTA | | | |
| GTGTCGGTAA GTCCACTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACA ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTC GTCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCAC 50 ATAAAGATGA AATAAAAGAT TATTTCTTG AATTAAATCG ATATGGTGAA CATGTC | | | |
| ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTC GTCAAAACGG TTATATTGCA GACACCCTG GATTCAGTGC TTTAGATTTT GATCA 50 ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGT | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358: | |
| GTCAAAACGG TTATATTGCA GACACCTG GATTCAGTGC TTTAGATTTT GATCAS 50 ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTS | GT | TCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACAAATG | 60 |
| ATAAAGATGA AATAAAAGAT TATTTCTTG AATTAAATCG ATATGGTGAA CATGT | A | TATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTCGAAC | 120 |
| | G | CAAAACGG TTATATTGCA GACACCCTG GATTCAGTGC TTTAGATTTT GATCATATAG | 180 |
| TAGGAATTGT AATCATATCA AAGAACCTAA TTGTAATGTT AAGCATCAAT TAGAGA | A | AAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTAAGTT | 240 |
| | TA | GAATTGT AATCATATCA AAGAACCTAA TTGTAATGTT AAGCATCAAT TAGAGATAGG | 300 |
| GAATATTGCG CAATTTAGAT ACGACCATTA TTTACAACTA TTTAATGAAA TTTCC | G. | TATTGCG CAATTTAGAT ACGACCATTA TTTACAACTA TTTAATGAAA TTTCCAAATA | 360 |

(2) INFORMATION FOR SEQ ID NO: 1359:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 392 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----|---|-----|
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359: | |
| • | CTGTTTTAGT CTTATTGATT GCCTGACCAT TAACTAAGTA ATTTGTGTTT GAAGCGGTTA | 60 |
| 15 | ATTGAGCAAT GATTGGAATG TCGTATTTCT TTCTCGTTCG TGAAATGACA TTTGTTAACT | 120 |
| 75. | CTTCTAGGTC GTAATACGTT TCGAAAAGTA GCGCGTCAAC GCCTTCTTCA ATTAAGGTGT | 180 |
| | CTATTTGAAT TCAGTATGAT AAAGAATAGT TTGTAAGCTG ATATCCCCCT GTTTGGATAC | 240 |
| 20 | CTCTAAACCC CACCAACTGG GGCCCAATAT ATACGTAAnC TnTAATTGGC nGGCTTTTTT | 300 |
| - : | GCGATGCGAC GGGGGGCTGG AGGATGCTTA ACCTTAACCT CCAGACCGAA CCGTTTAACC | 360 |
| | TTTCCAAAAT TGCACCATAG GAATGGGTGG AT | 392 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1360: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 base pairs (B) TYPE: nucleic acid | î |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360: | |
| | CCATGGTTAT TTTCTTCACA TTTCATGTAT ATATATTGT TTATTATCTG TCTCTACTAG | 60 |
| | ACTGTAACCT CCAACATATC TGTTTTATAA ACCAGAGAGC AGTCATTCAA TAAATAAACA | 120 |
| 40 | GATCTGAGGG CCAACTGGCA TGTTGTCAAC TTATGATATT | 160 |
| | (2) INFORMATION FOR SEQ ID NO: 1361: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 148 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361: | |
| | GTATCCTAAA GATTCAGTTA ATCGGAGCGT TGTATTGCAT GAAGGTACAT TGCGGAATGC | 60 |

| | ATATTTATTC ACGATNTTAT TTAGCGAC | 148 |
|-----------|---|-------|
| | (2) INFORMATION FOR SEQ ID NO: 1362: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 147 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . 4- |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362: | |
| 15 | AAAATTACTA TGAAGATTGC ATTAGGATGC GACCATATTG TTACAGATAC AAAAATGCGT | 60 |
| | GTATCTGAAT TTTTAAAATC AAAAGGACAT GAAGTCATTG ACTGACACTT CACTCATNAG | 120 |
| | TGGCGACAGT GTACGTATCA GACTTAG | 147 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1363: | |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 108 base pairs(B) TYPE: nucleic acid | |
| 25 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| . 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363: CTGGCAAAGA AGACAACAAC AAGCTGGTAA AGAAGCAACA ACAAGCCTGG TAAAGAGACA | |
| | ACAACAANCT GGCAAAGAAG ACGGCAACAA GCTGGTAAAG AAGCAACA | 108 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1364: | . 108 |
| 33 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 base pairs | |
| 40 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364: | |
| 45 | GACAATGTTG CTGTAATGGG GAAGGNAATG GGTTGGTACC GCGAATTGAA TAATTTAAAA | . 60 |
| | CCGTAATATA TAATCGTAAT TGTTAAGCCC TCATTTTTAT AAATTTTGGA CCTCTTGAAA | 120 |
| 50 | AAGTTACGTT TTCAAGAGGT TTTATTTATC CTA | 153 |
| | (2) INFORMATION FOR SEQ ID NO: 1365: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 184 base pairs | |
| 55 | | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ** |
|-----------|---|-------|
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365: | |
| | TAAGAGAATT ATATGCATTC CAAACGAAAC NAACAGAAAA ACGGACCAAA CTAACTGTCA | 60 |
| 10 | CAAGTACAAT CGCTGTACTA CTGCAAAACA CGCAAAACGA ACACTTACGT ACACACAAAA | 120 |
| | AGACCACCAT TCACGTCGGG ATTATTAAAA AGGTAGTCTC GTACATTTAT TAAACTACTT | 180 |
| | ACGT | 184 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1366: | • |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 452 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * |
| . (y. | | · · · |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366: | |
| 20 | ACATTAGATG GGTCAATCAT GTTATACACG GTGATTTAGG GGAGTCAATC AAATATAAAA | 60 |
| | GGCCGGTAAT TGATGTTATT GAGGAAAGAA TTCCAAATAC AATATTACTC GGTGCTATGT | 120 |
| 30 | CATTAATTAT TACTTATATT ATCTCATTTG CTTTAGGAAT AACGTCAGGT AGATATTCTT | 180 |
| | ACAGTTTGAC GGATTATACT GTGCAAATAT TTAATTATTT GATGTTAGCC ATTCCATCTT | 240 |
| | TTATTGCGGG AGTATTTGCA ATTTNTATTT TTTCTTTTGA ATTACAATGG TTCCCGTTTC | 300 |
| 35 | AAGGTTCTGT TGATATTAAC CTTAAAGAAG GTACTTTTGA ATATLATATG AGTAAAATAT | 360 |
| | ATCACACATT TTTACCTGCA TTCACTTTAG GTTTATTATC TACTGCTGGT TATAWTCAAT | 420 |
| | ATTTACGTAA TGATATTATT GAAAATTCTA AA | 452 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1367: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid | y . |
| 45 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| - | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367: | * |
| | TTGTGAGTAA TTGGACAATA TAAGTGTTGG TCTTGGATGG CATATCCTTG GTACGACCTG | 60 |
| | GGCAACTTGC TTCATAGCGC AGTTAGGAAC TGATCAATCA TTGGCGTTTT GATACCTAGC | 120 |

| | (2) INFORMATION FOR SEQ ID NO: 1368: | |
|----|---|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 126 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368: | |
| | TGGTGCAAAT TAAAACGGTT GCATATGCAC GTACGACGTA TTGCTAAATA CAATCAATTA | 60 |
| 15 | TTACGTATCG AAGATGAATT ATTTGAAACG CTAAATATGA CGGTATCAAA TCATTCTATn | 120 |
| | ACTTAG | 126 |
| | (2) INFORMATION FOR SEQ ID NO: 1369: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369: | |
| | TGNAAAGTTC ATCAGGGAGC CATTTTTACA ACACAGGGCA CATACGGGTT GTGTTTAGGT | 60 |
| 30 | GCAATTGCCC CAAGCGGACA AAGCATTATT TAAAGTTTCA AGTTCTTCAA CGATTTATTA | 120 |
| | GTGCACAGGA TCCTGTTAAG AGGTATTTTG AAGACTTCCG | 160 |
| | (2) INFORMATION FOR SEQ ID NO: 1370: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370: | |
| 15 | AGTAATTCTG CAAATGCCGC AGATAGCNGT ACTTTGAATT ATGAGGTTTA CAAATACAAT | 60 |
| | ACCAATGACA CGTCAATTGC TAATGACTAT TTTAATAAAC CGGCAAAGTA CATTAAGAAA | 120 |
| 50 | AATGGTAAAT TGTATGTTCA AATAACTGTC AACCACAGTC ATTGGATTAC TGGAATGAGT | 180 |
| | ATCGAAGGAC ATAAAGAAAA TATTATTAGT AAAAACACTG CCAAAGATGA ACGCACTTCT | 240 |
| | GAATTTGAAG TAAGTAAGTT GAACGGTAAA ATAGATGGAA AAATTGACGT TTATATCGAT | 300 |
| | | |

| | AATGGACCAD CTGATGTAGC AGGTGCTAAT GCACCAGGTA | 400 |
|-----|--|--------------|
| ٠. | (2) INFORMATION FOR SEQ ID NO: 1371: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 345 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | (b) Topologi: Timear | |
| | ing the second of the second o | ~ |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1371: | |
| 15 | CATCAAGAAC ATGTGAGACC ACAATTTGAA TCACTTGAAA AAATAAATAA AGACATTGTT | 60 <u>.</u> |
| ,,, | GGATGGATAA AATTATCAGG AACATCATTA AATTATCCAG TACTACAAGG TAAGACAAAT | 120 |
| | CACGATTATT TAAATTTAGA TTTTGAGCGA GAACATCGAC GTAAAGGTAG TATTTTYATG | 180 |
| 20 | GATTITAGAA ATGAATTGAA GAATTTMAAT CATAATACTA TTTTATACGG GCACCATGTC | 240 |
| | GGTGATAATA CGATGTTTGA TGTGTTAGAA GATTATTTAA AGCAATCGTT TTATGAAAAA | 300 |
| | | 345 |
| | CACAAGATAA TTGAnTTTGG CAATAAATAT GGTAATCTCC ATTGC | 343 . |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1372: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| • | (A) LENGTH: 154 base pairs (B) TYPE: nucleic acid | |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (2) 10102011 1211011 | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1372: | • |
| | TTGAAAAGCA GTTTGGATTT ATGCTCAAAC CATGGACGAC GGTTAGGTTT ATGAATGTTA | , 60 |
| | TTCCAAATAG GTTCATCTAT AAAAACTAGT GGAAAGTGGA AAAAATnAGT GGACCTTCGA | 120 |
| 40 | TAATACGATG TATTTATCGT TAGAAGCAGT AATA | 154 |
| | (2) INFORMATION FOR SEQ ID NO: 1373: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 45 | (A) LENGTH: 136 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 50 | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1373: | |
| | GAGCCTAATT ATTCAAGCCA AATCGCATAT GAAATTGATA AAGAAGTTCA ACGAATCGTT | 60 |
| | | |

| | CTATAChaga actatc | 136 |
|----|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1374: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 358 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 10 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374: | |
| 15 | ATCTTTAACA ATTAAAACCA TACTATCTTG AATCATCATC AAATTTAACG CATGTGCGTC | 60 |
| | AAGTTGTTTC ACTTTAAAGA CTTCATTATT AAGACCGACC TTAGACTGCT TTTTAAAAAT | 120 |
| | AGGTACATTC GTAATCATAC CTATACTTTG ATTGTCTAAG TGTAATTTGT TTTGGTGATA | 180 |
| 20 | TCGATTATAA TCTTGTGCAG TAAAAGCTGT AATCATTACT GATTGTCTTG AAAATATCGC | 240 |
| | GCCTTCATTA CCAATGAAGT CTATTGGAAT ATCATCACTA GCCTGTTTTA ACTTGTAATA | 300 |
| | AGCACGATTC THTTCTAAAG AAGCTCTAAA TAATGTCGTT TCATATACTT TGAAGTCT | 358 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1375: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 122 base pairs | |
| 30 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375: | |
| | ATATTGTGTG CTAAATTTGC TTAAGTATGT TTTTTGTTTG NAAGTAAGCA TATGTTATTG | 60 |
| | TCTTTTTAAT TGTTGTAAAA GTGCTGTTTT CATAGAATTA ATATCAGACA TCTTTATTAG | 120 |
| 40 | TA | 122 |
| | (2) INFORMATION FOR SEQ ID NO: 1376: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 467 base pairs | |
| 45 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376: | |
| | CATTTCTTC GGTTTCTGTC TTTTTATGCG TAGATTTATT TTCTTGTTCT TGGTTATTAC | 60 |
| | | |

| | CGATAATTAC GATGGTAATA AGAAGTTTTT TCAAATATAA CGCCTCCATG TTAATGAAAA | 180 |
|----|---|-----|
| | GTAGTTGATA CGTGAAGCTA AATAATTNAT TTCAATATTG CCATAATCAT TTTAAAAAAT | 240 |
| 5 | AAATATTAGA AAAGTAGGCG ATATTAATAT TTTCATTGTE TTTTGTGTAC TTCAATTAGT | 300 |
| | ATAACAAAAC TGTTATGTAT TTATAAATAT AATCATTAGT ATTTTTATGG CTGAAAAAGT | 360 |
| | TATAATAAA GTGTAAGGAA TAAAATATTT GTATGGAAAA GAGAGATAAT TATGAATAAA | 420 |
| 10 | ACCAGTAAAG TTTGTGTAGC AGCAACATTA GCATTGGGCA CACTGAT | 467 |
| | (2) INFORMATION FOR SEQ ID NO: 1377: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid | |
| ٠, | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| - | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377: | |
| | AGGTGTTAGA ATTTATTTTA AGTGTTATAC GTGTCTTCCA GAAATTGTAA TGGCATTATA | 60 |
| 25 | TTTATNAAAG TGTTGGCAGG TTATTTTCAG GTGTATTAGT TTAGGTATCA TTCGTAGTAT | 120 |
| | GCTTGGGA | 128 |
| | (2) INFORMATION FOR SEQ ID NO: 1378: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid | |
| 35 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378: | |
| 40 | GGACGCTAGA GGATCCCGGT CTGGAAAATA TCGTCCAGAA CTTAGAAATA TGAAAATATT | 60 |
| | CCCAAGACCA ATCGATAATA TATTGCCAAT ATGGCGTGCT GTTGGTGGTC CACCTGCAAG | 120 |
| | TGCTATTAAA GCGGGAAAAC AAGGTGTGCC AATGATGATT ACAACCCTTG GTGGCCCAGC | 180 |
| 45 | AATGAACTTT AAAGGTTCTA TAKATGCTTA TCGTCAAKCG GCAACTGAAG CAGGTTTCGA | 240 |
| | TGCTTCGCCT AAGTCTTTAC CAGTAAGTAC AGCGAGTCTG TTTTATACAG CTGAAACAAC | 300 |
| | TCAGGATGCT ATGAGAGAAT TTTATCCACA TTTGAATACA GGGATGTCAT TTATTCGTGG | 360 |
| 50 | THGTTGGTTA TCCGAAACAG CAATHGCTAA TTCGTCAGTT | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1379: | |

| 5 | (A) LENGTH: 108 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379: | |
| 10 | AACTACAACA ATTTAACGAC CAACCTTAAA ANAATACGCT CTTATGCATT GGATTAGTCC | 60 |
| | TGATTATACA ATTTAACTGA ACAAATACCC ATCATTTAAA AGACTTAG | 108 |
| | (2) INFORMATION FOR SEQ ID NO: 1380: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380: | |
| 25 | AAGTGGGGGG AATCAGTATG TTACATTTAC ATATATTAAG TATTAGCGAT TATTTTATTT | 60 |
| | ATCGCTACAT ACTTAACCAT TTCAAAAATT CAAGGCGGnT CACCATTTTC CAACCCGT | 118 |
| | (2) INFORMATION FOR SEQ ID NO: 1381: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 114 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381: | |
| | TCATGAAAAC ATTTATTTTA AAATTTGATA TTTGTTCAAT AATATTCGAA ATTAACTTnT | 60 |
| 40 | GTGTATAGAT TTTCTTTATA TCCTGAGAGA CATGTACTAT AATGTTTGTG AATA | 114 |
| | (2) INFORMATION FOR SEQ ID NO: 1382: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382: | |
| | CGGTATTGAT CATATAAATA GTGTTTAGAT GCTATAGTCG GnTGACTTAA GTAATTTAAA | 60 |
| 55 | | |

| | GTTTTCTTCT GCCTTGCTTA AAGATATATG ACAGGGTGCT GGCAT | 165 |
|----|--|-------|
| | (2) INFORMATION FOR SEQ ID NO: 1383: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383: | . 9 |
| 15 | TTTGGTGTGA TGGAGTATAT TTAGGTGTGG AAATCAAGAG GGAATTCCAT TTTCAAACAT | 60 |
| | CCAATTAGAG TCGNAATAAG AACTCGCTAT CGGTCCAATT AACTGATTCA G | 111 |
| | (2) INFORMATION FOR SEQ ID NO: 1384: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384: | |
| | CATTTAAATA ACGTTGTGAC CATGTGCTTT ATGCTATGTG CTAGAAAATC CATGTTTTTA | 60 |
| 30 | TCTAATTTCT TAATAAATTG ACATTAAGTT GGATTCTTGT CCnCTTCACG TTTCGACATT | 120 |
| | GGATGACTGA ACGCATGAAA TCAG | 144 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1385: (i) SEQUENCE CHARACTERISTICS: | . * . |
| | (A) LENGTH: 103 base pairs(B) TYPE: nucleic acid | |
| 40 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385: | |
| 45 | TCGTTGTGCA GCAACTGCAT TACGCTGTCT CATTAATGTA AGCGCAATGG CCATTTGGTT | 60 |
| | TTTCNATAGT GGAATACTTG TCAAAATTGA ACATTGTATC TTC | 103 |
| | (2) INFORMATION FOR SEQ ID NO: 1386: | |
| 50 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 533 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386: | |
|----|---|-----|
| 5 | CCAGNACAAA TACAACGTTA TATTCAACAA TTAGAAGACT TAGNATAGAT ATAAATTGAG | 6 |
| | GGAGGACATC GATATGGCAT TTGAAGGGTT ATCAGAAACC TTGCAAGCGA CGATGCAAAA | 120 |
| | AATGCGTGGT AAGGGTAAAC TTACTGAAGC TGATATAAAG ATAATGATGC GTGAAGTAAG | 180 |
| 10 | ATTAGCGTTA CTTGAGGCTG NACGTAAACT TTAAAGTGGT AAAAGAATTT ATTAAAACAG | 24 |
| | TATCAGAACG CGCATTAGGT TCCGATGTAA TGCAATCATT AACACCAGGG CAACAAGTTA | 300 |
| | TTAAAATAGT TCAAGATGAA TTAACGCAGT TGATGGGTGG AGAAAATACG TCGATTAANA | 360 |
| 15 | TGTCAAATAA ACCACCTACT GTTGTTATGA TGGTTGGTTT ACAAGGTGCT GGTAAAACAA | 420 |
| | CAACTGCAGG TAAATTAGCA TTATTGATGC GTAAAAAATA CAACAANAAA CCTATGTNAG | 480 |
| • | TTGCAGCAGA TATTTATCGT CCAGCAGCGA TAAATCAATT ACAAACAGTA GGG | 533 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1387: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387: | |
| | TTATTTACAA GCCATTAATA TATTTTAGGT TTGTTCTGCA TCGATTCATT GGTGCTATTT | 60 |
| | TATTTACATT CAATAATGAG ACTTTTACAn CAAACCAATT GGTCAAATAT AG | 112 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1388: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388: | |
| | ACACCTACAG TTAATAGTAT CAGTGCACAC TAAAGTCCTA ATACTTTCAA CCATGACTAA | 60 |
| | TGATGTATCm TCTTGCCCAA CGAACGCGTT GTGCCAAATT GAATTAGACT GGACGGAC | 118 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1389: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 147 base pairs | |

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

| | 5 | (wi) CEOUGNEE DECERTORION, CEO ID NO. 1200. | * + |
|---|------|---|------|
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389: | |
| | | CGACGACACA ACTITATAAT AAAATCITAG ACAATAACGA AGGGTATTAA CAGAACTTGG | 60 |
| | 10 | TGCTGTTAAT GCAAGTACTG GAAAATATAC TGGTCGTCGC TAAAGCAAAT TTTTGCTCTG | 120 |
| Ţ | **** | ACCTHCAATG GTACTTGTTG GGGAATA | 147 |
| | | (2) INFORMATION FOR SEQ ID NO: 1390: | • |
| | 15 | (i) SEQUENCE CHARACTERISTICS: | |
| | ŕ | (A) LENGTH: 161 base pairs (B) TYPE: nucleic acid | |
| | • | (C) STRANDEDNESS: double | |
| | 20 | (D) TOPOLOGY: linear | |
| | | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390: | |
| | 25 | TTTTTGATCA TGATTTTTGG GCATGGATCA ATCACTTGCT TGGCCAATGG TCTTTCAACA | , 60 |
| | • | ATTTGGATAT CTGACCTTAT TCGCTTTATC TAGCACTTTT GnCAATTTGT TGGCATTGGA | 120 |
| | | AAACATGTGT TTAGATTTTT GTATGCCTCT CGCAGGCTTT T | 161 |
| | 30 | (2) INFORMATION FOR SEQ ID NO: 1391: | |
| | | (i) SEQUENCE CHARACTERISTICS: | |
| | | (A) LENGTH: 102 base pairs | |
| | 1 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | 35 | (D) TOPOLOGY: linear | * . |
| | | | |
| | • | | |
| | 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391: | |
| | | GCCGCACGCG CGCGATTCTC GGCCTAATAA GAAAACAAAT AATTCCAATT CATATATGNA | 60 |
| | | CATTTTTGCC TCCTTATTTC TTGAAAATGT GGAATTGGAA TT | 102 |
| | 45 | (2) INFORMATION FOR SEQ ID NO: 1392: | |
| | | (i) SEQUENCE CHARACTERISTICS: | |
| | . • | (A) LENGTH: 412 base pairs | |
| | | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | 50 | (D) TOPOLOGY: linear | |
| | | | |
| | | | • |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392: | |
| | 55 | | |

| | AAAATGCTAT TAACAACGTA TTAAATAATC AAGATTACCA TGGTATTAAA GATAAACCAT | 120 |
|----|---|------|
| | TCGCATTATT CGTAACTGGA TTTTTCGACA ATGTAACAGA TAATACTGTT GGTATTAACT | 180 |
| 5 | TTAAGACAAA AGACGGTTCA ATAGCAGTAT TTATGCGTCC AGATATTGGA GAAACATTTA | 240 |
| | GCGAGTTTAG AACATTCTTA GCCGTCTTGT TAATGTTGTT ATTATTTATC TCGATTTCAT | 300 |
| 10 | TAGTTATCGC ATCANCCTAT TCAATCATTC GTCCAGTAAA AAAGTTAAAG CTAGCGACCG | 360 |
| 10 | AACGCTTAAT TGATGGTGAT TTTGAAACAC CTATCAAACA AACnCGCAAA GA | 412 |
| | (2) INFORMATION FOR SEQ ID NO: 1393: | • |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 186 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393: | |
| | AGCAANTGGA TTGCAATGAG TTTCTTATAT TTACAAGGTG GTAGATTGAT TGATGTTTTA | 60 |
| 25 | ACTGCGATAT TAGCAGTAGT CTAGATACCT AGTCACTGAG ATTTTAGATC GAGTTACACG | 120 |
| | CACATTATCC GATCTGTCTA TATGGATATC CGTATGACTA CCTATCCCAC GGACTGCACA | 180 |
| | TACTGG | 186 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1394: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394: | |
| | TCTTTAAAAG AATCAGGAGC TTGGAAGAAG TATATCAGGA TCATTAAGTC AACAAATTAC | . 60 |
| | GCGATATGAA AATTTGAATA ACAATTTGNA AAAGCATGCT TCCGATAATC AGCAAGCC | 118 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1395: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 175 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |

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| | GGTTACCTCG GATGGATGAT TACTATFITG GGCTGGGCGC CGGCTTTMGT TATTAGTGGT | . 60 |
|-----|---|---|
| • . | GGCAATAGTG GCAAAGTGTC ACAAAAAAT CCAATAGCTG GAAACCCGGG TATATTTGGG | 120 |
| 5 | TATTAACGCC GGTGGCCGGG ATTTGGCCAA TCGCATTAAT TTAATGGCCA TTGGG | 175 |
| | (2) INFORMATION FOR SEQ ID NO: 1396: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | • |
| 15 | (w/) CROUDING PROGRESSION OF TO NO. 1206 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396: | 8 |
| | AGAAACTTAG ACGATTAGTA TCATATATTA GAACACNGCA CCGAACTTGA AATCATGGCT | 60 |
| 20 | GATATCGCAC CTTGAAGAAG CAAAAATGCC GCACGACTTG GCTTTGATAT ATTGGCACGA | 120 |
| ** | CTTACATGGC AT | 132 |
| | (2) INFORMATION FOR SEQ ID NO: 1397: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | *** |
| 30 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397: | |
| 35 | AGAGGTCCGG CTATCTATCA AATAAAGTGG TCATTTAAAG CGTACACTTC GGGTGCGTTG | 60 |
| | ATTTCTTACT TTAGGTGTAG GACAATTGTA TCGCATCTAT CTTTACnCTA CCTGCATTGT | 120 |
| | $oldsymbol{	au}$ | 121 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1398: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 202 base pairs (B) TYPE: nucleic acid | • |
| 45 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | • |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398: | |
| | CGTTCGTATA ATCTCACTTG CATCnTGAAT TGAACAACAT CCTGTCATTT TAAGACTGCT | 60 |
| | AAAnGTACAG CTGAAAACCA AGTAAGTCCG TTTCGTCTGG CTGTGAAATG GATCAAGGAG | . 120 |

| | AAACACCTCA TCCAAAGTTC AG | 202 |
|------|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1399: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399: | |
| 15 | CGTTGGATCA CTGATGCATT CATAAATGGG TGAACnTAAT GTAATGTTAA ATCTATCACA | 60 |
| | GCGCGATAAC AGCAAGAATA TAGTGAACAC CATAAATTGA GCATATCAAT GCCATATTCA | 120 |
| | TGGATACACA TAGTTCACCT GGTGGTCGGT GAAAGCCTGT AGATG | 165 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1400: | |
| 25 ' | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400: | |
| | ACACCTTTGT TTTTGCAAAG CTGTACCACA AAGTACTGGG TAGAATTCTA CGTTATATGA | 60 |
| | GnCTTGGCGT ATAGCTTCTT TTAATTCATA AACTGTAAAT TTCTTCG | 107 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1401: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1401: | |
| 45 | TTTTGTCTAG NAACATCTGC TTCTAATAAT GATCGATCAG CAGCCATTGT GCTTAATCTT | 60 |
| | TCATCCCACA TCACAATCTC AATAGAAGGA TAAGCTTCTA ATAATT | 106 |
| | (2) INFORMATION FOR SEQ ID NO: 1402: | |
| 50 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 102 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| 55 | | |

| ٠. | | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1402: | |
|-----|----------|---|------|
| | | CAATGTTAAA CCTACACCGT TAACAGCACA CATGATACTA AATTGTTGGG GTGTCATATT | 60 |
| 5 | ; | ATACAATGTT GAGTAnTAAA TGGCGATGCA GATGAATAAC TA | 102 |
| | | (2) INFORMATION FOR SEQ ID NO: 1403: | * |
| 10 | o | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 169 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | | (D) TOPOLOGY: linear | |
| 1: | 5 | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403: | |
| | | TTTATTATTT GTGCTACAAC TACTTAAAAA AATCAGTAGA TATAGCATTA AACATATTTT | . 60 |
| . 2 | o | CATCCCCYTG AATTTTAAAA ACTTTTTCAA AAGCAACACC TCTAAAAATA AATaCAATAT | 120 |
| | | ATTATAGCAA ATAGAAATTA TTATTTTGTT AAATTATGTT GTnCATGTT | 169 |
| | | (2) INFORMATION FOR SEQ ID NO: 1404: | |
| 2 | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | ·· |
| 3 | 0 | (D) TOPOLOGY: linear | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404: | |
| 3 | 15 | TTAGTTGATA AGTAAATCCG AGTGACATTG GGATTCACCC CAACCGACTC TATTCCAGTC | 60 |
| | | TGAAATACGT GAACCCATAA nATCCTATGT CCAGATTTAT ATTTCT | 106 |
| | | (2) INFORMATION FOR SEQ ID NO: 1405: | |
| 4 | 0 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 309 base pairs | |
| | | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 4 | 15 | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405: | |
| | | TATTTTTGCA GCAGAGATGT TCGCGACAAG GTTTACGCCA AATTGTCACT GCTACTGCGA | -60 |
| 5 | 50 | TGTGTATTGC ATGCAAGTGC AGGNAATATA TTGAACATTT AAACGATCAG TTTAATTCGA | 120 |

| | CITIAATAAG CAATITGTAC TGACTGTCGA CATTGCGTCA TGGTCTGTTT TTGTTTAACT | 240 |
|----|---|-----|
| | ATACTATRGG TGCGAAGTAG GCCTATGTTT AGAGGTCTAA CATGCCGTAG GTCTAATGGA | 300 |
| 5 | TCAGGAACC | 309 |
| | (2) INFORMATION FOR SEQ ID NO: 1406: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406: | |
| | GTGGACCTGC AGTTAATTCA ACGATTTCAA GATGGGCGCC AAGAACGAAA CGTGGCCGAT | 60 |
| 20 | ACTTAGGATT CTGGAATCAT CACATAATCG TGTGCATGAG GTGTTTCACT TTGGGGTCTA | 120 |
| | ATGATTCTTC ATGGAAnGTA TAGG | 144 |
| | (2) INFORMATION FOR SEQ ID NO: 1407: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407: | |
| | ACCTTTGCGT CCAGAATTAG CTACATGGTA AAGCTTCGTG TTACTATTTT AGGGATATCT | 60 |
| 35 | TCAACnCGTT TCACTTGTAT AATTTGTTTT TGTAATTGGT GAAGTCATAG TATAG | 115 |
| | (2) INFORMATION FOR SEQ ID NO: 1408: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408: | 4 |
| | ATTGGTATTG GCGCTGTAGT ATAGCTTCAT TATCTGATGC CATTAGTATA CGCACACTnT | 60 |
| 50 | TTATTTATGG GCGTGGTATT CATCCTTATC GGGATCAATT ATTGGGTTAC ATTTT | 115 |
| | (2) INFORMATION FOR SEQ ID NO: 1409: | |

| 5 | (A) LENGTH: 123 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|----|---|-----|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409: | |
| 10 | AACCAGATGA AAAGCAAATA TACATATATA ACTCTACATG GGGTCGTGGT TTGGATATTG | 60 |
| | TTCATGATGC ATTCGGTATG CCAATGACAA AGCAATATAA AGATAAATTn CAAGAAGATA | 120 |
| | AAA | 123 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1410: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D)_TOPOLOGY: linear | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410: | 50 |
| | CTNTTTATAT TGAGGATTTT GTATCATATA TGGATAATCA TTAAAGGTGT ATGCTCTTGT | 60 |
| | TATCAGATCG CTACGGGTAA AATCGCTTCT ATAGGGCATT TACATGCGGG CTTCTGCCGG | 120 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1411: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 455 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| • | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411: | |
| 40 | TCTCGTATTG CGTTTAGAGA ACATGCGCAC AAAGGACAAA TTCCAGGTGT TAAAAAATCA | 60 |
| | AGTTGGTAAA ATCAAATTTC GTACTTTAGC CCATTTACAA TATCAATAAA ACAATGTACA | 120 |
| | GTATATACGA ATGCTATAAA CTGAATGTTT TCTCATATTA ATAAGGAAAC ATTCGGTTTT | 180 |
| 45 | TAATTTGCAT TTAAAAATAA TTAGTTTTTA AAGGGGCTAT TTAAAGTGAA AATATTTGAT | 240 |
| | TACGAAGATA TTCAATTAAT ACCTAATAAA TGCATAGTTG AAAGTAGGTC TGAATGTGAT | 300 |
| 50 | ACAACTATCC AATTIGGTCC GAAAAAATTC AAGCTACCTG TAGTTCCTGC GNATATGCAA | 360 |
| | ACAGTTATGA ATGAGAAATT AGCGAAATGG TTTGCTGAAA ATGATTACTT TTATAATCAT | 420 |
| | GCATCGTTTT GATGAAGAAG CAAGAATACC TNTTA | 455 |
| | | |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412: | |
| | ACAATGTCAA ATCACAATAG CTGTTGTAGG CATTTGATTA CAATGAACTA AAGGCAAAAT | 60 |
| | TGGAGCAGTT ATCCATGAAT GATTAATAAC AACANAAAGT ATGGGGTCAA GTTTAGGG | 118 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1413: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 245 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413: | |
| 25 | TGTTGACGAT ATAGGAATTA GCAAGAAATA GGCTAAGATA GTTTCGCACA ACTTGGGGCC | 60 |
| | CANCCACTTG CTTGTTTGTA GAATTAGGGG TCCATTTCTC GTGTTGGGGC CCGAACTAAT | 120 |
| | AGTATGAATA TATATATCTA ATATTAAAAC GGCAATATTT ATATGGTATA CATTTTTATA | 180 |
| 30 | TTTAGTnTTT GTATAGACAT GCTAATTAGC ACTTTCTAAA AAGGGTTGAA ATGATATACT | 240 |
| | GATGA | 245 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1414: (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 252 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414: | |
| 45 | TTTTTGTTAT TCAAAATTTA GAGTGTGTTA TATGATAACG GTTTTTTCAT AGCGACTTGA | 60 |
| | TCATTTTTCG AAATGATGAA AGATATGCAA GTTCAATCAA TCGGAACAAA AATACTATAT | 120 |
| | TATGGTAAGA ANTTCCCGAA GACTAGCGCA CTCACACACA AGTGCATCCT CGCGAACAAT | 180 |
| 50 | GCGCACTTTT CACAAGCACA CAAACACAAG GCACAAGTGC ACGCAnTATT AGACAATGGT | 240 |
| | CTACCTACCA GA | 252 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * . |
|-----|---|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415: | |
| ,,, | ATCTGCTGGA AGAGAAAAA GACGCTCTTA AAACTGGCTT TAGAAGGTCA AGATATAGAA | 60 |
| | GNTATTAAAT CTAAAAAGA AGGAACTTGA AAAAGTGATT CCAGGAATTT TC | 112 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1416: | |
| - | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs | |
| 20 | (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
| , | | *** |
| 05 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416: | * |
| 25 | CTCAATTACA TTCAAGAAAA TGGGTGGAAT TACACAACGT TGGACTGAGA AGTATAGTTA | 60 |
| | ATAGCGCAAA TGCnATAAGC CTTATATAAA AATGGGCACA ATTATTTCAT GTACCAACAA | 120 |
| 30 | GAAC | 124 |
| | (2) INFORMATION FOR SEQ ID NO: 1417: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417: | |
| | TTCAAGAGCA CATACTGTAA CTCGTACGAG AATTTTTCA AAATGACGCG TCAATCTCAA | 60 |
| 45 | TATCATCATA TGGTATTCCG AGTAATACCC CTCGnCACCT TTTTTAGGTA GCGTCAATAT | 120 |
| | ${f T}$ | 121 |
| | (2) INFORMATION FOR SEQ ID NO: 1418: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 123 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 55 | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418: | |
|----|---|-----|
| | CTACGCCATC AAGAGGGTGT TAGTGCTATT AACTATTGCG GCGAGAGCAA TTAGTCGAAT | 60 |
| 5 | GCAAATTAGG ACAAGTTGAT GAGTAACTAC nGCCAATATC GGTAAGTTTC ATGGCGGTTC | 120 |
| | AGC | 123 |
| | (2) INFORMATION FOR SEQ ID NO: 1419: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419: | |
| 20 | CTTATAATCC TTAChGCAAT TTCACCTTGT ACGGAATTAA ACAACGGAGG CATTTACTTA | 60 |
| | CCCCCTTTAC TTAATACGTA CCAAAACTTG GTCGTATTCA ACCATTGGG | 109 |
| | (2) INFORMATION FOR SEQ ID NO: 1420: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420: | |
| 35 | GCTGTmGTGC TGCCAAGATG CTGATTGAAA AGTATATATG ATTGCATCAG TAGAAGAGCG | 60 |
| | AGCAGAAAGA AGATATAAAG ATAATCAGTT AAGAGGTGTC GAATCAAATT TTGAAGATTT | 120 |
| | A | 121 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1421: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421: | |
| | TGTTTTTACA GTCACATACA CTAGGCATCC TAGCATTATC TAAATTTAAT ACCATCGCAA | 60 |
| | CTTGCGCTTT AATCTTCAAG GCCAATTAAA CCTCCTTCAT CTTTCTAACT GCTTANATAT | 120 |

(2) INFORMATION FOR SEQ ID NO: 1422:

| | • | |
|-----------|---|------|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422: | |
| • 11, | GCCAATCATT GTCAATGTTC AGGCATCANA TTTATCGAAT GATTTTCATT TGCCATGATC | 60 |
| 15 | AGTCAAGGCG GGGATTTATT CAAAAATTAT GACGCCTAGT AAAAAATTTT | 110 |
| | (2) INFORMATION FOR SEQ ID NO: 1423: | |
| 20 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 111 base pairs(B) TYPE: nucleic acid | |
| н - | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 97 - |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423: | |
| | ATTACCTTGC ATGAATTTCC ATCTGTCAAA TGTGCGCCTT CACGAATTTG TTCGATAAAG | 60 |
| 30 | ATACGTTGGT CACCGTGAAT AATTTCACCA GCTGCATTTn TCCATGGACC A | 111 |
| | (2) INFORMATION FOR SEQ ID NO: 1424: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 200 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424: | |
| | TGTTGTGTGA TTGCGTATTC TCAGGTGAAT TCTTACATAT ATAGTACTTT TTGTTTCCGC | 60 |
| 45 | TTGATTTGAC CTTGCATATC TTTCACATTC TTCGAAAATT GATCAAAGCn CTATTGAAAA | 120 |
| | ACCGTATCAT ATACANACCT CTAATTTTTT TGACTAACAA AAAGAATTCT TTGACGTATC | 180 |
| | AACTATATCA TCATGACTTC | 200 |
| <i>50</i> | (2) INFORMATION FOR SEQ ID NO: 1425: | |
| <i>55</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425: | |
|----------|---|-----|
| 5 | TTTCTATAAT TTTAGACTAT TTCTACCATG TTGCTGAACA ATTTACTTAG ATAAAAATTA | 60 |
| | THAAATTTTG GTCAATTAAC AAAGTTAGTT TGTTAAAACG TATACTTTAA TTATTCCGG | 119 |
| | (2) INFORMATION FOR SEQ ID NO: 1426: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | , |
| ,,, | (wi) CECUENCE DESCRIPTION OF TO MO 1406 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426: | |
| 20 | AAAATGGCGT TGCATTTTAC TCTAATAACG CTCAAGGCGA CGGCAAAGAT AAACTAAAGG | 60 |
| | CACCTATTAT CGAACATAGT ACTCCTAnCG GACCTGGAAT TTAAATCAGA GCGGCC | 116 |
| | (2) INFORMATION FOR SEQ ID NO: 1427: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 212 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 · | | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427: | |
| | TTTTATTTAC GTATAAGTGG GCGTTAGGTG TCACAGCGGT TGTCGATCAA AATATCATCA | 60 |
| 35 | TCAATCTTGT ATATGGGTTT GCGGATTCTT ATTTTATGAT TTTACAGAAC TATCCTAGGC | 120 |
| | TTATTCTTTA TTAAAAGATG CAACNAGTTA TATAAAAAGA CGAATCTATC AACGCGAGCT | 180 |
| 10 | GCTCACAAGG CATCTCnTAT AGCGTCCACA TC | 212 |
| | (2) INFORMATION FOR SEQ ID NO: 1428: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| ~ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428: | |
| | GAAAAATTGG TTCTGAATAT AATGGTGCCG TATACTTTAC GCCTCAAATC AAAGATTTTA | 60 |

| | ATTITAATGA AAAACATCGG TCGAATATAA CATAAAAAAA CGTCTATATC AAAAGCATCA | 180 |
|-----------|---|-----|
| • | TGAATAAACA GAGGAGCACA AAAATGAnTA AAAATATAAT CATCAAAAGT ATTGCGGCAT | 240 |
| 5 | TGACGNTTTT AACATCAATA ACTGG | 265 |
| | (2) INFORMATION FOR SEQ ID NO: 1429: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| , | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429: | |
| | CGTACGAAGG ATTTGCAAAC TTCTTCATTC AACAAGCTAA AGAAGAACGT TTCCATGGAC | 60 |
| 20 | AAAAGATTTA TAACTATATT AACGACAGAG GTGCACATGC AGAATTCAGA GCAGTTTCAG | 120 |
| , ; | CACCAAAAAT TGACTTTTCA AGCAT | 145 |
| | (2) INFORMATION FOR SEQ ID NO: 1430: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | - 8 |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430: | * |
| 35 | ACACCGCTAA GCGTATTAAG ACAGGATCTG AAAATGGACA CATCGCAATC GAATTATTGC | 60 |
| | AATGCCAAGT CATATCGGGG GTGAACCGCA ATTTCAGGNA TTAAGTGGAT AGGTA | 115 |
| | (2) INFORMATION FOR SEQ ID NO: 1431: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 211 base pairs (B) TYPE: nucleic acid | |
| * | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431: | • |
| 50 | natgtating tgaaaaggte etgagtggae aaaagaeeta aatatttaat ggtegattat | 60 |
| | CGCACGTCCA TAGTTGGTGA ACAGGAACTT ACACGTACAT CTAATCGCAG ACTATGCGTA | 120 |
| | AACTTTGGAA ACTGCTAGTC ATTGAAGCGT GGTATGTGTA TGCACGTAAA TATGCATTAG | 180 |
| | • | |

| | (2) INFORMATION FOR SEQ ID NO: 1432: | |
|----|---|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | (wi) SEQUENCE DESCRIPTION ORD IN NO. 1400 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432: | |
| | GGAATGATTG ATAAATTGGA CTACTTAAAG ATTTCGGTAT CGTGTCATTT GGCTCAGTCC | 60 |
| 15 | ATGTTTAATC ACCTATGNTG ACATGGTATG ATATTAGTGA CTACCAGAGA TATGGATGAT | 120 |
| | TTGGAACGTG GAGGACTTGA TCGTT | 145 |
| | (2) INFORMATION FOR SEQ ID NO: 1433: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 169 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433: | |
| 30 | TTTATTGCAT TTACATAATA ATATCCTTTT GTTGTTTTGG TATTTCTATT CATATACAAG | 60 |
| | ACCATACCTT TAACTTTCAG AGCTTCCCCC TTATTTTGAG TTGCCATTTC AGAACCAATA | 120 |
| | ATCCATGTAC CTTTATCATT TTTATCAAAT TCGTCATCAC GATAACCTn | 169 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1434: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434: | |
| | GATCTATAGT TCTGTAATCT GACGTGCTTT GCCATGTGCA CCACTCGTCn TAAAAATCAC | 60 |
| | TTACACTTAA CCCTTTTCCA CCTTTATCGT ATCCACCTTC AA | 102 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1435: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 55 | • | |

| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435: | |
|----|--------------|--|--------------|
| | • | TTCTTATTAT ACAAATAGAA GCCATGTGTG CTTATATCGC AGCATCATGA CTCCTTTTTC | 60 |
| .5 | | ATTTGAATAT ATAAATAATA CAGnCGCTTT CGAATAAATT TAGGCTAATT CTACCA | 116 |
| | | (2) INFORMATION FOR SEQ ID NO: 1436: | |
| 10 | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs | |
| | . . * | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | er ev |
| 15 | | | |
| | -(1)- | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436: | |
| | | GGGGGTTTAT GTACTGGTGG ATCTGCAAAC TACTTGGCGT AAAGAATATA CAGATATGGT | 60 |
| 20 | | AANGAAAAGT TTAGATTCAC ACGCCATCAC AATGGATTAG AAAAACCGAA TTTCTTCAGC | 120 |
| | | AATTCTACAA TTTCTAGTAT ACGC | 144 |
| | | (2) INFORMATION FOR SEQ ID NO: 1437: | |
| 25 | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 base pairs | |
| | | (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
| 30 | | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437: | |
| 35 | | GTTGCTGGGn AACCTATGGT CGAACATGTA TTGGTAAAGT GTGAAAGGCT CTGGTGGCGA | 60 |
| | | TCAAGTTGGT AACCATCGTA GTACATGGTG CTGTAAATGT A | 101 |
| | | (2) INFORMATION FOR SEQ ID NO: 1438: | |
| 40 | | (i) SEQUENCE CHARACTERISTICS: | |
| | o. | (A) LENGTH: 321 base pairs (B) TYPE: nucleic acid | |
| | | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438: | |
| 50 | | AAAGATGGTG ACATTTCATA TAATCCGAAT GTGCCAAGTT ATTCAGCAAA GTATCAATTA | , 6 0 |
| 50 | | AGTAATGATG ACTACAATGT GAAGCAACTT AGAAAGAGGT ATGATATACC AACTAHGAAA | 120 |
| | | | |

| | AATTTAGAGT TTACATTTAT AGAAAATAAA GAAGAAAACA TCTATTTTAC GGATAGTATT | 240 |
|----|---|-----|
| | AATTTCAAAC CTACTGAATA GGGTTAATAG AAGTTTGAAA TGAAAATTTC nTAAAGTGTG | 300 |
| 5 | CAAAATAATT TGTCGCTTTA G | 321 |
| | (2) INFORMATION FOR SEQ ID NO: 1439: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 135 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1439: | |
| | CAGTTGTAAT GGGACCTGGG CCAATCGGAT TACTTGTAGC ACAAGTGTTA AAAAGTAAAG | 60 |
| 20 | GCGCAACTGT TGTGGGTACT GGGTTGGGAC AATTGACCAA GTCAGATTAG ATTAAAGCCA | 120 |
| | GAANGCCATT GCCAC | 135 |
| | (2) INFORMATION FOR SEQ ID NO: 1440: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 30 | (D) TOPOLOGY: linear | 1 |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440: | |
| 35 | AAATTATTTT GAACACTTTA TGAAATTTTT ATTTCAAACT TCTATTAACC CTATTCAGTA | 60 |
| | GGTTTGAAAT TAATACTATC AGAAAAATAC ACATTTnCTT CTTTATTTCT | 110 |
| | (2) INFORMATION FOR SEQ ID NO: 1441: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 436 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 45 | (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441: | |
| 50 | TCTCTTTTGG ATTCATTAAG ATTGCnGCAT CGATACCAAC GTTMAACGGT GATTGTGTAA | 60 |
| | TGAATTTTTG CCACCAAGCT TTTTTAACAT TATTCTTTAA TTCAACACCT AAAGGACCAT | 120 |
| | AATCCCATGT GTTTGATAAA CCACCGTAAA TATCACTACC AGGGAACACA AAACCTCTGT | 180 |
| 55 | | |

300

GAAAACGCCC CATGGAAAAT AACAGCATAG TAAATATGCT TTACTTCCAT GGGACGAGTT

| | | AATATTTTAA ATTGTATATA ATACAAAANA AGTNACGTAT TTAACCCGCG GTTCCACCCA | 360 |
|---|--------|---|-----|
| | 5 | AATTAGTGTA GTCACTCGCT TTTATTTTAA AATGATTCGT TGCGCCAATC TTATTGTTAA | 420 |
| | | GCTTACACTA TCCTTA | 436 |
| | 10 | (2) INFORMATION FOR SEQ ID NO: 1442: | |
| | 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 461 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| , | | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442: | |
| | 20 . , | ATTTTTAGAA GCATACTGCG AACGTCATCA CATCGATTTA CATATCAAAA AGTTAGATTT | 60 |
| | | GTCGCATAGT CTCGACCGAA ATAACAGCAT TCAGAATGAA GCTCGAATTA AACGTTACGA | 120 |
| | | ATGGTTTGAT GAAATGATGA ATGTATTAGA AGCGGATGTA TTGCTAACGG CGCATCATTT | 180 |
| | 25 | GGACGATCAA TTAGAAACTA TTATGTATCG TATTTTTANT GGGAAATCAA CACGTAATAA | 240 |
| | | ACTAGGATTT GATGAGTTAT CGAAGCGAAA AGGTTATCAG ATTTATCGAC CACTTTTAGC | 300 |
| | 30 | TGTCTCTAAA AAAGAAATAY AACAATTCCA AGAGAGATAT CATATTCCAT ATTTTGAAGA | 360 |
| | 30 | TGAATCHAAT AAAGATAACA AATATGTTAG AAATGATATT CGTAANAGAA TTATTCCAGC | 420 |
| | | TATTGATGAA AATAATCAAC TTAAAGTATC GCATTTATTA A | 461 |
| | .35 | (2) INFORMATION FOR SEQ ID NO: 1443: | |
| | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 143 base pairs | |
| | 40 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | | |
| | 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443: | |
| | 45 | AAAGGTGATA AAAAACAAAG GCATTGTAAA TTACTTGAAA ACCAAGTGAG TTATTACACG | 60 |
| | • | ATTCTAATTG GGATAATGCG CGATATTTTA TTCCACACTT GTTACATTAT TGCTTTACGT | 120 |
| | 50 | GGGGGTTAGC GTGGAnTCAT CAC | 143 |
| | | (2) INFORMATION FOR SEQ ID NO: 1444: | |
| | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 90 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 1743 |
|----|---|------|
| 5 | | |
| | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1444: | |
| | TGGTGTTGGT TCATCAGTTG TAAACGCGAT TGTCACAAGA CTTAGAAGTA TATGTACACA | 60 |
| 10 | GAAATGAGAC TATATATCAT CAAGCATATA | 90 |
| | (2) INFORMATION FOR SEQ ID NO: 1445: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 218 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445: | |
| | ATTGAACAGT GACAACAAAT GACAACAATG AATGACCAAC TGAGTTGCAG AATTGACCGA | 60 |
| 25 | CCTGACTTGC TGTnAGATGT GCATTGCCTG TGACCAGTTA ACTGCTGTTT GTACATTATG | 120 |
| | ATTGTGCACG TGAAGTCTTT GCAAATGACT TTTAACATTA TGCTGCTAGA GCCATCTTTT | 180 |
| | AAAGATGTTT GGACTAACGT nCATGATGTG AATATCTG | 218 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1446: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446: | |
| | TTTGACTTGA CATTATAGAA CACAAATTCA TTTGAAACTA TGTTTTCAAA TTTATTTATT | 60 |
| | GTTACTGGGA ATTTCACATT ATTAGATTTA TTTATTTTCT TTTGA | 105 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1447: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |

1959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447:

| | AGACTGAAAA CTGCATATGC AGAGGCGATG AAACAAAATG CCAT | 104 |
|-----------|---|---------------|
| | (2) INFORMATION FOR SEQ ID NO: 1448: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 10 | (D) TOPOLOGY: linear | |
| • | | ** ** ** * ** |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448: | |
| 15 | TTGAATTAAC TGAAGAANTA GCAGTGCAAG CAGGATTGTT GATATGACAA CATTCGAGTC | 60 |
| | AGAATGGCAA CAACAACGTG ATTCGTGCAC TCCAAGCACG TGCA | 104 |
| | (2) INFORMATION FOR SEQ ID NO: 1449: | • |
| 20 | (i) SEQUENCE CHARACTERISTICS: | |
| = | (A)—LENGTH: 349-base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449: | |
| | TATTAATTTT TTTTAATATG GAATATTCAT TGCATCGCTT TCCTATTCTT CAAGCCCACT | 60 |
| 30 | TTTTATCTTC ATATACATTA ATTAACCACC KTCAAACATT GTCGTTAGAT TCGCCAAATT | 120 |
| - | GAATCTATTT TTAGCACAGC AAAAAACCGA ACTGCTGAAA TAATGCATCT CCAACAGTCC | 180 |
| 35 | GGTCTATTAA ACTATTTACT TATCTTTATT AAACAATTGA CATGATTTAT TAGAATAACC | 240 |
| | CAATTGGCAT GACCATGCAT CAGTAACATC CATGTTTAAT GGCTGCTGGT TTTTTAGGTA | 300 |
| | AACCAGGCCA GAGTCATGGn TGGCACCTGn GCAACGCnAC GATAAAGCC | 349 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1450: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid | |
| 45 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450: | |
| 50 | GATTTTATAT AAATATAGCT TTTCAACAAA ACAAATGATT GAATTTCTAG GAATTGAGTC | 60 |
| | ATTAAAAAA CACTTGAAAA ATTCAGGTGG GATTGCGCTA TTGCCGGAAT TTATTGTTGC | 120 |

1960 .

| | AGAAACAACA TIGATAATTA ATCCIGAATC GAATAAGCAM GTACITGAAT CITTIGTAAA | 240 |
|----|--|-----|
| | AGATGTTTT TTATAATTAT TGGTGAAAAC GTGTAGTTAT GGTGAAACTC AAAGATAATA | 300 |
| 5 | ATTTAAATGA GATGTTAATG AAAAAGTAAT TCAATATANA ACAGGTGATT TANATCTTAA | 360 |
| | TAAGGNTAAT TCCAGGTTGA ATTCCAATTG CGGGCATCAT | 400 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1451: | |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 124 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| 15 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451: | |
| 20 | TGCGTTATAG TTGCTATTCT CAATTATGTT CGCGATAATT TTAAGTAAAA GTAAGCACAG | 60 |
| | ATATTGAATT TGATAGGAGT TAATTGATAT ATACATACGA ACTTTCATGG ATCACTTAAA | 120 |
| | TTnG | 124 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1452: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 126 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452: | |
| | TGTATTAAAA ACCTTCCACC TTTAAAAGCA ACAATGCGGT GTCCTTTAAA TTCAAACATA | 60 |
| | ACCATATACG AATTACTCGA TAATTCTGTG TGTTTAATTG ACAGATGTCG TGTGAATTGA | 120 |
| 40 | TnATTT | 126 |
| | (2) INFORMATION FOR SEQ ID NO: 1453: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 280 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453: | |
| | ACTTTGGCAA CATCTGGAAT ATCATATAAA TCAAGTAACT TACCTAACCG ATGATTAATA | 60 |
| 55 | | |

| TGTAAGAAAT TAAAATCTTT TGAAGCATTA AGATTACTTA TCATTTHTAA ATTTCAATTT AAACTAACAG TAATTTATGT AGCTTTTGNA ATTCCATAA (2) INFORMATION FOR SEQ ID NO: 1454: (3) SEQUENCE CHARACTERISTICS: (A) LENGTH: 242 base pairs (B) Type: nucleic acid (C) STRANDENNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454: ATATTCTTTA AATTAAACTG ATCACTTGAA TAATTAACAT TACTTAATTC TATGGCATTC ATGATGATTC CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGTGACATTT. CGATGGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAATTGTT TCTCTTTTAA AATAAGGAACT ATTCTTNGCT CCTTAACAAA GGNCCCTTTT CCTCTAATTG 25 TT (2) INFORMATION FOR SEQ ID NO: 1455: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (2) INFORMATION FOR SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA 40 TTGATGTACA CAGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456: ACCAGTGGTT GCCTTTTTAA GTCCCGCGTG GGACAAAAAT TAACCTCTTT ACACTTGCAA ACCAGTGGTT GCCTTTTTAA GTCCCGCGTG GGACAAAAAT TAACCTCTTT ACACTTGCAA | | THE THE TAKE THE TAKE THE TAKE THE TAKE THE TAKE THE TAKE THE | 180 |
|---|-----|--|-----|
| (2) INFORMATION FOR SEQ ID NO: 1454: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 242 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454: ATATTCTTTA AATTAAACTG ATCACTTGAA TAATTAACAT TACTTAATTC TATGGCATTC ATGATGATTC CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGTGACATTT. CGATGGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAATTGTT TCTCTTTTAA AATAGGAACT ATTCTTNGCT CCTTAACAAA GGNCCCTTTT CCTCTAATTG TT (2) INFORMATION FOR SEQ ID NO: 1455: (1) SEQUENCE CHARACTERISTICS: (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (2) INFORMATION FOR SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTT TAATGTATATC GGTATAGATA TTGATGTGAC AGACTAGAT AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | TGTAAGAAAT TAAAATCTTT TGAAGCATTA AGATTACTTA TCATTTnTAA ATTTCAATTT | 240 |
| (i) SEQUENCE CHARACTERISTICS: (a) LENGTH: 242 base pairs (B) TYPP: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454: ATATTCITTA AATTAAACTG ATCACTTGAA TAATTAACAT TACTTAATTC TATGGCATTC ATGATGATTC CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGGGACATTT. CGATGGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAATTGTT TCTCTTTTAA AATAGGAACT ATTCTTnGCT CCTTAACAAA GGNCCCTTTT CCTCTAATTG 25 TT (2) INFORMATION FOR SEQ ID NO: 1455: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA 40 TIGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . 5 | AAACTAACAG TAATTTATGT AGCTTTTGNA ATTCTCATAA | 280 |
| (a) LENGTH: 242 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454: ATATTCTITA AATTAAACTG ATCACTTGAA TAATTAACAT TACTTAATTC TATGGCATTC ATGATGATTC CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGTGACATTT CGATGGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAATGTT TCTCTTTTAA AATAGGAACT ATTCTTnGCT CCTTAACAAA GGnCCCTTTT CCTCTAATTG TT (2) INFORMATION FOR SEQ ID NO: 1455: (i) SEQUENCE CHARACTERISTICS: (i) SEQUENCE CHARACTERISTICS: (ii) STPPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | (2) INFORMATION FOR SEQ ID NO: 1454: | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454: ATATTCTTTA AATTAAACTG ATCACTTGAA TAATTAACAT TACTTAATTC TATGGCATTC ATGATGATTC CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGTGACATTT CGATGGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAATTGTT TCTCTTTTAA AATAGGAACT ATTCTTnGCT CCTTAACAAA GGNCCCTTTT CCTCTAATTG TT (2) INFORMATION FOR SEQ ID NO: 1455: (i) SEQUENCE CHARACTERISTICS: (i) LENGTH: 110 base pairs (ii) TYPE: nucleic acid (c) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 10 | (A) LENGTH: 242 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | ýs |
| ATATTCTTTA AATTAAACTG ATCACTTGAA TAATTAACAT TACTTAATTC TATGGCATTC ATGATGATTC CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGTGACATTT CGATGGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAATTGTT TCTCTTTTAA AATAGGAACT ATTCTTnGCT CCTTAACAAA GGNCCCTTTT CCTCTAATTG TT (2) INFORMATION FOR SEQ ID NO: 1455: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: ATAAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA TTGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 15 | | |
| 20 ATGATGATTC CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGTGACATTT CGATGGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAATTGTT TCTCTTTTAA AATAGGAACT ATTCTTNGCT CCTTAACAAA GGNCCCTTTT CCTCTAATTG 25 TT (2) INFORMATION FOR SEQ ID NO: 1455: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA 40 TTGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456: | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454: | |
| CGATGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAATTGTT TCTCTTTTAA AATAGGAACT ATTCTTNGCT CCTTAACAAA GGNCCCTTTT CCTCTAATTG 25 TT (2) INFORMATION FOR SEQ ID NO: 1455: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA 40 TTGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456: | | ATATTCTTTA AATTAAACTG ATCACTTGAA TAATTAACAT TACTTAATTC TATGGCATTC | 60 |
| TCTCTTTTAA AATAGGAACT ATTCTTNGCT CCTTAACAAA GGNCCCTTTT CCTCTAATTG TT (2) INFORMATION FOR SEQ ID NO: 1455: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA TTGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 20 | ATGATGATTC CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGTGACATTT | 120 |
| (2) INFORMATION FOR SEQ ID NO: 1455: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA TTGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | CGATGGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAATTGTT | 180 |
| (2) INFORMATION FOR SEQ ID NO: 1455: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA TTGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | TCTCTTTTAA AATAGGAACT ATTCTTnGCT CCTTAACAAA GGnCCCTTTT CCTCTAATTG | 240 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA TTGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 25 | TT . | 242 |
| (A) LENGTH: 110 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA TTGATGTGAC AGATCAAGTG AGACTTGCAT AATGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | (2) INFORMATION FOR SEQ ID NO: 1455: | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA 40 TTGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456: | 30 | (A) LENGTH: 110 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA 40 TTGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456: | 25 | | |
| TTGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456: | 00 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455: | |
| (2) INFORMATION FOR SEQ ID NO: 1456: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456: | | ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA | 60 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456: | 40 | TTGATGTGAC AGATCAAGTG AGACTTGCAT ANTGGTATTT TATTCAGATG | 110 |
| (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456: | | (2) INFORMATION FOR SEQ ID NO: 1456: | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456: | 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| ACCAGTGGTT GCCTTTTTAA GTCCCGCGTG GGACAAAAAT TAACCTCTTT ACACTTGCAA | 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456: | |
| | | ACCAGTGGTT GCCTTTTTAA GTCCCGCGTG GGACAAAAAT TAACCTCTTT ACACTTGCAA | 60 |

| | AAAGCGCTTG CAATATATTT TCGATTTGTL ATTCAACMAA ACGTTTTATT LTATTCGCTG | 180 |
|----|---|-----|
| | TAGTCAAATG TATACCCTTA TACTGACTCG aTAATCATTT GCTTATHATT TGAGACTAGG | 240 |
| 5 | ACATAAATCA ATGCTCTAGA ATCCAAAAAG TCACATTAGT AGTAGTTAAC CGAACGAAAA | 300 |
| | TGCACTTGTA ACAAGCTTTT TTCAATTAAA GTCAGGGGCC CCAACATAGA GAATTTCGAA | 360 |
| 10 | ATGAAATTCT ACAGGCAATG CGAGTTGGGG TGGGACGACG AAATAAATTT TGCAAAAATA | 420 |
| | TCATTTCTGT CCCACCTCAC TCAAAATAAA TTTCACTATC CGTAAAATAA ACAACTAACT | 480 |
| | ATTTAAGTAT CATCTCTCCC CTAATTAACA ATTATAAAAA TAAGAACCAA TATTCGAGAC | 540 |
| 15 | AACCTAATTA A | 551 |
| | (2) INFORMATION FOR SEQ ID NO: 1457: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 20 | (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | • |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457: | |
| | ATCHGGGGCT GCATAAGCGA TATCAAGTGT GAGCATTGAA CGATTCAGGA CTGACCAGCA | 60 |
| 30 | CGCCGTTTGC CTGCTTTGAA AGATCCACCG ACAAATCCGC CAACATCGT | 109 |
| | (2) INFORMATION FOR SEQ ID NO: 1458: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 35 | (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458: | |
| | ACCAGAGCCT CTTTGACTTC CTAAGTCGAA TAGCATCGTT GATATAGTTA AAGATGACGC | 60 |
| 45 | TAGATTTAGn AATCCAAACT CATAACACCT CCACCATTCC ATCACATCTG GA | 112 |
| | (2) INFORMATION FOR SEQ ID NO: 1459: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 50 | (A) LENGTH: 224 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |

| | | CCCCAACCAA TTTTTTAAAA AAGGGGGCCT TTGGGGGGGCC CAACCAAGGG GGAACCCCTT | 60 |
|---|----|---|---------|
| | | AACCCCAATT TTGGCCAATT TTAAAGGGAA GGCCTTGGAA CCTTTTTGGG AATGGGCCGG | 120 |
| | 5 | TTTTAAACCC TTGGTTTCCG GAAGGGGAAA ATTTTTAAAA AAACCGGAAT TGGTTGGCCC | 180 |
| - | | CCTTTAAATT AAAAAGTTCC CTnAAAAAAA AATTCCCCCA AGGG | 224 |
| | 10 | (2) INFORMATION FOR SEQ ID NO: 1460: | |
| | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 135 base pairs (B) TYPE: nucleic acid | • |
| | 15 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460: | |
| | 20 | TTTCGACAAT CAATTCGACG TCAGTGCCAC TCCATCTATA GTAAAGCGTT GATACTTTCA | 60 |
| | | ATAATAACTG GATCACTGTC TAATTATAAA TGGATTCTTA CATCCCACCA TAATAAATTn | 120 |
| | | CATATGTTCA TCACC | 135 |
| | 25 | (2) INFORMATION FOR SEQ ID NO: 1461: | |
| | 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 114 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | , | | |
| | 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461: | |
| | | TTATAGAACC TCGTACTCCT nTCGACACTT GAATTTAAAT CAGAGCCGCC AGTGGAGAAG | 60 |
| | | CATGAATTGA CTGGTACCAC TCGCAGAAAG TAATGATTCT AAGCCACTTG ATTA | 114 |
| | 40 | (2) INFORMATION FOR SEQ ID NO: 1462: | |
| | 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | · · · |
| | 50 | (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462: | |
| | 50 | GTTGAATTGT TGGTGATGTG GTTACACGAA TTTCGAATAA TTGTTCTTTA CGTCAAAACG | , 60 |
| | | TATCGTTCCA AAGTAATCCC CNGGTAATAG TTACCAACAA GTTCA | |
| | | INICOTICCA ANGIANICCE CHOGINATAG TIACCAACAA GIICA | 105 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 162 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-------|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463: | |
| 10 | TTGTATGACT CTTCGGACTT TGGTAAAATT GTGAACGCTG GnTGAATGAT TTTTGTTTGA | 60 |
| | CAATTGGCCT TATCATCATT AATCGTATTT TTAAGCTGCT CGGATATAAG TTCTCAGCGA | 120 |
| 15 | GTTCTTTTG ATGTATCATT AGTGTAGAAA ATAGCTGTTT GT | 162 |
| | (2) INFORMATION FOR SEQ ID NO: 1464: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 103 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464: | |
| | TARATTGGAR AGTCACATTC ARRATGCGAR ARTGTTTTAR RATGTCCTGT AGGTGCTTAR | 60 |
| 30 | TAGTITTGCA TITGCAAATT TTACTGAACC GGTTTAAACG AAT | 103 |
| | (2) INFORMATION FOR SEQ ID NO: 1465: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465: | |
| | AAATTGTATA ACTACCAAGC TTATATGAAA TGGTAAACAA AATATTATCA CTTGTTTGAT | 60 |
| | AAGTAGCGTG GAAAATATTG TATCTTTCTA AATGTACACG TTAGAANTCA TGCTTATGTA | 120 |
| 43 | TTACACGCGG GGCACTGGTA CCTAAGGGCC TAT | . 153 |
| | (2) INFORMATION FOR SEQ ID NO: 1466: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1466: | |
|----|---|------|
| | TTTCAGTAAC ATATGAAAAC TTAATTAACG ATGTTCAGTA GGTTCATACA TTTTACTTTA | 60 |
| 5 | TGATGCTTAA TTGAATTACA NTTAAGATAT GACCAGCTAA AAAGAGTTAA TGTGATATTT | 120 |
| ٠. | AACC | 124 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1467: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 354 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | *** |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1467: | |
| 20 | AAGGAATTAA GTTTGCGACA CCAGCAAATA GTACTAATAA AGGAATATAT GGTAAGTCAA | 60 |
| - | TAATTGAATA ACCGATATAT AAGAATATAC CTAAAATAAC ACTGACAGTT ACTTGACCTT | 120 |
| 25 | GAATGTAAGA TTTTAATGTA AAGTTTAAAT CAGTTAATAA ATCTACGAAA AATACTTTAC | 180 |
| | GTTCACCTTT GADAAATTTA GCAACAGCTG GGATAAATTT TTCATGGTCT TTTAACATAT | 240 |
| | AAATTAAGAA GAATGGAACC ATAATCAATA AGAAGATGGT TGAAATTAAT GATGTAATGT | :300 |
| 30 | ACTGTAATGA ATTAGATAAn ATATTAGAAA CGCCATCACC CATTGATTTA ACCA | 354 |
| | (2) INFORMATION FOR SEQ ID NO: 1468: | i. |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 40 | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1468: | |
| | TGCAAACTAG GAACAATAAT GTTAATATAA CTATGATGNA AGTTAAAAAA TAAAAAGGAA | 60 |
| 45 | CACTCTATAA TATGAATTAG GGTTTACAGT TTTTTGAGTA TTTTACAGTA TCAAAGTTTA (2) INFORMATION FOR SEQ ID NO: 1469: | 120 |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 476 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | o) - |

| | TCTAAATGCT GACTAAAACT AGCAACACGA GACTCATTAT TATTAGACAC GATTGTAATA | 60 |
|------------|--|-------|
| | GTGATTCCTT TTTCATTAGC TTCCTTAAAC CATGCTTTAA CACGTTCTGT AGGTTCTTTA | 120 |
| 5 | ACATCCCAAC CTACTAGCGT ATTATCTAAA TCTGTAATAA TACCTTTAAC GCCTTTGTCC | 180 |
| | ACTAACTTGT CTAAATCAAT TTGAAATATT GATTGAACAT ATGAATTCGG CATAAAAAAC | 240 |
| 10 | TTGCGAACTA AACCCATTTA ACTCACCTTT ACCTTTTAT AATTGAGACA CTAATGCTTC | 300 |
| | AACAGTTTGA CTTGATGATA CAGCTGCTTT TTCTAAAAAT GCTTCGAAGC TCATTTCCGC | 360 |
| | TTCTCCATTT GCTAAGTCTG AAACTGCACG AACTACAACA AATGGTACAT TAAATTGATA | 420 |
| 15 | ACATGTTTGT GCAATTGCAG TTGCTTCCAT TTCAACCGCC ATCGCATTTG GAAATG | 476 |
| | (2) INFORMATION FOR SEQ ID NO: 1470: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 156 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 2 5 | | |
| _ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1470: | |
| | CACGATACAT GGGTAAGGAT ACTACTCAAA TCAACTTGAA ACCAATAATn CATGACCATA | 60 |
| 30 | TGTGTGCCAA TGAATTCAAT TGGAAAGACA ATGATGAGAT ACTATTAAAA CGATTATATT | 120 |
| | TATTGTCACT TGTTCAAACG CACTCCTTTT CCAAAT | 156 |
| | (2) INFORMATION FOR SEQ ID NO: 1471: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1471: | |
| | AACAAAAGTT TTGAAAAGCC GGGTGCCAGC GAAAACTTAA AAAGCACTTT ATCAGAAAAA | 60 |
| 15 | GCTAAGAAAA AAGATTAATA TTCATTCATT AAATATAAAT CCAATTTAAT TTGTTGTTTA | |
| | AGGTCTACAA GTGTATGTTT AATATACAAT TCATCGTTTG ACGGTAAATC AGATACTTTG | 120 |
| | AAATCTTGTC GCTCAACCTC TAGTAAATCG AAATCGCTAC CAGCTGAATT ATAGGTTTTA | |
| 60 | AGTTCACCCT CTTCAATGAT TCTGTTTTCA AAGTCTTTAA TAACTATAAA TACTGGTTTA | . 240 |
| | CONTRACTOR TABBOARCH CONTRACTOR TO TOTAL TRACTOR TO A A A A CONTRACTOR TO TABBOARCH TO | 300 |
| | | |

| | (2) INFORMATION FOR SEQ ID NO: 1472: | |
|------------|---|----------|
| 5 . | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | - 18 |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1472: | e y Mari |
| | CTAGGATTHC ATCTATTTGG GATGAAAATA AGCGTTTCCT GAATCCACAA GAATATCCAG | 60 |
| 15 | TCGATTTAAG CCAGGCATGT TGGGGTAATA ACATAACGTT TTTTGA | 106 |
| | (2) INFORMATION FOR SEQ ID NO: 1473: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid | |
| • • • | (C)-STRANDEDNESS:-double | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1473: | |
| | TATCTTACCT ACATTGTTAT CTGATGGCTG TAATCATTAA ATCTATAACA CCGAGTTCTT | 60 |
| 30 | CCATTAATTT TCAGCTTCAT TCGACTGCCT TTTTAThTTT CGTACTATTA CGAATTT (2) INFORMATION FOR SEQ ID NO: 1474: | 117 |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 164 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1474: | * |
| | ATGCATGGCA CTGGAAnCAG CTGGGAGATA TAGGTAGTAT CCTAAAGAAG TTCAGTTAAT | 60 |
| | CGGAGCGATT GTATTGCATG AAGGTAACAT TGCGGAGTGC CAACAGGCGA AGTAAAACTT | 120 |
| 45 | AACGGCAACC ATGCCTTATA TTAAATGCCC TTCCGGGAAA GGAC | 164 |
| | (2) INFORMATION FOR SEQ ID NO: 1475: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 210 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| <i>55</i> | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1475: | |
|------------|---|-----|
| | ACAGCAAGAC GTGACAAATC AGATACTATT AGTCATCAGC GTTAACATGT GGATANGTGT | 6 |
| 5 | GAGGTACGAA TANCCGAAAG GAAATACGAC CTTTAACATT CGCGCACAAA ATGAGCTCAG | 12 |
| | GCGCCTGCCT TGCCCATTTT TTAAATTATT TCCCTGGAAA TGATTCGCTG TGTGCTGTTC | 180 |
| 10 | TGTCCACAAC AACACGATTA ATGCCATGAC | 210 |
| | (2) INFORMATION FOR SEQ ID NO: 1476: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 128 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1476: | |
| | AGGGTGATTT CACGGTTCGT CTGCCCATTT AATTGCGCAT TTTGCACACC ATCTACCGTT | 60 |
| | TGCAATTTTG GTATTAATTG TTGCATGCAG TACTGTCCGT TGACTTTGnT GCAAGTGCAT | 120 |
| 25 | GCTCTTTC | 128 |
| | (2) INFORMATION FOR SEQ ID NO: 1477: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 641 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 3 5 | | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1477: | |
| | AAAATCTGGT AAAGTAACTA GAGTTTAATA AATATATTGC ACATAAAAAA TGTGACCTTA | 60 |
| 40 | TGTGGAGGAC ACATTTACTT AAGAACTAAG AGCTCAACCT CTTAGTTCTT TTTTTGTTAC | 120 |
| | CAAACAATAC ATAATGGTTC ATAGTGAAAT TCGAACTATC AATATAATTT GGTTAATACG | 180 |
| 45 | TTTAATAATG GTTCTCTGTC AAATTGGACT TATGGGTTCA ATATCGATTT TGGCACATAA | 240 |
| 43 | ATCAATGTAC TAGGACCTAC AATTTTCCTT TCAATAATAA ATCACGCCAT AATCTTCATT | 300 |
| | AATTACAGCG TGATTCATCT ATTATTATGT TATAAATKCT ATCTATAAAC GTCACTTTAT | 360 |
| 50 | TARATAACTC ATGCACTTTA TTARARATCC TCACAAATTT GAATATACTT AATTTAAATC | 420 |
| | TGTACTTCTA ATTTGCAAAA TCAACCCATC ATGTACAGTT ACTTTCGCTT GCAAAGACTC | 480 |
| | AATTTCATTT GAAATAGTTA AAGTAGAACC TATATHAAGC ATTTGTCTAG CTAAATTATA | 540 |

| | GATAACTCTT ATCTTTTCA ACTGTAGGTG ACCTTTAGGG C | 641 |
|-------------|---|-----|
| 0 | (2) INFORMATION FOR SEQ ID NO: 1478: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | د ادا د د ادامه در ادامه ادر از | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1478: | |
| 15 | TTAACCGTGA TGCAGAGTAG TAAGTGGATTN CATGCTCTGT TATGGATGAC AAGACAAAGC | 60 |
| | AGCGAATATT GCGTACTGCG ATTGATGAGC AGATGCATAT GATTGGATTG | 120 |
| | c | 121 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1479: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 30 . | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1479: ACCATTGCTT AGATAAATAC CTCGCAGTGA ACCGCATTAG TATAGCACTT CTAGCTGATC | 60 |
| | GCATCAGTAA AGTATGCTAT TAATGTCTCA GTTTTATCTG TAATGCATGT TTAAGTTAGT | 120 |
| 35 | CATAGCATTA TTn | 133 |
| | (2) INFORMATION FOR SEQ ID NO: 1480: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 201 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1480: | |
| | TTTTGGGGNT TTTAAATTTT AAATTCCCGN TGGGGGAAAT TCCCTTAAAA ATTCCCAACC | 60 |
| 50 | CTTTTAAGGG GTGGGGGTTT TTTTAGGGAA AAAGGGGCCC GGGGTTAATG GTTCCCAAAA | 120 |
| 30 | AATTGGGGAA AATGGCCCCC CAAATTTTAA ATTCCCGGTT TTAAAATTGG GGTGGGTTAA | 180 |
| | ATTGGAAAAA CCCCCAAATT T | 201 |

(i) SEQUENCE CHARACTERISTICS:

| 5 | (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1481: | |
| | CAGTATCAAG CATAGTAAAA AATGAGGGTA GGACTGAAAA TACGGCGTTA TTGGTGGTGC | 60 |
| | ATTCACGGTA AATATGTTGC ATGACCAGCA AGTTTTGGnC TTCTGATGCA CC | 112 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1482: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1482: | |
| | CAAAAACAA GTTCTGATAT GCAGTAGCTG AATAATTTTG CTAGTTACAC CAAAGTGATC | 60 |
| | TTCTGGTGTT TTACTTTTTA TAAATGTTTT CATATATTTC ATATGTATAA AAATGGGATT | 120 |
| 30 | TAGCGTA | 127 |
| | (2) INFORMATION FOR SEQ ID NO: 1483: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 83 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1483: | |
| | AGTGGTGTAT TGGGTGAGTA ATGCTTAACT TCATACCTGG TGCATTGGCT GTTCAGTATC | 60 |
| 45 | ATTATATCTG CATGGGCGAT ACT | 83 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1484: | * |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 201 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | | 80 |
|--------|---|----------|
| | CGTTAGCTGG AACCTAGNCA AAGGGATGGG TTTAGTGGTC TATTGTGGTAT | 120 |
| 5 | TCCGTGGGCC ACCCCATGGG GCCATTATGG TTTGGGGAATT TTGGGAATAA ATTAATTTnC | 180 |
| | CCAACCAAAA ACCAGGCCAA G | 201 |
| | (2) INFORMATION FOR SEQ ID NO: 1485: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 210 base pairs (B) TYPE: nucleic acid | egi er e |
| 15 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| • | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1485: | |
| 20 | CTCACAGCAA CATCAAAGAG GCAGATATTA GTCAAGTTCA ACGTAATAAC ATCTACCTTC | 60 |
| | - ACAAGTEGAT AAAGGAGCAC CATCATTAAT AAGTAGATCA ACAAGTCAAC GAGAATTTTA | 120 |
| | ATGTGCAGAA TAGAGAAGTA CACCACACAN ATAATCAAGC GATGTAATTA CTACTACATT | 180 |
| 25 | TTnCATGACA GAGTGAACCT CAACAGCGGT | 210 |
| | (2) INFORMATION FOR SEQ ID NO: 1486: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 158 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| 33 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1486: | |
| | CAGGTTATGT TTGCATTAGA AGTTCTTGGA AAATCTTTAT GGAACGTGGT TTACACCCTG | 60 |
| 40 | ACTTTGAATT GCATCGATCT GATGAAGATA AATGAAATTG AATGGGATGG CCnACATGGA | 120 |
| | ATGCAACCTA TGACTTGGAT GGAATTAGAT GAAGCGGG | 158 |
| | (2) INFORMATION FOR SEQ ID NO: 1487: | , |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 114 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | , |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEO ID NO: 1487: | |

1972-..

| | TTGCAGCATA TAGAGGTAGA GGCATCGCGA CAAAGTTATT AACGTCATTA CTTG | 114 |
|----|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1488: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1488: | |
| 15 | TGCTAAGTGA TAAAAAGAAT GATAAGCCAG GTGTACCAAT GGGTCCTGGA TTAGACCATT | 60 |
| | TGGGAGATAT CGTTGTACCA CATGTTGATC AACTAACGTT nCCACATG | 108 |
| | (2) INFORMATION FOR SEQ ID NO: 1489: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1489: | |
| | CAANACGTAA TTTCATGATG AAAGTGGTCG ATAATTTCTT GAAACATCGC TTTCAGTAAT | 60 |
| 30 | AACGCCTGCT TTAAGGTCAC GTTCCGCATA GGTGTACTGA GGATGTTGAT GT | 112 |
| | (2) INFORMATION FOR SEQ ID NO: 1490; | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1490: | |
| | CAGAACGTTT AAAACAAAGT TGGAAAAGTT TTCTAATCGT ATTAGCTGCA TGTTTAATAC | 60 |
| 45 | TTATTATTGC AAGTGAAACG CTTATTTTCC TTTAGTCATT TGACCGATGT TAAAGAGGTG | 120 |
| | AGATGGTTAT TTAGAATCAT TGTATTGATT GTTTTTGCGG TAGTGATGTT CACAATTTAT | |
| | ATCTCTTATC ATCATTATAT GAATGACTTT TTAGTTACTA AGTTATTTAA TATTTCCGCA | 180 |
| 50 | | 240 |
| | GCGACGCCAL AGTTATTATG TCTAT | 265 |
| | (2) INFORMATION FOR SEQ ID NO: 1491: | |

| 5 | (A) LENGTH: 113 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----|---|-----|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1491: | |
| 10 | Charattggc Caggggctca tccartatta arataggcgt acgagggatt artagaccac | 60 |
| | CTAATGAAAC GCGTTGGTTG TTGGACCTCC AGATAAATCC TGGGGGTCGG TGG | 113 |
| | (2) INFORMATION FOR SEQ ID NO: 1492: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| -00 | (D) TOPOLOGY: linear | |
| 20 | | |
| - | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1492: | |
| 25 | ACTAAGAAAA TCCGAAATCT TTTCCGCTTC TTTTAAATAC GTAATACTTC CTTTTTTCG | 60 |
| | CTCTAAATGT TTGGCATTCA ACTCATAACT ATTCATTAGT TTCGTTAAGC CTTCTGCATG | 120 |
| | ACTCTCATTT TGAGAAAAA TTTCCAAATG GTACGAAGAT GTTTCAGGGT TATTCACTGA | 180 |
| 30 | GCCACCTGCC AGAAAAGCTC CTCTCAAGTA ACTGCGTCTC ATTTCGTCAT CTTGAATCAT | 240 |
| | TGAAATGATC AATTTCATGG CGnnAAAATG CCGTCT | 276 |
| | (2) INFORMATION FOR SEQ ID NO: 1493: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 110 base pairs | |
| ٠ | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (b) TOPOLOGI: Timear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1493: | ٠ |
| 45 | GATGACGAGC GCCAATTATG TCACTTTAT GGCAAAAGCT GGAACTAAAC AACCNAGCCT | 60 |
| | GCCAGTAAAA TTGGCAATTG GGACGTTCTT AGCAGGTGCG TCATACATAC | 110 |
| | (2) INFORMATION FOR SEQ ID NO: 1494: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 200 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 55 | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1494: | |
|----|---|-----|
| | AAAAAAAAGG TTTTTTACCC GGAATTCCAA AnTTTTAATC CCTTAAAAAA AATTCCGGCC | 60 |
| 5 | AACCCCCAAA CCCAAGGTTT TTTCCTTAAC CTTGGAAnTA ACCAAGGTTT TTTTTCCAAA | 120 |
| | AAATTTTCCA AAAAAGGAAT TACCCAAACC CTTAAAGGTT TTAAAATTGG GGGGGGAAAA | 180 |
| 10 | AGGCCCTTTT AGGGGGGGAA | 200 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1495: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 253 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1495: | |
| | AAAAAATTTG GTGCATTTAT CATATGGAGT ATTAATCTGT AGAAGTAAAG GCGATATAAA | 60 |
| 25 | TGTTACTTTG GTAATAAAGA TTACAGCGAA CGTTATTATT GCTCAGGTCA GATCAAGAAA | 120 |
| 25 | TTGGTGTCCG GGTGACAAGA CTTGGTGGCG CGGTGTAGTT TGTCAGTTGT GTGGTCATCT | 180 |
| | TARATARCGC TATCGTACGG TGTGTATCAC ATGARGGGAC TCTTACTART TCTGCAAGTA | 240 |
| 30 | CACGTCACGC nnT | 253 |
| | (2) INFORMATION FOR SEQ ID NO: 1496: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1496: | |
| | ACGCTAGCTT CTGAAAAAAT AAGTGAACTA TGGATGCAAT GAnCCTATTC CTGAATGATA | 60 |
| 45 | TTAGACGTAG CGCACCTGGT GCAGAACGCC AATAAAAAGA CAAG | 104 |
| | (2) INFORMATION FOR SEQ ID NO: 1497: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | i) |

| | AGGGAGGCGC CCAAATGGCT CTATATTAAA AAAGGACTCT CAGAGCATTA ATGAAAAGTT | 60 |
|----|---|------|
| | GAAGCTCAAA AGGAAnCGAA AGAAACAAGT ATCAAAACAT | 100 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1498: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 base pairs (B) TYPE: nucleic acid | ٠, . |
| 10 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1498: | |
| | TGGAACTTTG GGGAAGTCAA ACGGTTGTAA TCGTTGAACA TAAAGTTAAA CACATTCTGG | 60 |
| | ATCATGTCGA nCGCGTCCAT TTGATGGATA TAACGGGAAT A | 101 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1499: | |
| - | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid | |
| 25 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1499: | |
| 30 | AGTTCTGGTG CATCGTTTTT CATTGTATTT GTGACGATTA TCATTCCAGC ATTAGAATAT | 60 |
| | TATGCATTAT ATTTAGGTGT GATAGGTGCA TTTATAGGTG GTTTAACTGT TTATACACTT | 120 |
| 35 | TCAGGTG | 127 |
| | (2) INFORMATION FOR SEQ ID NO: 1500: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 560 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1500: | |
| | TCCCCGCTTT AATACCTTCC ACGATTTCTT TAATTGCTTG CGGTTGGTCA CCTTGAGGCT | 60 |
| 50 | CAAAATCAGA ATGTATTTTA AAAGGATAAT GTTCAACCAT TGTCACATAT GCCTCCTCTT | 120 |
| | TCAACGTATT ATTTATATTT CCGCTCAACT CTTTGCTTTC TCATnACATA TnTTAGCAAA | 180 |
| | GTAGTCACAC AAAAaGCAAA CGTTKGTTCG TAAAAATGTC GAACAAaGAA AnACAAACAT | 240 |
| 55 | | |

| | | 300 |
|-------------|---|-----|
| | AAGTTAATCT TAGCGATCTT CATCTTGATG TTTATGAAAT TCGAGTTGAT CTATAATTAA | 420 |
| 5 | ATAACCAGCT AATAATGACA CTACATCAAT AAAAATAATC CACTCGTTAT GGAAATACTC | 480 |
| | TITATAGATT GAGGCACCAA TTAAAATTAA TGTCAGAATA GTACCGACCC ATTTACTTCT | 540 |
| 10 | TGTTATTACA CTAAATAATA | 560 |
| | (2) INFORMATION FOR SEQ ID NO: 1501: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (b) Torollog1. Tilled1 | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1501: | |
| | ATTAAATCAT ACTHACAATT ACCGATGACA TTATTCCAAT TCAATCTAAT TCCGTGATGA | 60 |
| | AAGAGCCACG TTTTGGTTAC TTCGTGGGCG TGAATTATTA TG | 102 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1502: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| i | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1502: | |
| | TATGGTAGCT CCAAATGGTT GTATCGTCAC ACCATCATCT TCAAGTGCAA TGCGATGTAA | 60 |
| * | TCGATTGGCT GTTGTTTCTG TTACCCATAG TACTTTTTCA TCTGTACTTA AAGCAATACC | 120 |
| 40 | ATTTGCTACG CTAATATTTT GAATGATAGG CGTCACTGTT CTAAAGTCCG GCGAAACATA | 180 |
| | ATAAACGCCT CCTAGTGGAT TGGTAGAGTA TCCTCTAAAA TCTGTAAAAT AAAATCCACC | 240 |
| 45 | TTTAGAATCA AATACCATGT CATCAATACA ATATGCTGTT GAAAGATCTT CAATAATATC | 300 |
| | TTGTAAGTTG TCACCATTTT CTGTAGCTGC AAAAATGCCT CCnGGAGATT TAAAATCTCC | 360 |
| | NAAAATAACC AACGNATAAA TCGGGCANCT TATGGAATTG | 400 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1503: | |
| · <i>55</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 168 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1503: | • . |
|------------|---|-----|
| 5 | TACAGGTAGT TAACAGTTGA TGTTAAATGG CGTACTGGAT TCTTTACGCA CGATTTTTTG | 60 |
| | TTAATAAGTA TGGGATAGCA CATTACTATA TCCTACTTAC GACTTATTGG ATATGTCnTA | 120 |
| ٠ | GCTATTCTTA AGCTCGAAAA GTTTCACAGG ATACATAAGG GACCAACT | 168 |
| 0 | (2) INFORMATION FOR SEQ ID NO: 1504: | • |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 237 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * |
| , | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1504: | |
| 20 | CTACTGATTG TGTAATGTCG TTGGTAGGCT TGGGCTGTAC GCAGTATTAG GTGTAGGCAA | 60 |
| 5. | CTTGGCTTTT GGCATCTACC TTGTATGTGT CGTGTATCTA nGGCTGGGGC TTGCTCCTTC | 120 |
| 25 | AGTTGTTAGA CAGTAGGGGG TAATCTCAGG GGTGCAATGT ACTCCCTCCG TCCTAAAATA | 180 |
| | CTHTATATGC TCGTGCCGAA TTCCTGCAGC CCGGGGGATC CACTAGTTCT AGAGCGG | 237 |
| | (2) INFORMATION FOR SEQ ID NO: 1505: | 0 |
| 3 0 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 209 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1505: | |
| | CGCATTTACC ACCATATGAT GGATCCANCG ACGTTTTAAT AAAGATAAAA GTGACAGTAG | 60 |
| 10 | CGGGAAAACA GGnCCATAAT TCACATCTCT TTTGAAAAAT ATGTTCAAGC TAGGATCATT | 120 |
| | AGGAGAGTCA TATTAATAAT AAAAATGTTG CAATCAATCG ACGTGCGTTG AATCTTAAAT | 180 |
| | ACATAATAAA TGTTGTAGAA GATATGGGT | 209 |
| 0 | (2) INFORMATION FOR SEQ ID NO: 1506: | ٠, |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1506: | |
|----|---|------|
| | AAAATGTGGC TATTGATTTT GACTTGGAAC TTTTTGAACA TTTCTCTCAA GGATTTAAAT | 60 |
| 5 | GTAGGTAACA GGGCAGGTAC TACGGTACTT NCCTATTTT TTATGCAAAT TTTAAAAAAC | 120 |
| | A | 121 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1507: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1507: | |
| 20 | AATGACAAGG TCAGCATTAA AACCATTTAA AAATAAACGC GTTATGGTTA CTGGACGTAT | . 60 |
| | ACAACGTGTT TTGTTTAAAA ATTATTTAGA TAGACATAGC ACATTTAAGC CGAATGTAAG | 120 |
| | GATATTATTA AAAGANGTAT TTGT | 144 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1508: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 139 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1508: | |
| | CCGATTGAAT CTGTGTACAC TTCACCAAAG ATATCTTTCT TCGTTTCTTC AGATAAACTT | 60 |
| | TCCATTGCTT TCTTATCAAC ACTTGTTTCT ACTAATAAGT GTGTTAATTT GTGCTTnTTA | 120 |
| 40 | ACAAACTCAA TAGCTTGTC | 139 |
| | (2) INFORMATION FOR SEQ ID NO: 1509: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 155 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1509: | |
| | TCTGCCTGCC TCGGCCTCCC AAAGTGCTGG CATTACAGGC ATGAGCCACC ATGCCTGGCT | 60 |
| 55 | | |

| | CAAGTTAAAA TACAGATGTA AGACTTGACT TGATC | | 155 |
|----------|--|----------|-------|
| | (2) INFORMATION FOR SEQ ID NO: 1510: | | |
| <i>5</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs | | |
| | (B) TYPE: nucleic acid | | |
| | (C) STRANDEDNESS: double | | |
| 10 | (D) TOPOLOGY: linear | | |
| | . A company of the second of t | <u>.</u> | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1510: | | |
| 15 | ATCCCAATGC TAATGAATTT GCATATACGA TAAATAATGC TTTTTATCAT CAATAAAGC | r | 60 |
| | ATGAATCTTT CAAGATCTTC ATTGAAC | | 87 |
| | (2) INFORMATION FOR SEQ ID NO: 1511: | | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | | 3 |
| - N | (A) LENGTH: 217 base pairs (B) TYPE: nucleic acid | | |
| | (C) STRANDEDNESS: double | | |
| e | (D) TOPOLOGY: linear | | |
| 25 | | * 7 | |
| | (xi) SEQUENCE DESCRIPTION: SEO ID NO: 1511: | | |
| | | | |
| 30 | ATAGGCGTTT ACCAGTTATT TTCGAATCCA TATAATTATG TTTGTCCGTT TGGTTTAATC | 3 | 60 |
| | CAATTAATTG ATTAAGTTTT TCCAATTCCT TTTTTTTTAA TTAAAATTCC AATCCTTAA | A | 120 |
| | AAAAATTGGA AAAAAGCCTT AAAAAAAATT GGTTAATTTT CCCAAGGGAA TTAAAAATT | r | 180 |
| 35 | TGGGGTTTTT TnAGGnCCCT TTTGGGAAAA ACCCAAC | • | 217 |
| | (2) INFORMATION FOR SEQ ID NO: 1512: | · | • |
| | (i) SEQUENCE CHARACTERISTICS: | | |
| 40 | (A) LENGTH: 101 base pairs (B) TYPE: nucleic acid | | |
| | (C) STRANDEDNESS: double | | 1 |
| | (D) TOPOLOGY: linear | • | 1 |
| | | | |
| 45 | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1512: | | |
| | TGACATTGCA TCGGATTATG TTACATCANG GACAACGGGC CTCAAAAAGC GGTGCACAAA | ¥ | 60 |
| 50 | CGTTCCGTAA TCATATGCCA GTGCAATCGG ATGTAAAGAG A | | . 101 |
| , | (2) INFORMATION FOR SEQ ID NO: 1513: | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 114 base pairs | • | |

(C) STRANDEDNESS: double

| | (D) TOPOLOGY: linear | |
|-------------|---|-----|
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1513: | |
| | GATTTTATTG AAATGATTTT ACCTGTGATC AATTATTGTA ACAAATCTAC AATAAAATTG | 60 |
| 10 | TCTTACTGCA TGACCTAATA ANATAGCAAC AGATATCATA CACACTTGTA ATTT | 114 |
| | (2) INFORMATION FOR SEQ ID NO: 1514: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 77 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1514: | |
| | ACATATACAG GTACGTGTTT AGTCCGTCGT ATACTGCAAA ATTATGTCCG ATGAAATTAG | 60 |
| 25 | GGGAAAATTG TAGAACG | 77 |
| | (2) INFORMATION FOR SEQ ID NO: 1515: | • |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · |
| | | |
| <i>35</i> . | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1515: | |
| | CCTTATAAAG TTAATGCAAG CAACATGGAC AAATTATTAN TTGAATAAAC TGCAAGAAAG | 60 |
| | ACAACAATCA TTCTTCGGAA TGCTAGGAGA ATATATTTTA GA | 102 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1516: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 89 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1516: | |
| | CAATTITAAA TAGGATTITI AAGACCITGG TTGGGTTTTG GTACAATTAA TGGGGACATG | 60 |
| | ACTAGGTCTT GCCACGTTTA TATGCATCT | 89 |
| <i>5</i> 5 | | |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-------------|---|-----|
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1517: | |
| - • | GTAAGAGTGC ATAGTTTTTA AATGTTGCTT GTCTGGTnTC ATTTTGGCAC CATACAGTTC | 60 |
| | GTACCTGGAT TAGGGAAATG CCAAATGTCC GCGTAGTGAT AT | 102 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1518: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 448 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1518: | • |
| 23 | GAGAACTCCT TACCACAATC AAAAGTAATT GATTTAAATA TATGAGAAGA TAAAATGAAA | 60 |
| | AGGTGCAAGC AGTATTAAGA ATTTAGGTAG CAAGAAAACA AGAAGTGGTA CATACGATGC | 120 |
| 30 . | TAACCTAAAA AGAATTGGAG ATTAAAATGA TTATTAACCT TGAAACACAA CAAATACATT | 180 |
| | TIGATITAGA ACATGAAATT CCCTATTTC AAGCACCTGA GAAAAATAGG ATACGCTTAG | 240 |
| | ATATTGATGT TCTCAATAAA AAGCNAATTT CTAATATTAT TAATGTTATA TTTAATAACC | 300 |
| <i>35</i> ' | AATCAAAGAC GAAATGTACA TTTTTGTCTG AATACTTATA TCCTGTTAAA TTTAGAGAAA | 360 |
| | AAACAAGAAT TGGTCGTTTT TTTAATATTA CTAACTGGTA CGAAGAAATC CATTCTACCG | 420 |
| | ATGAGAAGTA TGThATTGCA ACTATTAA | 448 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1519: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1519: | |
| 50 | ATGGACGAAA GAAGATGTCA TTGCTTTTGA AAACCTAACA AATATTAAAG TAAATTTAAA | 60 |
| | AGGTAGCGGT TTTGTGTCCC ACCAATCAAT TAGTAAGGGA CAAAAACTTA CTGAAAAAGA | 120 |

| | ATTCAAATTC AGATGGTmAA GAAGAAATCT GACAGTTAAA ACTGACAGGG ATAAGTCGGG | 240 |
|------|---|-----|
| | ACTHAACAGG AATGGGCTAC HTTTAAATTT AGGGATGGTA TTGGGCCACT ATTTGGTTTT | 300 |
| 5 | TGAC | 304 |
| | (2) INFORMATION FOR SEQ ID NO: 1520: | |
| 10 . | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 322 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1520: | |
| | ATGACGTCGC ATGCACGCGT ACGTAAGCTT GGATCCTCTA GAGCGGCCGC CCTTTTTTTT | 60 |
| 20 | TTTTTTTTT TTTCTGTTGG CCTTTGATAA TTTTATTGGA TCAGTAACAA CTTTTTGTGT | 120 |
| | TTCAACTAAG ATAGCTAAAA TTCTAACACT TATATGTAAA AATTACACTC CATTTTAGCA | 180 |
| | CAAATGTTAA CAGAAATTAA CAGCACAGTG CCATGAAGAA ATGAHAAATA CACAGCTTTG | 240 |
| 25 | GTAGGGNAAT GGTCCTGGAA ATAATGTAAT GCCAAGTNTC TGATCATTTA ACATATCACT | 300 |
| | CACCTCCTTC TTCATCTGAT GT | 322 |
| | (2) INFORMATION FOR SEQ ID NO: 1521: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | . · · · | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1521: | |
| 40 | TAAATACAAA CCCTTTAAAC ATATTTACTA AGTCGTTCAA TTGTTGATTT GATAAnTGAT | 60 |
| | GTGATGTGGT ATTTTGCATC GGTCCTGCTT GATTCCAGAC ATGTC | 105 |
| | (2) INFORMATION FOR SEQ ID NO: 1522: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1522: | |

| | GATCGTATTT CCCAGATGTA AATTCNGTGG ACAATTGGCG TCAAATAGCT TCTAGTGG | 118 |
|----|---|------|
| | (2) INFORMATION FOR SEQ ID NO: 1523: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 base pairs | |
| - | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 10 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1523: | |
| 15 | CNGCATATAA TCCCGCGACA TGTCTTTTAC GGGTGCACTT GTAATATTAT TACCCCCCGT | 60 |
| | ATAACCCATG TATATCTATA CTTTACCACA TAAAATAATT CCGGGACTAT TTGGCACATG | 120 |
| | TTTTGGGTGA ATTTCTTTAG TGGCACACCA CCCCTGG | 157 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1524: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 82 base pairs | |
| 25 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (b) 101030011 1111041 | |
| -1 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1524: | |
| 30 | ACTGAGGTAG GTTATGTAGG ACGAGATGTT GAAAGTATGG TTAGACATCT TGTTGATCCT | 60 |
| | TGAGTAAGAT TAGTCAAGGC CG | 82 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1525: | |
| • | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid | |
| 40 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1525: | |
| 45 | GATACAAAAA AGAAGTTCAA TITGAACTAT GAAGAAATTT ATATTTTAAA TCATATTTTA | - 60 |
| | AGAAGTGAGT CTAACGNAAT CTCATCTAAA GAGATTGCTA AGTGCTCAGA GTTCAAACCT | 120 |
| | TACTATTTAA CTAAAGCTTT ACAAAAGCTA AAAGATTTAA AATTGTTATC AAAGAAAAGA | 180 |
| 50 | AGTTTACAAG ACGAAAGAAC AGTTATTGTT TATGTTACAG ATACACAAAA AGCAAATATT | 240 |
| | CAAAAACTGA TTTCAGAATT AGAAGAATAC ATTAAAAATT AAATCAAGGT TAATTGCGTT | 300 |
| | | |

| | AAAATTAACT TAAAATTTAA ATATTGAAGA GCTTAATTAA | 400 |
|----|---|-------|
| 5 | (2) INFORMATION FOR SEQ ID NO: 1526: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 base pairs (B) TYPE: nucleic acid | |
| 10 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1526: | |
| 15 | ACTGTCTAAT ATTCACTCCC TTAAAGTGTT TTTCATATTT TTCTATTAAT GTTCATATTG | 60 |
| | TAGGGTGTTG AATGCATCTA AGCATTNCAA GTTATTCTCC AAGTTCATCA ATTTCAAAAT | 120 |
| | GGAAC | 125 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1527: | |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 112 base pairs(B) TYPE: nucleic acid | |
| 25 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1527: | |
| 30 | CATGITTATT TATGITTCGG CTTTAATGIT GAAGAGITTT ACAAAGITTA CCGATTGCAT | 60 |
| | TITATAATTT TAATGCATTA TTGGAGCATT GGCTATCATC TATTACTGCG na | 112 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1528: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 115 base pairs (B) TYPE: nucleic acid | |
| 40 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1528: | |
| 45 | GCGAAGATGA GGATGAGATG ACTAAAGGAA AATATTGAAA AACAACCAAA AAACTGATGA | 60 |
| | ACATTATTAA AAATTTACAA AATCAAATCG ACAACTTGAG CGCAAGAACn AACAG | - 115 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1529: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (C) SIRMIDEDINESS. COUNTE | |

| • | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1529: | |
|----|---|------|
| 5 | ATGGATCTTC CGCTTCTCTT AATTGATCAA TTAAATCAGA CATTTCATGT TTTTGTAAAT | - 60 |
| | AATGATTCGC TTTAATGGAT TTTTTACATG ACATCATGAT TGCTACATCT TCACGTAATT | 120 |
| | TTTTGATATC TACTTTTTC TCTTCCAAAA TTAGCTCAAT CATATCTTTA ATAATTTCTT | 180 |
| 10 | CTACTTCATC TTTAGGGAAC CAAACTGGAT AGCTACTTAC AATATAATCA TGACCACCAA | 240 |
| | AATGTTCTAA CATGATACCT ACTTGTTGAA GCTCATTTTT ATATTGATCA ATGACTAATT | 300 |
| 15 | GTTCATCTTT TGAAAAATGA AATGTTAACG GGATTAATAA ATCTTGTACT TCATTGGTAA | 360 |
| | CCTCACCTAT TTNATCTCGA AAATATTCAT ATNTTATNCT | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1530: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 97 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1530: | |
| | TAACAGTCAA CCCACCCATT AATATATATT CAACGGCTGA CTGATACGAC GAACGTCAAA | 60 |
| 30 | GAATATGAGA GGAATAGGGA CAAGATCATC ACACATA | 97 |
| | (2) INFORMATION FOR SEQ ID NO: 1531: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . * |
| 40 | | |
| ÷ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1531: | |
| | TCATAACGGT GCAACTTAGA GCTGACGTAT AGTTCATTCC AACTATATAC GATGTATCAA | 60 |
| 45 | CACCATGTTC CAGTTTTAGG TTAACGATAC TGTATACCGT ATTATGTCAG nGGCACCTTA | 120 |
| | TCTTCACGTA CTTTACGGCG AGATGATGAC | 150 |
| | (2) INFORMATION FOR SEQ ID NO: 1532: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 138 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1532: | |
|----|---|-------|
| 5 | ATTCATTCTG CTAACCAGTA AGGCAACCCC GCCAGCCTAG CCGGGTCCTC AACGACAGGA | 60 |
| | GCACGATCAT GCGCACCCGT GGCCAGGACC CAACGCTGCC CGTCCTATCC TGAAGCCAAA | 120 |
| | GGAAATGAGA TCGGAATT | 138 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1533: | • |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 460 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1533: | |
| | GGGGnCCnGG CAATGGAGGC GTGCTTGGAT GGTGCTTGGA ATCATCCCTT TGGCCTCGAT | 60 |
| | CATAAGCTTA ÄACTTTTGGT GCTGGNGCCA CTGGAGGGAA ATCTTCAATT CTGGCAAATG | 120 |
| 25 | GTAATTHCCT ATACCAACAT TTAAGGCATG TGGTAATGCT GGCTACTCCC GCTTCGTTAT | 180 |
| | CAGCTACATG ACAAATACAG ATGCCATCAC CTTTGCGTCC ATTTTAATCG TTGATGCTTG | 240 |
| | GAAATGTTTT TTGTAAATAT CAATGTTATC CTTCGCTGTA TGTATCGCAT TTATATCTGG | 300 |
| 30 | TAGCAAAAAT GTTCCAACAG AAAGCCCTAT ACCTAGTTCG GCAGCTATTT TGGCAGATGT | . 360 |
| | TGCGCTACTA CTTAATAACC ACATTTCTGG AAAATGATCA TGTGTGGTGC ACTACGATCG | 420 |
| 35 | ACTTGGTTAT CTTTATTGTT AGATAATACG GAATACGNAA | 460 |
| | (2) INFORMATION FOR SEQ ID NO: 1534: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1534: | |
| | | _0 |
| | TACGCTAATA AATAGTTCAC TTTTCCATTT TGTGTAGTCA GCTCATTGTA TTCTTCAATT | 60 |
| 50 | TGCTCTTCAT TTAATGCCGC ATAAGCTTGA TCAATAATAT TTGGATTAAG TTGTCCAATA | 120 |
| - | TACTCTAACT GGTCATGATA AACAn | 145 |
| | (2) INFORMATION FOR SEQ ID NO: 1535: | |

| 5 | (A) LENGTH: 151 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1535: | |
| 10 | ACGCGATTTA ATCGTTCGTT CCAACGATGT CCACTCCCCT ACTAATAATT AAAATCATTA | 60 |
| | CAAATTATTT CAAACTTTAC AATTMAAACT AACAGTTTTC TCAATAAAAT GCAAGCTTTT | 120 |
| | CTCATTTGTT ATTTAGAATG ATTATGATTT A | 151 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1536: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 86 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1536: | |
| 20 | ATAATAGAAT CATTACAAAT TATTTCAGAC TTTACAATTA AGACTAACAG TTTTCTCAAT | 60 |
| | AAAATGCAAG CTTTTCTCAT TGTTAA | 86 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1537: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1537: | rui |
| 40 | ACCAAACTGT AAAGCCATAT ACTGAACATA TTGATAGCAT ACTCAATGAG ATCAAATTAC | 60 |
| | ATCGTGAATT TATTATAGAA GTACCTTATA TGAATTCAAG GAAATTTGAG CTACTGATTG | 120 |
| 45 | CTAACATTGA ACAACTTTCT GTCGAATGTC ATTTTAAGCG AACAAGTCGA AAGTTATTTA | 180 |
| | TAGAAAAGCT TAAAAGTGTT CAATATGATT TACAAAATAT ATTAGATGGC GTAACAChAG | 240 |
| | AGGGTACTGA TGGTTAAAAC AGTTTATGTA ACAGGTTACA AATCATTCGA ATTAAACATT | 300 |
| 50 | TTTAAAGATG ACGCACCTGA AGTACATTAT TTAAAACAAT TTATAAAACA TAAAATTGAA | 360 |
| | CAACTGTnGG ATGAAGGATT AGAATGGGNG TTAATACAAG | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1538: | |

| 5 | (A) LENGTH: 136 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | ٠ |
|------|--|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1538: | |
| 10 | ATATCGTTAC TGCTGTATGT TTCAATATCT ATATTCATAA ATTTCAAATh CTGACACCTC | 60 |
| | AATTTCTTTA AAATAAGGGG CAGAACCCAC TATGACTATA GGATCTCTCA CAGGTCAATT | 120 |
| | CGCAAATCAC TCGTGC | 136 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1539: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 85 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1539: | |
| | TAAATATCTC GGCACAATGA TGCGGGATAT TTTTTTACAA TAGGCATAAA GGCTGGAAAA | 60 |
| | AACATATCTA GTGCTATGAT ACTTA | 85 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1540: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1540: | |
| 40 . | ACAATTTGTT TATTTCAACA AATTATCTTT ATTCCACGAT GTGCACAAGT GGTTGAAATC | 60 |
| | AGCTGAAGAC ACG | 73 |
| | (2) INFORMATION FOR SEQ ID NO: 1541: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • . |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1541: | • |
| | | |

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| | TGCAGGAATT CGATATCAAG CTTATCGATA CCGTCGACCT CGAGGA | . 106 |
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| | (2) INFORMATION FOR SEQ ID NO: 1542: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1542: | No (a.) |
| | ACATCAACTC ACCCATAATA TATATTCACG GCTGACTGAT ACGACGAACG TCAAAGAATA | 60 |
| 15 | TGAGAGGAAT AGGGACAAGA TCATCAC | 87 |
| | (2) INFORMATION FOR SEQ ID NO: 1543: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic-acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | 13 |
| + * | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1543: | |
| | GCTTATTCTG AAAAATATTT AAATTGAAGA AAAGAATATT CTAACTACGG AAGTGGTATT | 60 |
| 30 | AACTAATAAC TAGTATCCTT TATAAATAAA CATAAAAATA TTCAAACGAA GGTCTACTAA | 120 |
| | ATAACTATCC ATAAAGTGAG TATAAGTTTG TTTGTAAAAC TGAAGTAAAA AGCATAAGGA | 180 |
| | ATTACACTTT AAATACATAT AGTACTTACG AATAGAAAAT AATCCCTTCA ACAGTAATTT | 240 |
| 35 | TTAAACAAAA ATAAGTGTTG TITTATGTTG ACTCTACTAG AATAACTTGA TATTATATAA | 300 |
| | AAGTCGTCAA ACGGCACTAA TATTTANNAA ACAAATGTTT TAAGTTGTTG GATTTNAAAA | 360 |
| | TATTGAATTA AAGTGTAAAT TTGGACTATT GGAAATTGCG | 400 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1544: | * |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 103 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1544: | |
| | ATAACGCTAA TCAGCCACAT TCAGTATTGT TAAATGGACA CACAAGCAGT TGATGAAAAT | 60 |

(2) INFORMATION FOR SEQ ID NO: 1545:

a.

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| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| 10 | (add) energy on programmer, and to No. 1545. | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1545: | |
| | GGCTGTTATT GTTGTGGAGT TAAAAATGAA GGAAAATTAT AAACATGGTA AGCGTGTTTC | 60 |
| 15 | TCGTATTACT TTACTTAAAC NAACGGTATA ACCATACCTA ACTTAGTA | 108 |
| | (2) INFORMATION FOR SEQ ID NO: 1546: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 554 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1546: | |
| | AANTATGTTT CATATATTAT GAATCTAGCC TTAATCATAT TGCATTCAAA ATAATTTTAA | 60 |
| 30 | AAAATGAAAA GAAAGGATTT AGCATGCAAA AATTCAAAGA CTTTTTTTAC GATGATTTAT | 120 |
| | CGGTTACACG AGGAAATTAT TTTTTAACTT TAATGGCAGC ATTTTTTATT ACTATCATTT | 180 |
| | TATTTATCGG CATAGTTGTC AGTGAAGTAC ATTTACTTTA TAGCATGCTA ATTGTATTAG | 240 |
| 35 | TAGGTTTAAT TCTATTGAGG CTATTCAAAA TCAATTTATT CTCTTTTAAA AAATTAACAT | 300 |
| | TGTCTCAAGT TATTTATATT ATAGGCGGTG CACTATTAAT TTATGGGTTA GATAATCTTT | 360 |
| | ATTTATATTT TCATGACGTA CCGGCAATGA ACAACAATTA GAGCAAGCAA TACGGAAATA | 420 |
| 40 | CACCATTCTA TATTTCTATT TECACTGTAC CATCATCCCC GCTATTGTGG AAGAAATTGT | 480 |
| | TTTLCGCGGT ATGATAATAA GGGKTATCTT CAGAAAACAC TTGTTTTTAG GGTTAATTGT | 540 |
| 45 | GTCTAGTTTA GTTT | 554 |
| | (2) INFORMATION FOR SEQ ID NO: 1547: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | , |

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| . * | TAAAGCAACA CTTTTAATCC CTTTTGAACT TAGTTTATCC GCTAAATCAT AAGCTTCTTT | 60 |
|-----|---|-------------|
| * | TTTGCTACTT ACAAAAATCA ATCCTTGTAA AATTTCACCT GAATATCCAT AGTAATCTGT | 120 |
| 5 | CTTTTGAATA ATATAATTAA CTCTTTCATC AGAAGTTAAA TATCTCAGTT TAGTTACATC | 180 |
| | ATCTTCTTTA ATACCTTGAT GTACATAATC AGTCACACCA AAATAATGAA ATGGGACATA | 240 |
| | AAATATCACT TTCTAATGCT GCTTGTAACC TTATTTCATA TGCAATATTA TAATCAAACA | 300 |
| 10 | GTTCAAATAT ACTTAATTCA TCTGGATCTT TCTGGTGGTA GGCAGGTCAT TCCCAGCANG | 360 |
| | AACTTAGGGT TTGGAGGTAG GTTAAAATAC TCGGTTGGAT | 400 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1548: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 20 | (D) TOPOLOGY: linear | · · · · · · |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1548: | |
| | CGCTCTAGAA CTAGTGGATC CCCCGGGCTG CAGGAATTCG GCACAGCATA TCTAGTATTT | 60 |
| | TAGGACGGAG GGA | 73 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1549: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1549: | |
| 40 | GTATCCAAGC AGCTTTTAAA CAATATGGCA TAAACATTAT TAACGGCTAT GGTTTAACTG | 60 |
| | ATGGCACCTC TTG | 73. |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1550: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1550: | |

| | GTAACATGTA TAGTGAAGTG ACTACTAAGA AGNCGTATTG TGATATTGAT AGCAGCTGAT | 120 |
|-----------|---|-------|
| _ | (2) INFORMATION FOR SEQ ID NO: 1551: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 192 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | o)(e |
| 10 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1551: | |
| 15 | GGTATGTATT AATTAAAATG TGGTCATGAT TGAAACAGCA ATGTAAAAAT AGCACAACAT | 60 |
| | AATTMATAAA GGAGAGAAAC GGCATGCATG AACAAGATTT TAGAATTTTA GAGGGTCAAG | 120 |
| | ATATTACTTT GCCAGAATTA GGTAGAGAAT TAGANAATAT TACAGGACAT ACGATTGCTG | 180 |
| 20 | ATTCTACTGG CG | 192 |
| | (2) INFORMATION FOR SEQ ID NO: 1552: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 76 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1552: | |
| | CTAAGTTAGA TGCTAGTATA CAAGATTTAC AACAAAAGGT ACTGGAATCG AATTGTGAAC | 60 |
| <i>35</i> | TAGACAAACT AAACTC | 76 |
| | (2) INFORMATION FOR SEQ ID NO: 1553: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 135 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | . 1 - |
| | (D) TOPOLOGY: linear | |
| 45 | | |
| 1 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1553: | |
| 50 | TGTGTTGGGG CCCCGTATAT TGAAAATTTG TTATAGGTGT ATTTCTTTGG TTAACTATTG | 60 |
| 30 | TTATATAACT TGTAGTTTTA GGATGTTGAT TTTGCTTACC TTGTCTGCTA TGTAATGTCA | 120 |
| | CATCAACATG ATTnA | 135 |
| 55 | (2) INFORMATION FOR SEQ ID NO: 1554: | |

| <i>5</i> | | (A) LENGTH: 104 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | * . | • |
|--------------|----|--|---------------|------------|-------------|------|
| | | | | | * | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ I | O NO: 1554: | | | |
| 10 | | TTTGANATCA AATTCACTTC GCAAACGTGT CCAA | CCTGA GCAAAC | GGCT AGA1 | GATTAA | 60 |
| · 20 · · · · | | TAGTTGCCCC ACTAACGGGA TCGCCCCAGT TATC | CAACTT ATCT | 20.8 | 00 I | 104 |
| | | (2) INFORMATION FOR SEQ ID NO: 1555: | | | | |
| . 15 | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | i e | | | |
| .20 | | (D) TOPOLOGI: Timear | | | | * |
| | | | - × | | . " | |
| | • | (xi) SEQUENCE DESCRIPTION: SEQ I | NO: 1555: | | | |
| 25 | | AATAAGAAAC AngaCACTAG CTCACCACGA CGCG | CACGGC CTGCGT | GTAA AAAT | GTTGGT | 60 |
| | | GGCGCGGGTT GGAGATCGTG TTCAACCAGA GCAG | AAAATA | i e | | 100 |
| | | (2) INFORMATION FOR SEQ ID NO: 1556: | | | | |
| 30 | , | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 86 base pairs(B) TYPE: nucleic acid | - | | * | |
| | | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | | |
| 35 | ; | * | | | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ I | NO: 1556: | ٠, | | |
| 40 | , | CAATGAAATT ATTTATTATT TTAAGTGCAT TAAA | CCCCGA TGATGO | CTGT CCG | TACCAG | 60 |
| 70 | | GTGCATTTTG GTGCCCATGG TTTACC | | | | 86 |
| | | (2) INFORMATION FOR SEQ ID NO: 1557: | | | | |
| 45 | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 78 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ý. | ** | • • | |
| 50 |). | | | | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ I | NO. 1557. | | | |
| | | | | 00000 220 | A TOTAL CO. | |
| 55 | 5 | GTCATGTTCC CATCAAAACT AATTTGTACT TACT | MANGGC TCAGCA | AGUGU AACA | WI TWOO | - 60 |

| | (2) INFORMATION FOR SEQ ID NO: 1558: | |
|----|--|----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 82 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1558: | |
| | AACTGGTTAC AGAAATACCA CGTTCTTGTT TCAACTTTCA TCCAGTCACT TGATCGCAAA | 60 |
| 15 | TTTACCAGTC TTCTTCCCTT TA | 82 |
| | (2) INFORMATION FOR SEQ ID NO: 1559: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 78 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1559: | |
| | CCACAGCGGC ACTATAGCCA GCCCCTAATA TATACAGTAT TTGCATCTGA CTCATTGGTT | 60 |
| 30 | CATAAGTATA TGCAGTGA | 78 |
| | (2) INFORMATION FOR SEQ ID NO: 1560: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 76 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1560: | |
| | ACCATTIGCT AACTITITAG CAGCGCAATG TICTTATTAA CIGCTTACGC CATCTATAAA | 60 |
| | AATAAACGTT CAACAA | 76 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1561: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 50 | (A) LENGTH: 200 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |

| | | | . 60 |
|-----|----|---|------|
| | | GGGTTTTCCT TGGGGGCCGG GGGTTAATTC CACCCGGGGT TAAAATTTTC CCAAAAATTA | 120 |
| | 5 | ATTITINGAAA AGTITIAATT TAAGGAAACC CATTINGTCCG GAATTITTAC CCCATCCTTA | 180 |
| | | TGGGGGGTCC CAAAGATTCC | 200 |
| 1 | 10 | (2) INFORMATION FOR SEQ ID NO: 1562: | |
| | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | • |
| 1 | 15 | (D) TOPOLOGY: linear | |
| | | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1562: | |
| | 20 | AACACAGAGA ATAACCAAGA GAAGACGTTT TCATCTGAAG AAAGTAACAG TAMGCCATTT | 60 |
| ** | | ATGGAAGAAA ATCAAAACGA TGAGATAGTT ATAAAAGAAG ATTCATATAA TCCATTCGTA | 120 |
| , | 25 | ACGAAAACAT CTGAAAGTTT AATAGCTGAT GATGAATCTT CTGGTTATAA TAATACACGT | 180 |
| _ | | GAAAAAGATG AAGACTACTT CAAAAAACAA CAAGAAATTT TACAAGAAAT GGATCAAACA | 240 |
| | | TTTGATTCAA ATGATGGTAC AACTGTGCAA AATTATGAGA ATAAAGCGTC TGATGATTAT | 300 |
| . 3 | 30 | TATGATGTAA ACGATATTAA AGGAACAAAA AGTAAAGACC CTAAACGAGG AATTCCATAT | 360 |
| | | ATGGAATTGT TGGnCAGTCA TGGAACGTTA TTATTGCTCA | 400 |
| | | (2) INFORMATION FOR SEQ ID NO: 1563: | |
| 3 | 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 454 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 4 | 10 | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1563: | |
| | | TCTTCATCAT CTTCTAATTT ACCAGCTGGA ATTTCTAGCA ATGGTTTTC TACTGGTTTA | 60 |
| . 4 | 15 | CGATACTGTT TCACTAATAC GACTTCTTTT TTAGGTGTCA CTGCACAAAC ArCAACTGCA | 120 |
| | | CCATTATGAT AAACTAATTC TCTTGTTGAC GTTTCACCGT TTGGTAATGT CACTGTATGA | 180 |
| 5 | 50 | ATTTCTACAT CTACAATTTT GCCATTATAA ATAACTGTTC GATCAATTGT TTTTTCATTT | 240 |
| | | AAATCCATTA TAATCACGTT CCTTTAAATT CATATTATAT ATTGATACAC TATGCTTGTT | 300 |
| | | AGCTAAAGTG TATCGAAAGG AGAACAGACA TGCAAAAAAA TATATTAAAA AGTGGTATTT | 360 |
| | | | |

| | AAATTATAGG ATTGTGCTGT TGAAAATGGG TATC | | • | 454 |
|------------|--|------------|---------------------------------------|---------|
| 5 . | (2) INFORMATION FOR SEQ ID NO: 1564: | | | |
| J | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 base pairs | | | |
| | (B) TYPE: nucleic acid | . : | | • • • • |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | |
| 10 | (b) lot disout. I flicat | | | |
| | * - () | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: | 1564: | | |
| 15 | ACATCTCGCA TCGTCACGAC TTGCTTGAAC CACTAGCAG | TCAAACAAAG | CTGTACAGGC | 60 |
| | AACATCTGC | | | 69 |
|)) | (2) INFORMATION FOR SEQ ID NO: 1565: | | * - | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | | · · · · · · · · · · · · · · · · · · · | |
| | (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid | 0 | | * |
| , | (C) STRANDEDNESS: double | | | |
| 25 | (D) TOPOLOGY: linear | | | • * ' |
| 25 | | | | |
| | (ALL) CHOUNNESS OPERATION CHO TO NO. | 1565 | | 1 * |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: | • | | |
| 30 | TCCAGAACCA TTTTAAATCC CGGGAAATAT AATTACCTCC | ACTAANGTAA | TATATCCAAG | 60 |
| | CCAAGACTAA TCCTCCTTAA GCCGGTTTAA GTAACCAGG | TGAGAAGGAT | TTTTTGG | 117 |
| * | (2) INFORMATION FOR SEQ ID NO: 1566: | | * | |
| 35 | (i) SEQUENCE CHARACTERISTICS: | | | |
| × | (A) LENGTH: 103 base pairs (B) TYPE: nucleic acid | | | |
| | <pre>(C) STRANDEDNESS: double (D) TOPOLOGY: linear</pre> | | | * |
| 40 | | | | |
| 16 | * | | * . 4 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: | 1566: | * | |
| 45 | TATTGAGATT AACAGTCTGG GAAAAATGAA CAGCAATTG | | GATGCTGATT | 60 |
| | ACTITITAAC AGTATCATTI AATAACTCAG AGATGCGCT | TAT | | 103 |
| | (2) INFORMATION FOR SEQ ID NO: 1567: | | * | |
| 50 | (i) SEQUENCE CHARACTERISTICS: | | | |
| | (A) LENGTH: 81 base pairs(B) TYPE: nucleic acid | | | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | |
| | | | * - | e . |

| | (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1567: | |
|----|---|-----|
| _ | AATGGATGGG ACAGCAATTA GTGCATAACG ACAATATATG CTCAATTTGT CGGCAACTGG | 60 |
| 5 | TTAAGAATCG TATTGTCACA A | 81 |
| | (2) INFORMATION FOR SEQ ID NO: 1568: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 80 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1568: | |
| | AATGGATTCA GTAGGTATTG GTGAAGCGCC AGACGCAGCT GATTTGAAAG ATGAAGGTTC | 60 |
| 20 | ACATACTTTT AGCATACCTT | 80 |
| * | (2) INFORMATION FOR SEQ ID NO: 1569: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 95 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1569: | |
| | TTTTTAAATA CGATTTTAAG GAGGCCATTA TAATGGCGAG TAAAAGTAGC GAATTAATGG | 60 |
| 35 | TTTTGGTTAG GAATTGGTCG TTTAGGCATT CAGGA | 95 |
| | (2) INFORMATION FOR SEQ ID NO: 1570: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1570: | , |
| | CCCAATAAAA AAAGCCTGTT GTCACAATGG TCATAGACAC GTACATACTT TAAAGGTTTC | 60 |
| 50 | TGTAATATAA ATATTTCATA TGCCACTTTA AAGTTGGNAC GTTCGTATGT TGTACTAA | 118 |
| | (2) INFORMATION FOR SEQ ID NO: 1571: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 base pairs | |

(C) STRANDEDNESS: double

| | (D) TOPOLOGY: linear | |
|-----|--|-------|
| | • | |
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1571: | |
| | GACTTGATCA ATGAAGCATT GTGTGACAAT TGGTCTGTTT GCACACCGCA CGGATTGnGC | 60 |
| 10 | GTCATTTATT TGTACTAATT CAAAAAACAT TGTTGTTTTC CTAG | 104 |
| | (0) TUROPUS TO THE TO THE TO THE TOTAL TOTAL TO THE TOTAL | |
| | (2) INFORMATION FOR SEQ ID NO: 1572: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 118 base pairs | |
| 15 | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | è |
| | | |
| | | 1.0 |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1572: | |
| | CCGAACTGTA ATGGTCCTAA TGTTTTACTC ATACCATATT GCGTAACCAT TGAGCGGCGA | 60 |
| | | |
| 25 | TTGTGTTGCA CGTCGAGCAT TGAGACCGTT GTACTCGTAA nGTATATCTC TGTACACG | 118 |
| | (2) INFORMATION FOR SEQ ID NO: 1573: | |
| | (a) apostore and appearance | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 74 base pairs | |
| 30 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | (b) Topologi: Tillear | |
| | | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1573: | 0 |
| | AGGGATCAAA GGTCCATCCC CCATGCATTG GATAGTGGGG GATGACTTTT GATCCTATGT | 60 |
| | TCCAGTTGCT TATT | . 74 |
| 40 | | , , , |
| ••• | (2) INFORMATION FOR SEQ ID NO: 1574: | |
| | : | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 341 base pairs | |
| | (B) TYPE: nucleic acid | |
| 45 | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1574: | |
| | | |
| | AACCTTTTGA GTAAATTCAC CAATACTCAT CCCCTTATCA TTTAACAAAC TTTTATTAAT | 60 |
| | GTTTTTGGTT ATATTATGAG TCTTTACTGC TTTTAGATTG TAAAAATTAT CGTCATAAAT | - 120 |
| 55 | | |

| | GIAATTAATG TAATAATAGA AAAGTGTATA TATCTCATAT CGCCACCTGC TATACAACTT | 240 |
|----|--|-----|
| | ATTANATAAT TAATTCCAAG ACATATTAAT TATCTAATTA TAACCTTAGT THACGTTATT | 300 |
| 5 | ACATAATATA AAAATATATA ATAACTTATC Cnccggcncc T | 341 |
| | (2) INFORMATION FOR SEQ ID NO: 1575: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1575: | |
| ٠ | ACGTGTACCA ACTTTTGGGC ACCATTGATA ATANGTGTCA TAGGGTGACT CAGCATAACG | 60 |
| 20 | GGCAAGCCTA TTAATGATAG CCAGATTAAG ACATACAGTA CATATGTTC | 109 |
| | (2) INFORMATION FOR SEQ ID NO: 1576: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 79 base pairs | |
| 25 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1576: | |
| | GCTAGATTGC GGGAATTAAC AATCATCAGC GATTTAATAT TTGCACTGGA GACGTCATGG | 60 |
| 05 | TAATAAAAA TTGATGAGA | 79 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1577: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 40 | (A) LENGTH: 69 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1577: | |
| | ATGATGGCTA TCATGAGATT GAGATGATAA TGACAACAGT TGATTTGAAA TGATCGTGTA | 60 |
| | ACTITICAT | 69 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1578: | - |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1578: | |
| | AAATTGTCAC THCAGGTCAT AACCAACCAG GTGGGACTGC ACGAGCGTTA CTAATGATCC | 60 |
| 10 | AACGGTCTTG CTTTGTGATG AGGCAACAAG TGCACTTGAT CCGC | 104 |
| | (2) INFORMATION FOR SEQ ID NO: 1579: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 89 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | ٠ |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1579: | |
| | GCTCAATAGA TACAACTATT AGGACAACGG ACTATCGTTT ACAATTTATT CCAGATAAGG | 60 |
| 25 | ATCGCGCAGG TCGTATGCGT AACTATGCA | 89 |
| | (2) INFORMATION FOR SEQ ID NO: 1580: | • |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1580: | |
| | TTGTCTCTAA TAATGGnTTT GGCTTTTTCT AAAATTTCAG ATGTGGGTGC TGGTGAAGCA | 60 |
| | CCGACTGGTT AATTITCTTG TCGTCACGGC CACTTTTTGT TT | 102 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1581: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1581: | |
| | AAGGTGCTGT TATTAGGATA ATGNATTTAA ACCCCATGGT ATGAAGGATA TCTGGAAGTT | 60 |
| | AGATTGGATA TCCCTTAACC ATGGGGGGTT TTATTTTTGG GG | 102 |
| 55 | | |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|---|------|
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1582: | |
| THE TODAY | TTCAGGGGAG CTGAACATAT TGACGACTTT TGGGTCAATT CATTTTGCAT TTTACTTTTA | 60 |
| | AATGCGTTGT TGCATGTAAT TGTATTAACG ACATACATGG TGGGGCTCTA AATNAATGCT | 120 |
| 15 | TGACTAATTT CTTGGATGGA GACCACGATT TACCAACTCA | 160 |
| | (2) INFORMATION FOR SEQ ID NO: 1583: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 348 base pairs (B) TYPE: nucleic acid | - |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1583: | |
| • | TAAAAGCAAG TACATTAGAG GTTAGATCAC AAGCTACTCA AGACTTGAGT GAATATTATA | 60 |
| 30 | ATAGACCGTT CTTTGAGTAT ACAAATCAGT CAGGATATAA AGAGGAAGGA AAAGTGACGT | 120 |
| | TTACTCCTAA TTATCAACTT ATAGATGTAA CTTTAACTGG GAATGAAAAG CAAAATTTTG | 18,0 |
| | GTGAAGATAT TTCTAATGTA GATATATTTG TTGTAAGAGA AAATTCTGAT AGATCTGGTA | 240 |
| 35 | ATACAGCTTC AATTGGTGGT ATTACTAAAA CAAACGGTTC AAATTATATT GATAAAGTAA | 300 |
| | AAGATGTAAA TTTAATAATT ACTAAAAACA TCGATAGTGT TACATCAA | 348 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1584: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 45 | (D) TOPOLOGY: linear | |
| • () | | |
| ٠. | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1584: | |
| 50 | AGCCAGCAGT AGATAGATAT ATTAATGAAT TCTTGGAGAA AGGTAGCTCA AATTGTCCAA | 60 |
| • | TTGAGATATT GAA | 73 |
| | (2) THEORYAMION DOD GEO TO NO | |

(A) LENGTH: 255 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1585: | |
|------------|---|-----|
| 10 | GTAAGGAATG GTCACGTATT CCACACTTCT ATATGAATTA TTATGTATAT CAATACGCAA | 60 |
| | mTGGTTACAG TGCAGCTCAA AGCTTAAGTC ATCAAATTTT AnCAGAAGGT AAGCCAGCAG | 120 |
| | TAGATMGATA TATTAATGAA TTCTTGAAAA AAGGTAGCTC AAATTATCCA ATTGAGATAT | 180 |
| 15 | TAAAAAATGC TGGTGTAGAT ATGACAACAC CTGAACCAAT TGAACAAGCT TGTGAAGTTT | 240 |
| | TTGAACAAAA ATTGA | 255 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1586: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ı |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1586: | |
| 30 | TTATTAGGTG ANTCCATTGG CAACATTGAT TGGTTTGTCA TTAGGACAAA TTTTATTATA | 60 |
| | CATTGGCGTT ATTTTTACTA TCTTATCTGG TATTGAATAC TTTTATAAAG GTAGAGATGT | 120 |
| | TTTTAAACAA AAATAAATAT TTGTTTATAC TAGATTTCAT TTTCATATGG AATCTAGTTT | 180 |
| 35 | TTTTAATCCC AATTTTAGAA ATTAGCCACG CAATTGTTTA TAATGATATA TTGTAAAACA | 240 |
| | ATATTTGTTC ATTTTTTAG GGAAAATCTG TAGTAGCATC TGATACATTG AATCTAAAAT | 300 |
| 40 | TGATGTGAAT TTTTAAATGA AATACATGAA AAAATGAATT AAACGATACA AGGGGGATAT | 360 |
| | AAATGTCAAT TGCCATTATT GCTGTAGGCT CAGAACTATT | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1587: | |
| 45 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 561 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1587: | |
| | CAAAGCGTCT ATTATTGTTT GATTTTGATG AAACATATTT TAAACATAAT ACAAATGAAG | 60 |
| 5 <i>5</i> | | |

| | AAGTGATCAC TGCTGTATTG ACAGGAAGTA CATTTCAA | AG TGTCATGGAT | AAAATGGATC | 180 |
|-----------|---|---------------------------------------|------------|----------|
| | AAGTTAATAT GACGTTTAAA CCATTACATA TCTTTTCT | GA TTTGAGTTCT | AAAATGTTCA | 240 |
| | CTTGGAATAA TGGCGAATAT GTTGAATCAG AAACATAT | AA AAAGAAAGTO | TTGAGCGAAC | 300 |
| | CATTTTATT TGAAGATATT GAAGATATAT TACGTCAT | AT TTCTGCGCAA | TATAATGTCG | 360 |
| 10 | AATTTATTCC ACAAAGAGCA TTTGAAGGTA ATGAAACA | CA TTATAATTTI | TATTTTCATT | 420 |
| | CAACAGGTAA TCACAACAAT GATAGTCGTA TCCTAGAA | GC ACTINITCAGA | TACGCAAATG | 480 |
| | ACCAAAACTA TACAGCGAGA TTTAGTCGAA GCAATCCA | TT AGCTGGTGAT | CCTGAAAATG | 540 |
| 15 | CGTATGATAT TGACTTCACA C | | - | 561 |
| | (2) INFORMATION FOR SEQ ID NO: 1588: | | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 79 base pairs | * . * | t . | |
| 20 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | | |
| | (D) TOPOLOGY: linear | · · · · · · · · · · · · · · · · · · · | * | |
| 25 | | ·() | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO | : 1588: |) | * |
| | CCAACAGTTT TATCATTATG GCAAGTTCTG TTAAACCTC | GC TGAGAGTTAT | TTTGCACTGA | 60 |
| | | | | |
| 30 | TTGCAAAACC AGAAATTGG | | * . | 79 |
| 30 | TTGCAAAACC AGAAATTGG (2) INFORMATION FOR SEQ ID NO: 1589: | | | 79 |
| 30 35 | (2) INFORMATION FOR SEQ ID NO: 1589: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid | | | 79 |
| , | (2) INFORMATION FOR SEQ ID NO: 1589: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs | | | 79 |
| , | (2) INFORMATION FOR SEQ ID NO: 1589: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | : 1589: | | 79 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1589: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | AGCTTTCAGA | 79 60 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1589: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO | | AGCTTTCAGA | |
| <i>35</i> | (2) INFORMATION FOR SEQ ID NO: 1589: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: GCAGATATGC AGCAATTTAT AGAGGACTAG TAAACGCAT | | AGCTTTCAGA | 60 |

| | TCATTITATG GTTGATCATA GGCGTCGTCT TTTTCCTTGG GGATTTTATC TTTAAATACA | 60 |
|-----------|---|-------|
| | CAGATTGGCG C | 71 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1591: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 78 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1591: | |
| | ATACAATACA ATTCACACCA TATATGGATA AAATGCAAGA TGCAATTACT GCAGTTGCAC | 60 |
| | AGTGCAAGTA GCAATACC | 78 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1592: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 168 base pairs (B) TYPE: nucleic acid | |
| 25 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * * * |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1592: | |
| | CCAATTAATT AAAAACCGGA AAACCAATTT TTTAAACCAA TTAAGTTAAA AATTTTTTAA | 60 |
| | AATTGGGCCC CAAACCTTGG AAAAAGGTTT AATTTTCCTT TCCCAATTTT CCCAAAATTT | 120 |
| 35 | TTAAACCCAA AAATTCCCGG TTTTGGGTTA AATTTCCCTn GGTTAAAT (2) INFORMATION FOR SEQ ID NO: 1593: | 168 |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| - | | • |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1593: | |
| | TGCTAGAAAG TATAGAACCT GGTTCAAACG CATGGTTTTA TGTCCCTTTT TAAACnGATG | 60 |
| 50 | TTTATTAAAA AAATATGGAA ATTGGCCACG TCCGCCAATT TCCTTAGAAA AGAACGT | 117 |
| | (2) INFORMATION FOR SEQ ID NO: 1594: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|---|------|
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1594: | |
| | AGACGAAGCC AAAAAGTTAT TCGCCAAATC TGAAATATTT TCAAAGACCT TAAAGGCGTA | 60 |
| 10 | AAATAC | . 66 |
| w | (2) INFORMATION FOR SEQ ID NO: 1595: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1595: | |
| | ATTTTATTTA GGCCAATAAC TGnCTACTTC TGAAATAAGT TGCTTTGCAT AGTCTGACGC | 60 |
| 25 | GGGATGTTTG GATAATATCT TCTGTGTTAT TGCATTGCAA | 100 |
| | (2) INFORMATION FOR SEQ ID NO: 1596: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · |
| 35 | | |
| - | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1596: | |
| | GACCAGACGG CCGTAAACCT GGATGAAACC GTCCATTAGA TTCTGAAGTT GGTATTTTAC | 60 |
| 40 | CTAGAACGCA TGG | 73 |
| | (2) INFORMATION FOR SEQ ID NO: 1597: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1597: | |
| | CTTTATAAAA TTGTCTTTGA CTAACAGGAT TTTCAACGCT ATTCACAAAC CATGGTTTAA | 60 |
| 55 | CATATT | 66 |
| | | |

(i) SEQUENCE CHARACTERISTICS:

| 5 | (A) LENGTH: 139 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|----|---|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1598: | |
| | TATGGCACCC TCTTTGATnT TGTGACCGTT TTTGGTAATT CACCATTATT GTACGAACCA | 60 |
| | TGGAATTCGC TGCCTTCCTT TAGGCAATAA CATAATTATA TTTATCCCCT TCTTGTCACT | 120 |
| 15 | AGAGGTGCTG ACAACACCA | 139 |
| | (2) INFORMATION FOR SEQ ID NO: 1599: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1599: | |
| | CTCCTCTGCA TGCACATCTT GTTGTAGCAA GGTTCACATG TAATTTATTA AATCGAAACT | 60 |
| 30 | CTATCCAACT ATGTTATAAA GTTCATTCTA AACAAATHAG T | 101 |
| | (2) INFORMATION FOR SEQ ID NO: 1600: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 172 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1600: | |
| | TTGTACCAAG GTTCACATGT AATTTATTAA AGCGAAACGC GTATCCAACT ATGTTATAAA | 60 |
| 45 | GTTCATTCGT AAACAAATAA GTATAAAAAT TCAATATTTT TATTACTAGA ATATGGTTAA | 120 |
| | ATACATTTAT TTCTTATAAN AATTTGATGT TTAAGATATT TTGCCAAATT GA | 172 |
| | (2) INFORMATION FOR SEQ ID NO: 1601: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 55 | (D) TOPOLOGI: Tinear | |

| | (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1601: | |
|----|---|------|
| 5 | TTGGCACTGG CCGTCGTTTT ACAACGTCGT GCACTGGGAA AACCAAAnCA CGACGTTGTA | 60 |
| | AAACGACGGC CAGTGCCAAG CTTGCATGCC TGCAGGTCGA CTCTAAGAAG GA | 112 |
| | (2) INFORMATION FOR SEQ ID NO: 1602: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 679 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1602: | |
| 20 | TGCAATGGTT AATCATCTCA TATAACAACA CATAATTTGT ATCCTTAGGA GGAAAACAAC | 60 |
| | ATGACAAAAC-ATTATTTAAA-CAGTAAGTAT-CAATCAGAAC-AACGTTCATC-AGCTATGAAA | 120- |
| | AAGATTACAA TGGGTACAGC ATCTATCATT TTAGGTTCCC TTGnATACAT AGGCGCAGAC | 180 |
| 25 | AGCCAACAAG TCAATGCGGC AACAGAAGCT ACGAACGCAA CTAATAATCA AAGCACACAA | 240 |
| | GTTTCTCAAG CAACATCACA ACCAATTAAT TTCCAAGTGC AAAAAGATGG gCTCTTCAGA | 300 |
| | GAAGTCACAC ATGGATGACT ATATGCAACA CCCTGGTAAA GTAATTAAAC MAAATAATAA | 360 |
| 30 | ATATTATTTC CAAACCGTGT TAAACAATGC ATCATTCTGG AAAGAATACA AATTTTACAA | 420 |
| | TGCAAACAAT CAAGAATTAG CAACAACTGT TGTTAACGAT AATAAAAAAG CGGATACTAG | 480 |
| 35 | AACAATCAAT GTTGCAGTTG AACCTGGATA TAAGAGCTTA ACTACTAAAG TACATATTGT | 540 |
| | CGTGCCACAA ATTAATTACA ATCATAGATA TACTACGCAT TTGGAATTTG AAAAAGCAAT | 600 |
| | TCCTACATTA GCTGACGCAG CAAAACCAAA CAATGTTAAA CCGGTTCAAC CAAAACCAGC | 660 |
| 40 | TCAACCTAAA ACACCTACT | 679 |
| | (2) INFORMATION FOR SEQ ID NO: 1603: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 85 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | • |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1603: | |
| | CATTTTAATT GATATAATTT AGACTTTAAC ATTTCATGCT GTTCACGGTT TTAATTTGAG | 60 |
| | ACGTCATTTG GTATAACAAC TATAC | 85 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 68 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
|-----------|--|---------------|------|
| | | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1604: | y. | |
| | ACTGGTGTGA ATAGCTCCAG CAATTTCTTT AACCGCGATC ATAATCAA | CG TCACCTTTTA | . 60 |
| | ATTTGCCA | • . | 68 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1605: | | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | | | 1 |
| <i>25</i> | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1605: | *** | |
| | TGGGGGGTnT TTTTGGGTTG GGTTAAAAA AGGGAATTGG CCCAAGGG | GG GAATTCCCTT | 60 |
| | AAAAAAACCC CCAACCCCCT TGGGAAATTA AAAATTGGGT TAACCGGG | Α . | 109 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1606: | | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1606: | | |
| | GCTTATATAC ATGTTCCATT ATAAAAGGAG TACGAACGAA AGTAACGC | AT GACGTTAATT | 60 |
| | TAAAAATATT GTAATAATTA TGGATTAAAT TTAAAACCAN GGGGTATT | CC AT | 112 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1607: | ÷ . | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | * | | |
| 55 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1607: | | |

| | GTTCAAGTTG GTAACCTAAC AACACGNAAT TAGTTTAAAC GTTTGG | 106 |
|----|--|----------|
| 5 | (2) INFORMATION FOR SEQ ID NO: 1608: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 83 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 10 | (D) TOPOLOGY: linear | * |
| | in the second of | . 4- 2 3 |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1608: | |
| 15 | CACACTGATA CCATAGGATT TATGATAGAT CAACAGCATG ACCAAATGTA TGACCTAAAT | · . 60 |
| | | , . |
| | TTAAAAATTT ACGTACACCT TGT | 83 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1609: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs | |
| | (B) TYPE: nucleic acid | |
| 25 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | (D) TOPOLOGI: Timear | 0 |
| | | |
| ÷ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1609: | |
| 30 | AAAAGAATAA AGTCACTGAA CAATGGTCTT TCACAATGAT GTTGCGTCAA TGCACAAGCG | 60 |
| | CATTATGTnT GTGACTTGGG CATTTTGGCT TATCAGCTGA ATATTATACG CATTTACATC | 120 |
| | CCAATTAACG TA | 132 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1610: | |
| | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs | |
| 40 | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1610: | |
| | TTTAATGCAT ACGCTTCTCG CTTAGCAATT TCTTTGCACG TCTAACAAGC ATTAACGCTC | 60 |
| 50 | TTANTACTAT AATCACAACA AAACCAGCGA AATATAACAT GCGTATA | 107 |
| | (2) INFORMATION FOR SEQ ID NO: 1611: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 84 base pairs (B) TYPE: nucleic acid | |
| 55 | (C) STRANDEDNESS: double | · . |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1611: | |
|----|---|-----|
| 5 | TTCGCACCTG GTATCGTTCA AACCACCAAT GATGGCCCGT CTCGCCGTGG CAACAGCCGA | 60 |
| | AGACCGCAGG TAAACCCTGA ACGC | 84 |
| | (2) INFORMATION FOR SEQ ID NO: 1612: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1612: | |
| 20 | ACTCACATGT ACGATAACAC CCTTCGTAAA TCCATCTTTG GTTTGCCAAG TTCGTCGTTG | 60 |
| | TARACTGTCT ATACTCGTTA AACCGCTACA TGTTTTCCTA AANCCTGTGC CTAAATGCTT | 120 |
| | TACTGAA | 127 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1613: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | ; | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1613: | |
| | CGTTCAACTT TTTCAATTTC TAACGGCGTT TTACTATCTT TATCTGTAAC TAATTCAACT | 60 |
| | CCAAACATTA AGCCTCGTCC TCTTACATCA CCAACATTTC GATGACGCTT CAGCGCATGT | 120 |
| 40 | AACTGTTTC | 129 |
| | (2) INFORMATION FOR SEQ ID NO: 1614: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 348 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1614: | |
| | nCAACTAGTG GATTTAAnAT AnACATAATT ATAAATGCAA ATGCTAATAG CTGAATACCC | 60 |

| | | GCACIAGGIG CATAATTTGT GTATTGAGCA AATAAAGCTA ATACAATGAT TGTAATTCCT | 180 |
|---|------------|--|-------|
| | | TTAATGACAA ATAAAGGTAA ATTTAATCGT TTTAAAGGTT GGTAAATTAA AAATACAATT | 240 |
| | 5 | GCAGCTATAT GCGAGCCACT AACTGCCAGC AAATGATATA TACCTATCTC TTTAACACGT | 300 |
| | | TCCTTAAATT GCTCATTAAC TTCTTTTACG TCACCAGTAA TCAATGCC | 348 |
| | 10 | (2) INFORMATION FOR SEQ ID NO: 1615: | 340 |
| • | 10 | (i) SEQUENCE CHARACTERISTICS: | |
| | | (A) LENGTH: 72 base pairs (B) TYPE: nucleic acid | |
| | 15 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1615: | |
| | · | GAGCTCCACC GCGGTGTCGC CCGCTCTAGA ACTACTGGAT CCCCCGGGCT GCAGGAATTC | 6.0 |
| | · | GGCACAGCAT AT | 72 |
| | 25 | (2) INFORMATION FOR SEQ ID NO: 1616: | |
| | | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs | • *** |
| | | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| • | 30 | (D) TOPOLOGY: linear | |
| | | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1616: | |
| | 35 | CATCACGTTA AATCATAACG CGTGACGTGC TTTTGCTATT TGTCTCTCGG TATCTCTATA | 60 |
| | | TCT | 63 |
| | | (2) INFORMATION FOR SEQ ID NO: 1617: | |
| | 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 113 base pairs | |
| | 45 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | 43 | | |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1617: | |
| | 50 | ATTGAATTCA AGGGTGGAAC TCATGAATTG GCTGGAAAAA GGTAGATTTA ACTGGATGGT | |
| | | TGNAGCCATA TATCGGTGCG TTTATTTATT TGGTATTTTA AAAATCAACC TCG | 60 |
| | | (2) INFORMATION FOR SEQ ID NO: 1618: | 113 |
| | <i>5</i> 5 | | |

| 5 | (A) LENGTH: 80 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|----|--|------|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1618: | |
| 10 | GTACAATAAA GTGGTAAACA ACATGCCAAT GGAAAAAGGG ATTAAAGGTG TTTATGTCAT | 6 |
| | TCTTAAAGAT AGTAACGGTA | . 80 |
| | (2) INFORMATION FOR SEQ ID NO: 1619: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 20 | (D) TOPOLOGY: linear | |
| | | |
| ٠ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1619: | |
| 25 | ATCTTATGTT TTTTTCCTAA AACTTCTGCT ACTTCATTTA TTTGATGTAT GGTAGATAAT | 60 |
| | TCTGTTTGGA TACTCATATC AACTTTTTCT ATCATATCTG AAATCTCTTT TnTGGCA | 117 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1620: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs | |
| 35 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1620: | |
| 40 | CGATAAACCC TTCGTAATCA ATCTTTGGTT TGCCAAGTTC GTCGTTGTAA CAGTCTATAT | 60 |
| | CGTTAAAAGC TACATGNTTT CCTAAGCCTG TGCCTAATGC TTTACTG | 107 |
| | (2) INFORMATION FOR SEQ ID NO: 1621: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1621: | |
| 55 | AATATCGTGT CTCTGTCCAG TGCTGTCCAA TCAATTTTGA TCCACCGATT GTCATACGTA | 60 |

| | 10K 55Q 1D KO: 1822: | |
|----------|--|------|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| ` | | |
| 10 | | |
| , , | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1622: | |
| | ACCATCTGAC ATCATCAATT ATGAATTAAT GATGATATTA AAAATAAATT TGAAACATTG | 6(|
| 15 | CCAATTGATA GTGCC | - 75 |
| | (2) INFORMATION FOR SEQ ID NO: 1623: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 78 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | , |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1623: TACCTGTGTA TCAGCTCTAT TAACAACCTA ACATATGTGA ATAATTTGCG ATCCTTGTTG | 60 |
| 30 | ATAATGCTGT AATTTGAC | 78 |
| | (2) INFORMATION FOR SEQ ID NO: 1624: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 95 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (D) TOPOLOGI: Tillear | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1624: | 8 |
| | GCAAGCTTTT GCGGCTTCTG ATGCACCATT AACTTCTGTA ATTAAACACA CAAAGTGAAA | 60 |
| 5 | CAGGTAGGTA ATGCAAAACT GCAACGGACA ATCGA | 95 |
| | (2) INFORMATION FOR SEQ ID NO: 1625: | |
| 0 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 76 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * |

| | ATTGCGATTA CACAGTAGTG AATGAGATAT TTGACATGAA AGCTCCTGCA GCTTCTAAAG | 60 |
|----|---|-----|
| | AAGAGTTAGC AGGTTT | 76 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1626: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 126 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1626: | |
| | AAAAGCTAAA AAAGATTATC AGGTGTATCA CAAACTCAAA TTCTCATTAC CATTTATCTC | 60 |
| | AGTGTGAACG TCTTAATTGA GAACTAATCT NAATTGAGAT ATTAGTCATA TAAGGATGGA | 120 |
| 20 | CAAGCA | 126 |
| | (2) INFORMATION FOR SEQ ID NO: 1627: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1627: | |
| | TGATACGATA GAACATAGTT CAGCACATTG TTTGTTGAAA TTGGATATTA CCGCCATTTT | 60 |
| 35 | TTCACAATAT CAATAATACC TGAACGTGTT GGTTnTTCCA CATTATGATT GTACAT | 116 |
| | (2) INFORMATION FOR SEQ ID NO: 1628: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 91 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1628: | |
| | ATTTTGTCCT ATCTTGAACA AATCCGATTT TTCTCAGACA CTGAATCCAA AGTATTCATG | 60 |
| 50 | TACCATAAAC CATCTGCATG TTGATTTATG C | 91 |
| | (2) INFORMATION FOR SEQ ID NO: 1629: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs | |
| 55 | | |

(C) STRANDEDNESS: double

| | (D) TOPOLOGY: linear | |
|-----------|---|-----|
| | | , |
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1629: | |
| | ACAGAAAGTC AAACAGTAAA AGCGGCAGAA TCAACTCAAG GTCAACACAA TTATAAATCG | 60 |
| 10 | TTAAAATACT ACTATAGCAA GCCAAGTATA GAGTTAAAAA ATCTTGATGG TTTGTATAGA | 120 |
| | CAGAAAGTGA CAGATAAAGG AGTATATGTT TGGAAGGATC GAAAAGATTA TTTTGTTGGC | 180 |
| | TTGCTTGGTA AAGATATTGA AAAATACCCT CAAGGTGAGC ATGATAAGCA AGATGCATTT | 240 |
| 15 | TTAGTCATCG AGGAGGAAAC TGTTAATGGA AGACAATATT CAATTGGTGG TTTAAGTAAG | 300 |
| | ACAAATAGTA AAGAATTTAG TAAAGAAGTC GATGTTAAAG TAACAAGAAA AATTGATGAA | 360 |
| | TCATCGGAAA AGTCTAAAGA TAGTAAATTT AAAATTACTA | 400 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1630: | : |
| - | (i) SEQUENCE CHARACTERISTICS: | |
| • | (A) LENGTH: 400 base pairs | |
| 25 | (B) TYPE: nucleic acid | |
| 2.5 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (b) Torobodi. Timear | |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1630: | * |
| . = | GCTTTCCTTT TCGAAATCTA TAAATCTAAT CCATTGAAGT AAACTAATTA TGATAATTAT | 60 |
| | TAATTCTATA ATTGTnGTTA TCTTTAAATA ATTTGGAAAC CTTTCATAAT CTAAACCAAA | 120 |
| 35 | AAAGAAAGTT AGACATGAAA AAAGTATCAT AAATAATGAT GCTAAACTTA AGGCTTGTGC | 180 |
| | ACCTGGCTTT CGAAGAATGT CTATATTTTC CTTAGTAGTC ATATTTACCT ATCTCCTATA | 240 |
| | CATTGATTTT GTAATAGCAT ATTAAGTATT TAAAGTTATA AGTACTTAGA TTCTTTTCGA | 300 |
| 40 | TTAAAAGTAT AAAAGCCTAA AATTATCTTT ATATTATTAT TTGATGACAA CTTTATGGTC | 360 |
| | TCTATTGTTT TTTACTTAAA CGCTAAAAAG CTANACAAAG | 400 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1631: | |
| +5 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 70 base pairs | |
| | (B) TYPE: nucleic acid | |
| 50 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| <i>50</i> | | |
| | • | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1631:

| | TCTAGAGCGA | 70 |
|------------|---|----|
| | (2) INFORMATION FOR SEQ ID NO: 1632: | |
| <i>5</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 62 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 10 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1632: | |
| 15 | CAACGAAGAT ATTCAAGTGT TCAGTCATTA TTTTTGACTG CTAATGAAAC TGATTCTTGT | 60 |
| | GG | 62 |
| | (2) INFORMATION FOR SEQ ID NO: 1633: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | (b) Torobosi. Illieat | |
| | (with applying programmer, one are to be accessed | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1633: | |
| 30 | CTAATGATTA GATTCAAACT AATAAAGACT ACAAAAACAA GTTGATAATG GTAAAGATAT | 60 |
| | TATCCAACTT GACATCTAAA G | 81 |
| | (2) INFORMATION FOR SEQ ID NO: 1634: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1634: | |
| | AATTTCACCT TTGTCTAGTA ATTTATTTGT GTAGTGTAAT CATTAATTGT TTTAATATCT | 60 |
| 4 5 | AGT | 63 |
| | (2) INFORMATION FOR SEQ ID NO: 1635: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 579 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1635: | |
|-----|---|-----|
| | ACCAACTAGC TAAATGCCAG CGCGGNATCC ATCTCANAAG TGCACAGCAA GACCGTCTTT | 60 |
| 5 | CCAACTITIG AACCATGCGG TICAAAATAT TAITCCGGTAT THAGCTACGG TITCCCGAAG | 120 |
| | TTATCCCAGT CTTATAGGTA GGTTATCCCC AGTGTTACTC ACCCGTCCGC CGCTAACATC | 180 |
| | cagagaagca agctictcgt ccgticgctc gactigcatg tattaggcac gccgccagcg | 240 |
| 10 | TTCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA | 300 |
| | TACTAAATAA TGTTTGTAAC TAATAGTTAC GTTTTTGGAA TTAACGTTGA CATATTGTCA | 360 |
| 15 | TTCAGTTITC AATGTTCATT AATGTTCAAT CTCTTTTATT CTACTTCATT TATTTCTTGA | 420 |
| | AGTCAATAAC TTTTTGAACG ATTACTTTAT TTATTCTATA TTGTTTTTAT AGTTATTTCA | 480 |
| | ATGGLAAGTn TTACACTTTT GABATTCTTC TTTAAAAACA ACTGCGTCGL TTTTGaCGCT | 540 |
| 20 | TTATCATATT ATCMACTTTG GGAATTTAAA GTCAATAAC | 579 |
| | (2) INFORMATION FOR SEQ ID NO: 1636: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| - 1 | (D) TOPOLOGY: linear | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEO ID NO: 1636: | |
| | TCGACATTAA GCAACGTTCT TCGCAAAAGG TAGCGAGCGA CACGAGTTAA CTTTGCACGT | 60 |
| 35 | TTCATTATT | 69 |
| | (2) INFORMATION FOR SEQ ID NO: 1637: | 0,5 |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | (vi) SPONENCE DESCRIPTION, SPO. ID NO. 1627. | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1637: CTGTGACTTC GTCGCGATGA CCTTCGCCGT TGTTCTCATG GTAAGCTTTA AGTATCGTCG | 60 |
| 50 | ATGCAGTCHG TTCGCCATGT GCGCCAGCAG ACTGGTTGTA ATGTCGCCTC GTCCGT | |
| | (2) INFORMATION FOR SEQ ID NO: 1638: | 116 |
| | | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|---|-----|
| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1638: | |
| | | |
| | ACAACATTTA GGTACTTTCA CGCATATCAC TACAGCTCAA CGTGATGATT TACCAAATCA | 60 |
| 10 | AATTTCACAA G | 71 |
| | (2) INFORMATION FOR SEQ ID NO: 1639: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1639: | |
| | GCGTGGCTTT GTGATTAACA TTGACAAGCA CGTGCAACAA CATATTCGAC GCGATAAAGC | 60 |
| 25 | GACATCTAAT ATT | 73 |
| | (2) INFORMATION FOR SEQ ID NO: 1640: | |
| <i>30</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • , |
| 25 | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1640: | |
| | CGCGATCATT TTCATTTCTA ATTAATCTTC CAAGTCCTTG TCTAAAACGT GTAACTGCAT | 60 |
| 40 | CAGGTAATAC ATATTCCTTG AAAGTTGAAG TGAATTCAGA ATCCATAAGC CAATATTTTG | 120 |
| | CATTATGCTT GTTCATAAAC GGTAACTTCG CTATCATCAC ACATTTAATA CCATTTGCTT | 180 |
| | GAAAATCAAA ACCTTCAAAA AATGTTGACG TACCAAGCAG TATGGCCTTA TCAAAATTAT | 240 |
| 45 | TAAACTGTTG TACTATTTTA TAATTTTGGT TCTGCTGTTG TGTTAATACA ACATAATCTT | 300 |
| | CAAATTCTGG CAATTCATTT AAGCATATCT TGTACCATAT GCATCATTTT ATAACTCGTA | 360 |
| | AATAAGACTA AACATTTTGA TGACGTTATA GTCGTATATn | 400 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1641: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 66 base pairs | |
| 55 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (AI) SEQUENCE DESCRIPTION: SEQ ID NO: 1641: | - |
|-----|--|-----|
| 5 | ATTGTTGTAC CATGTATACT AACAATTGTA ATGTCTCATT TCAGTAAACA AAAAGCGAAA | 60 |
| 3 | GACATT | 66 |
| * | (2) INFORMATION FOR SEQ ID NO: 1642: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1642: | |
| | ATTTCGTCGG GAATAAATTT TGCCATTACA TAGAAATATC TAATAGATAA CGAAAAAGTA | 60 |
| 20 | TCGTATGTAT TTTTAATATA GTGTAAAATA TTATATGTAA AATAAAATGT AGGTTTTTAG | |
| | TTAGAGGCAT TATAAGANAA TTTTGAGTAT AGGTTAGCTT TTAATTATGA ATCTTATTGA | 180 |
| 25 | AATTTGATTA ATAAAAATAT GATAGGGGAT TAAAATGAAA CTATTTTATA TCGTATTTCT | 240 |
| e e | TATTATTATA TGGCTGAATA TATTTTTAGG AAATGAAATC ATCCATACAC TGACTGTTTT | 300 |
| | AATAACAACA TTGTATATTG TTAATTCACG ANAGGGGATT AAAAATGACA GAGTTGAATA | 360 |
| 30 | ATATTATAAA CGCGCnTGCA ATCNTTGTTT GAGTCCGGAA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1643: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . ' |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1643: | • |
| | AACTAGAGGA GGACATCCTA ATGGAAGCAA AACCCGTTGC TAGAACAATA AGAATCGCAC | 60 |
| 45 | CTCGTA | 66 |
| | (2) INFORMATION FOR SEQ ID NO: 1644: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1644: | |
|----|--|----|
| | TATCAATTTC ATATGCGATT TGGCCTTGCA ATAATTAGGT CTCACCTTGC CATATCTTTA | 60 |
| 5 | CCTAAGCAAT ACTTG | 79 |
| | (2) INFORMATION FOR SEQ ID NO: 1645: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 70 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1645: | |
| | CATTCTCCTG CATCATAAAA ATCAACAATT GTATCATCAA AGTGTATCAA AATATTTTAA | 60 |
| 20 | TATCCCAATT | 70 |
| | (2) INFORMATION FOR SEQ ID NO: 1646: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1646: | |
| | AGTGACACTT TCGTTCCACC ACATCGTAAA GAAGTACTTC AAGCACGTGA AGATGACATC | 60 |
| 35 | AAAGAAAAAG TTG | 73 |
| | (2) INFORMATION FOR SEQ ID NO: 1647: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 4- | - | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1647: | |
| | CTGTGATTGG TGTTGTGATT GTCTTGCTTC CTGGTTGTCC TTCTTGTTTC GCTCGCTC | 60 |
| 50 | CGCCGGGTTG T | 71 |
| | (2) INFORMATION FOR SEQ ID NO: 1648: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs | |

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

| 5 | | |
|----|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1648: | |
| | AACTATAGAA AAATTCGGAA TTATACCAGA AATGGAATAT GAAATGGAAG AGGTTAAACA | 60 |
| 10 | AAnCGAGCAA TATATTAGAG AGCAAGAAGA AGCTGGAACA ATAGAGGCGA TAACA | 115 |
| | (2) INFORMATION FOR SEQ ID NO: 1649: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ÷. |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1649: | |
| - | TGTTGTCATG ATCTGAAAAG TCAAAGTCAA TAGAACATTG GCTTTGGCTT TTTATTTGG | |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1650: | 59 |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| • | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1650: | |
| 35 | ACCGATAATA GTACACGGCA TAATGNAACA ACTTGGCATG CACCCTTTTT ACGTTCCTTT | 60 |
| | ATCTCTGCAT GATTGTCATG TTCATCATGG TTTGGCTTGC ATTAATAGAG AGGGTTGACG | 120 |
| 40 | CAGAA | 125 |
| | (2) INFORMATION FOR SEQ ID NO: 1651: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1651: | |
| | TGATTAACGC GAATGCCACT TTTACTACCA ATGTTCCCAA AGCTGCTTCT GACAAACGCC | 60 |
| 55 | ATTGTACTCT G | 71 |
| 33 | | |

(i) SEQUENCE CHARACTERISTICS:

| 5 | (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|------------|---|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1652: | |
| | TCACTACATG CACCATAAAT ACAGTATGAA CGTATTGAAA TGGGCATTAC ATGATACAGA | 60 |
| | (2) INFORMATION FOR SEQ ID NO: 1653: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 123 base pairs (B) TYPE: nucleic acid | |
| * . | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | (5) 10102001 211002 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1653: | |
| 25 | TTAATTGAAA CAATTGACAA ATGCAATTTG ACGCCAAACT TTGAACTTTG AATGGATTAT | 60 |
| | CACATTATGA TTGTTCATCC ATGGnCAATT AGCATGGACG TATTACATTC TGGATTATCA | 120 |
| | AGC | 123 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1654: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 76 base pairs (B) TYPE: nucleic acid | |
| 35 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1654: | |
| | CTATGACGTC GCATGCACGC GTAACTTGGG CCCCTCGAGG GATCCTCTAG AGCGGCCGCC | 60 |
| | CITITITIT TITITI | 76 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1655: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1655: | |

| ATGTGAACCT GGTATTGACG GCGCT (2) INFORMATION FOR SEQ ID NO: 1656: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid | 145 |
|---|--------|
| (2) INFORMATION FOR SEQ ID NO: 1656: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: Public acid | |
| (A) LENGTH: 73 base pairs (B) TYPE: Dugleig acid | |
| (B) TVPE: pugleig agid | |
| (C) STRANDEDNESS: double | |
| (D) TOPOLOGY: linear | |
| | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1656: | |
| TTTAGAATTC CAATACGCTA TTGCCAGCGA TTTAGCCACT TGTGGGTAAT GATATTG | AAG 60 |
| GTGTTAGTCA AGT | 73 |
| (2) INFORMATION FOR SEQ ID NO: 1657: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 93 base pairs | |
| (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1657: | |
| CTTCTGAAAA GTAGTAATGT AACCTATTGG ATGCGAATGA ATCCCCAAAT TTAGTGG | ACG 60 |
| TATGTGGCTT CATCTTCAGA ACCTGTATCT GGT | 93 |
| 35 (2) INFORMATION FOR SEQ ID NO: 1658: | |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 58 base pairs(B) TYPE: nucleic acid | |
| (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1658: | • |
| 45 AAGTTAACAT GCAAGTTGAC GATGTAATGA CTCAAAAAGA GTGGAAACAA AAACACGA | 58 |
| (2) INFORMATION FOR SEQ ID NO: 1659: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1659: | |
|----|---|-----|
| | TTAATCCCAC AAACAAATGT ATGAAATTGA GTCAGTGATA TTAAATATGG GCTTGAAAGT | 60 |
| 5 | GTCTA | 65 |
| | (2) INFORMATION FOR SEQ ID NO: 1660: | • |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 91 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1660: | |
| | TGCATTTTTG TAAGAACGCA AAGCATTGTA AATTAGTTTT TATAAATTAG GATATTATCA | 60 |
| 20 | TGTGTATTGA AAACAATGAA GTGTGCTATG A | 91 |
| | (2) INFORMATION FOR SEQ ID NO: 1661: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1661: | |
| | ACATATCTGT CCACACAACA AGGACCATTT GTCTGAAGGG ACAGTGAGTG GGGAATATGT | 60 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1662: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 169 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (5) 101020011 1211001 | |
| | (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1662: | |
| 45 | TGGGGTTTTA ACCAGGGGAC CTAAAACCAG CCCCCATTTT CCAAGTTTGG ACCCCAAATT | 60 |
| | CCCHAAATTT AAAAAAAATT TGTTTGGGGT CTAACTTGGG CCGGTGCCTT CCTGCCTAAA | 120 |
| - | TTTAGCCCAT GTCTAACATA GTACTTTGGG AACGTAAAAG TTTAATTTA | 169 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1663: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 677 base pairs | |
| 55 | X., | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|------|
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1663: | |
| | TGGCACAATT GCACCAATTA AATGAATAAC TTTATCATTT TTATATACAG GTACAACAAT | - 60 |
| 10 | CGCTTCTTTT ACGAACTCAG ACTGGCGTAA TTGTGTTTCA ATTTCTTCTA ATTCCATTCT | 120 |
| | GTAGCCATTC AATTTGATTT GGAAATCAAT ACGACCTTGA ATGAACCATT GACCATTTTC | 180 |
| 15 | AAACTTCGCT TTATCACCAG TGTGATATGT ACGAATACCG TCATCGAAAT TAAATACTTC | 240 |
| 15 | AGCTGTTTTT TGGTCATTTT TTAAGTATCC TAAACTTACA CTTTGACCTT CGATAACAAG | 300 |
| | TTCACCTTCA TCTGTAGTAG ATAATCTTGC GCCTGGTCTT TCAACGCCAA CAGGTAATGT | 360 |
| 20 | CGGATATTGA TCTAAGATTT CTTGTGTAAT TTGAATACTT GTAACTGCTA CCGTAGCTTC | 420 |
| | - AGTTGGACCA-TATGTGTTGT-AAATCGTCGC-ACTTGGGAAA-CGGTTTACTA-ACGCTTTTGC | 480 |
| | TGCTCTGTGA GGTAGAATTT CACCACAGAA GAAGAATTCG TTAAGACTAC CATATTGTTC | 540 |
| 25 | TTCATTAAGC GTTGGTAATA ATAAACACAT TTCCATAAAT GATGGTGTTG ATACCCAAAT | 600 |
| | GTTAATCGGT GTTGCTGTTA GCATTTCATT TAATAATTTA GGTTTATTAA TCATGTTTTT | 660 |
| | ATCTACAAGA nTnAAnG | 677 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1664: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 62 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1664: | |
| 40 | GTTACAACAA TAGTGGTATA AAACGGGAGC AATTAGAGAT CAATATATGA TTATTAAGAG | 60 |
| | CA CA | 62 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1665: | 02 |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 342 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | · | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1665:

| | GITTACGCAA ATGATAGCTC GGTAAAACAT GAGCAACATG TTGAAGCCAA TTTGGAAATG | 120 |
|----|--|-----|
| | TGTTTATCGG AAACCACAAT CCACCTAATA CTGCTAAACC AATTGTTACG ATATTAGCTA | 180 |
| 5 | AAGCACTTGT TTTTTGAATA TCATTTAACA AAGAACCATA ATATGCCAAA AGTTATTAAT | 240 |
| | AGAGACGCAC CTAACCATAA AAATATTCCT GACTCTAACC ATTGAACTGC ACTCATTGCA | 300 |
| | ACACCTTTAT AAAAATGTCC AACCATAAAA ATAACTAATA TC | 342 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1666: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 5. |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1666: GTCCAAGAAT TCAAAAACGT TTTCAACTTC GGCCAAAGCC CAATTINTCT TTGTGGTTTA | 60 |
| | ACTITITAAT TITGAACGIT TTAGGGCATA AAAAAAAAAA GG | 102 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1667: | , |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 122 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1667: | |
| | TTGATAGTAG CCATAATCAT ACCACTTAAA TAATATGTTT GATCATCGGC ATAATTTTTA | 60 |
| | TTTATTGTCt.GTTCGCAATA TTTTGAGCAT TATCATAATT ACCACTAGTC ATATCATCTT | 120 |
| 40 | TG (2) INFORMATION FOR SEQ ID NO: 1668: | 122 |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1668: | |
| | AGAGATGAAA TTAAAATCGC AATTGAAAAT TTCAAATCAC GATGAGAGTG GGACAGA | 57 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 70 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: doubl (D) TOPOLOGY: linear | | ĝ. |
|-----------|--|---------------------------------------|-----|
| | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: | 1669: | |
| 10 | AACTACTGCC AATATTAATA GCATTGGTAC ATCTTAGAGG | CATTGAATTC CTTACTCAGA | 60 |
| | CTCATAATGC | | 70 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1670: | | · |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | • |
| 20 | | · · · · · · · · · · · · · · · · · · · | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: | 1670: | 60 |
| | GCCCGACCCG TAC | | 73 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1671: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 140 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | * | |
| <i>35</i> | (D) TOPOLOGY: linear | * | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: GAAGAATTGT ACTGTTAAAG TGACTCTAAA CTATCGCGGA | AATAACAGTG AAATCACCAA | 60 |
| | TTAGACTAGC GACACTGAAG TCATTAAAAA CAGACATTTG | TAGTGGTGCn CTTATCACCG | 120 |
| | CAAATACAAG AGAGTTTCTC | | 140 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1672: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | |
| 50 | (D) TOPOLOGY: linear | | |

| | AACAACGITI ACTATIGGCA CAGAACGGTT GGTACTTAGT CTAATACCAT TGTCATCAA | 59 |
|-----|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1673: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 10 | (D) TOPOLOGY: linear | |
| | | • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1673: | |
| 15 | ATCTCTTTGA CTTGAAGGAT TGGATTTAAA TCTTGGTGAT TTGGGCCGTG AAATATTTCC | 60 |
| | AGAAAATTCC TCAGACGTAT TAGTATAATT GTAACGnTAC ATTCTAATAT ACCTTTCTTC | 120 |
| 3 * | GATG | 124 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1674: | • |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid | |
| 25 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| * | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1674: | |
| 30 | CACCACCAC ACACACAC ACACAAACAC ACAACCCCC CACACAAAA CCACACCAC | 60 |
| | AACACACCAA CACAnCACAA AAACCCACCA CACACACCAC ACACCAACC | 109 |
| | (2) INFORMATION FOR SEQ ID NO: 1675: | 103 |
| 35 | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1675: | |
| 45 | THETCAACTE ATTTATGAAA TEGCAGAGCA TATEGCETCA AAGGTTCTTA ATCETTAAGC | 60 |
| | CAGACCACTG GAGGACCATT AGATGCAGCG TTGCTTTCAA G | 101 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1676: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 55 | | |

| | (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 16/6: | | |
|-----------|--|------------|-----|
| | TTTTTAAAAT TTGAAAATTT TAGACCTTAT TTCACGTGCG ATTTAATCGA TGTGTTAAT | (A) | 60 |
| 5 | AAACAATACT GGCATTCAAC ATGTAATCCG ATAATAAAAT AAGGTTGCAA TTATGTTAT | PT , | 120 |
| .* | GCATATTTTG TTTATTACTT AGAATAATAC GATGGTTAAG ATGAAATATA TGACAAAGA | AT · | 180 |
| 10 | AAATAATGAC ATTAAATTCA AGATGTTTAC GCCTTTTAGA TCTTTTTTAA GCATTTTAA | VA | 240 |
| | TCCTGTCACT TCKACATTAC CGACTAAGAG TAATAAGACG ATAAATACCC ACCAATTST | rc | 300 |
| | TTTTGGAAAA CTCATCGTCG TTAATGCTAA GACGAATAAT AACAACACAC CCATAATAA | AT | 360 |
| 15 | TCTCAAAATG CGAGTAAATA CAACTTCCAT TTTAAAAATA | | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1677: | | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 64 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | |
| | (C) STRANDEDNESS: GOUDIE | | |
| | | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1677: | | |
| | TCTTACTCAT GCATATGAGT GCAAGGGCCT GAGCATTCAT CAGCAAGATT AGAGCGATT | r r | 60 |
| | | | |
| | TTAC | * | 64 |
| 30 | TTAC (2) INFORMATION FOR SEQ ID NO: 1678: | * | 64 |
| 30 35 | | * | 64 |
| | (2) INFORMATION FOR SEQ ID NO: 1678: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | * | 64 |
| | (2) INFORMATION FOR SEQ ID NO: 1678: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | 64 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1678: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 'A | 64 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1678: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678: | `A | |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1678: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678: ACAGCTGATT TATTAAATGA TACTAAGTCC AAAGGCATGC GCATTATATC AGTTGGTAC | ·A | 60 |
| <i>35</i> | (2) INFORMATION FOR SEQ ID NO: 1678: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678: ACAGCTGATT TATTAAATGA TACTAAGTCC AAAGGCATGC GCATTATATC AGTTGGTACTTTCA | ¥. | 60 |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1679: | |
|----|--|-----|
| | AGCGCCACCA ACTGACGAAT TAGGTGGTAG TTGGACACTA TGGAAAAATT TAGCGCGACA | 60 |
| 5 | AAGTCCTGAA TTTGGTAATC CTGATAAGTT TTGCCAAAAT ATTCCTAMAA AAAGTTGGTT | 120 |
| | TGTTTCAGCA ACTTCTACAA CAAACAATAA AGAGATTATC GATACAATAG AAAGTATTTG | 180 |
| 10 | TARACGTGAC CCACTTGGCA GGCAAAACAG TTACAGGCGG TATTATTACA ATCAATGATT | 240 |
| | CTGCATGGCA AATGAGTTTT ACAATCAATC GTGCAGCAAC AGTTTGAAAG ACCAACCTGG | 300 |
| | AAAATGGAAA TATCTACATG GGGTTTGATG CCTTATGATT CnGGnGTAAA CGGCGGTTGA | 360 |
| 15 | TG | 362 |
| | (2) INFORMATION FOR SEQ ID NO: 1680: | • |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1680: | · · |
| | AGATACTICA GATTIAGCAT CATGAAGCAA CTTTAAAAGC AATCGCTGAC GCTGGTATTC | 60 |
| 30 | AGCCCGAGG | 69 |
| • | (2) INFORMATION FOR SEQ ID NO: 1681: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | * |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1681: TAACCATTC TTTTGACGTT TTATGTTGTT TTAAGAAATA AATACCAGTT AATGTA | 56 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1682: | • |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1682:

| | (2) INFORMATION FOR SEQ ID NO: 1683: | |
|----|--|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1683: | |
| | CCCCAACACA ACAAACAACA CACCCACCAC CCAACCCCAC CACACCCCCA | 60 |
| 15 | ACCCACCACA ACACCACICA CCAACACACA CCACACAACA ACCCCACAC | 109 |
| , | (2) INFORMATION FOR SEQ ID NO: 1684: | r · |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 62 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | - |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1684: | |
| • | ATTATGTTCG CGATAATTTA AGTAAAAGAA GCACAGATAT TGAATTTGAT AGGAGTAATT | 60 |
| 30 | GT | 62 |
| | (2) INFORMATION FOR SEQ ID NO: 1685: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1685: | |
| | CATAAGGTAC TTAAATTAAG GCATATCTGC TGTCTAGCAG TCGCATAAAT CATTAGA | 57 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1686: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1686: | |

| | | (2) | INFO | RMATI | ON FOR | SEQ II | NO: 16 | 87: | | • | | | | |
|-----------|------|--------|---------|---------|--------------|-------------|--------------------|-----------|--------|----------|--------|---------------|-----|-----|
| | | | (i) | _ | | | RISTICS base pa | | ٠ | 0 | ÷ | * | | * * |
| 5 | | | | | | | c acid | | | | | | | |
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| 10 | | | V | | | | | • | 7 | | • | | | |
| | .) | | (xi) | SEQ | UENCE I | DESCRIP | TION: S | EQ ID NO: | 1687 | | | e' | | |
| | | CTT | TATAG | TA TA | TTGCTT | T TGTI | TTTCTT | TTTCGTCAT | A TTT | CACTITI | TAAAT | AGATAC | | 60 |
| 15 | | CIG | CAACAC | AA TY | TTAATA | G ATTA | ACATAA | TACTAGTT | LA TAT | TAAnATI | | . I | | 110 |
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| 25 | | | | | | | | | .1 | | | | | |
| | | | (xi) | SEQ | UENCE I | DESCRIP | TION: S | EQ ID NO | 1688 | • | | | | |
| | 1.44 | -AATT | TACTAC | T CT | CTTGT | C AAAG | ATTATT | TATATTCTA | G CTC | AACATTA | ATTT | CTTTGA | | 60 |
| 30 | | TTT | rggtac | C AT | CTATCGT | G TCAC | CCATGC | GATGCGGTT | G TAG | | GTAA | STTCGA | | 120 |
| | ** | AAGT | AAATA7 | A CT | TATCATO | T TCCA | AATTTT | CTACAATTI | T ACC | TTTTCTA | TTAT | TAACAG | | 180 |
| | 7 | CACC | ATATA | A TT | TTCTT | T TCCA | TCAATT | TTTT | -10 | | | | | 214 |
| <i>35</i> | . 0 | (2) | INFOR | ITAM | ON FOR | SEQ ID | NO: 16 | 89: | | | | . • | • | |
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| 45 | | | (xi) | SEQ | JENCE I | ESCRIP | TION: S | EQ ID NO: | 1689 | | | | · | |
| | Ė | GCTA | GTTGT | A AC | STGCTTI | TTCAC | CACCAG | ATAAATCAT | A ATA | TCTTTTA | ACAT | CTCTG | · y | 5,9 |
| | | (2) | INFOR | ITAM | ON FOR | SEQ ID | NO: 16 | 90: | | * 100 | | | | |
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| 50 | | 5- | (i) | | | | RISTICS | | | (+ | | | | |
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| | | - | | | | | : doubl | e | | | | | _ | |
| | | | | | TOPOLO | | | | | | | | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1690: | |
|----------|---|----|
| | CCAAACTTTA TAATATGAAA TGCTTGGTAA TTACAAAGAT AAAATCATAC TCACG | 55 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1691: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 64 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1691: | |
| | TAGACAGCAA TCCATTGCTA TAGGGGTGGA TATCTCATTT GCGTTTGGAG CTGTGCTTGT | 60 |
| | TATG | 64 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1692: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1692: | |
| | TGCATGGGAT TGCAGCTAAG AGAATCATAA AAATATATTA CTTTAATAAG TGTAGTA | 57 |
| | (2) INFORMATION FOR SEQ ID NO: 1693: | |
| 35 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 74 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1693: | |
| 45 | CGATGTGTAC GTCTCACCTG ATTTCGCACG GTAAGCTAGT GCATATTCAG CACCGCTACT | 60 |
| | CGCCCAGCCT AGAC | 74 |
| | (2) INFORMATION FOR SEQ ID NO: 1694: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 162 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 55 | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1694: | |
|----|---|-----|
| | AACTTTTCAG ATGTTGATAG CTATAGATTT AGGCGCTATT CACCANGTCT ACATGCAATA | 60 |
| 5 | CGTACGTTAT AATGCACTGC AACGAATCGC GCGTTATGAG TTGGTAATTG TTGTTCAATA | 120 |
| | TTGGGTGTAT AGTTTTCAAC GTGGTTACAA GCAACTACCT AA | 162 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1695: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1695: | |
| 20 | AATTATCTCT ACACCTTTTC TTTCACATAA TTGACGCAAT ATAATCCCTA TATCT | 55 |
| | (2) INFORMATION FOR SEQ ID NO: 1696: | ٠. |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1696: | |
| • | ATGCAACGTT GGCATTGGGA AATGGTCCTG CCTAAATTAA CACGCAATAA AATGTG | 56 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1697: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1697: | |
| | ACTGTGTAGA AGATGCTATT ATTGTAAAAC ATAGTTTTAA TTTTATTTTC TGATATA | 57 |
| | (2) INFORMATION FOR SEQ ID NO: 1698: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1698: | |
|-------|---|-----|
| | AAAATTTTCC CCCGGGAACC CGGTTTTTTA AACCCCCCGT TTTAAAAAAA TTTTGGGGGG | 60 |
| 5 | CCCAAAATTT CCCAAAAAAA nAAAAAATTT TTTTTTTCCC GGGGAAAAA | 109 |
| | (2) INFORMATION FOR SEQ ID NO: 1699: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1699: | |
| , | GTGTTAACGT GGATTATATC AAnGAGGCGG TCAGGTACAG TCCACACGCA CAGCGCACAG | 60 |
| 20 | AAGTATCACA TCCAGTAAAC AAGGCTAGTA CAGCATTGCA | 100 |
| -, -1 | (2) INFORMATION FOR SEQ ID NO: 1700: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1700: | |
| | AAGGTTAAAT GAATTAGGTT GATCAATGCT CTATACTCAT TGCTAAGTCA ACGCACCTTT | 60 |
| 35 | ACCACCTTTT CCCAACTCAG TAAGGCATTC GACGTATTTC TTAGCCAAGN TTACATATCT | 120 |
| | ACTCTGCAC | 129 |
| | (2) INFORMATION FOR SEQ ID NO: 1701: | • |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs (B) TYPE: nucleic acid | |
| 45 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1701: | |
| 50 | CAAGAGGAAC AACTCGGTAC TGCGCATCAG CAGAGATGGC GAAATCACAC TTAGAAGACA | 60 |
| | AGG | 63 |
| | (2) INFORMATION FOR SEQ ID NO: 1702: | |

| <i>5</i> | (A) LENGTH: 400 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|----------|---|-----|
| 3 | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1702: | |
| -10 | TATTTAATAA ATCTTCAATA CCTTGTTCAT CAGTTTGTTG ATAAATAAGA CCTCTCCATT | 60 |
| | TTAAATCTTC AATTAATACA TTCGTCATTA TTATTTCCTC CTATTTATAA TTATTTATTG | 120 |
| | AATACTTGTT AAAATACTTT AAAGKTTTTT GAACGTAAAA AAAACCCTTA CAACAAATAT | 180 |
| 15 | GTAAGGGCGC GATTGCACGT TACCACCAAA CTTAAACATA ATCATAAGAT AATGTTCACT | 240 |
| | CTATTAATGA TACGTTCATT AATAAACGTA GGACATGTTA GTTATAAAGG TGTATTCATA | 300 |
| | TTATTAAAAA CACTAGTTCA CAGCGACCAC TAGCTCTCTG ATGATTTCAA ATAATATTAC | 360 |
| 20 | TTGTCCTTTT ATCCTATTCT GTATGCATTT TCCCTAATTA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1703: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 208 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| · | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1703: | |
| | TCAATATTGA TATCGAAACG CTTTGCAGAT TGATATAAAT TATCAGAATC AAGTAATTCA | 60 |
| 35 | TTTATTTTCT TTGGTGAAAG TACTTGGAAA ATACTATACT | 120 |
| * | ATGAAGTATG GAAGTTGTTG CTTTGGGTAA GCHAAATTTC TAATACATAC TGATTAAACT | 180 |
| 40 | GTTTGTTTAT TGnGAATTGC AACGCATC | 208 |
| | (2) INFORMATION FOR SEQ ID NO: 1704: | : |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 67 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1704: | • % |
| | AAGCCGATGT AATTATTTAT GCAACACCTG TTCTAATGCA CAAAGAAATA TCTTAGCGAG | 60 |
| | CTTATAG | 67 |
| 55 | | |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear |
|---------------------------------------|--|
| ** | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1705: |
| | CCAACTIGCA TGTTATTTTA AGCTGACTTT CCACCAACTT CTGAGTTTGT GGCC 54 |
| | (2) INFORMATION FOR SEQ ID NO: 1706: |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 61 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double |
| 20 | (D) TOPOLOGY: linear |
| · · · · · · · · · · · · · · · · · · · | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1706: CAACTACACG AAAGGGTAGT GCTTCAAGAT AATAACGTCC AATTATTAGG AACTGTGGCG 60 |
| 25 | A |
| | (2) INFORMATION FOR SEQ ID NO: 1707: |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear |
| 35 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1707: |
| 40 | ACCATTCCAA ATGAACCTAA ACCACTTGAT ACGTTGACGA CAACAGGTTG TTCA 54 |
| ٠ | (2) INFORMATION FOR SEQ ID NO: 1708: |
| 4 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear |
| <i>50</i> . | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1708: |
| | AAATTTGAAT AACTGTACAC ATTTTTTTGA TCATAGTCTA TATACTTTGT GAATTAATT 59 |
| 55 | (2) INFORMATION FOR SEQ ID NO: 1709: |

| 5 | (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-------------|---|----|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1709: | |
| 10 | GCACAATAGC CAATTAGATG GGGCCGGTGC GGTAACATTT TGCTTCATTC CTGCATTAT | 59 |
| | (2) INFORMATION FOR SEQ ID NO: 1710: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1710: | • |
| | TTACAATTCA ATCAAGTTCT TCATTATCAG ACGAAGAAAT CCACCGTATG GTAAA | 55 |
| 25 - | (2) INFORMATION FOR SEQ ID NO: 1711: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 30 | (D) TOPOLOGY: linear | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1711: | |
| | TTTCTGCTTA TTGTCATTCG ATATCGAATT ATTAGAAAGT GCAGATTTCG CATCAG | 56 |
| | (2) INFORMATION FOR SEQ ID NO: 1712: | |
| 40 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 55 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1712: | |
| | TAAACCTTTA GGATTGCTGG CAATAGTAGT GCAGTTGGCT GGACTTGTCA TGCCC | 55 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1713: | • |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 207 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| 5 | CAAGAGGATT CGTGCANTGA ATTCATGGAG ATATTTAGAT AAAAGAAGAA AAGAGTAACC TTTAGATTGC TGGATNTGTG TTAGGTGGCA TAAGGAGGCT ATACGCAGAC AACCACCGTC | | | 60 |
|-----|--|---------------------------------------|--|-----|
| . * | | CAGTGGCTGC | mmo o o ma o o m | |
| • | TTAGGTGGCA TAAGGAGGCT ATACGCAGAC AACCACCGTC | | TIGCGIGCCI | 120 |
| | | CCGGGGTTTT | ATTGTACACT | 180 |
| 10 | GTGTAGGACG CAGACTTTAT GTGGTTG | | 1. | 207 |
| | (2) INFORMATION FOR SEQ ID NO: 1714: | * * * * | and the state of t | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | |
| 20 | | , | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: | 1714: | | |
| | TGGTTATCGA CTGCTCGTAT ATTTTGACTGT | TGTTTCCGTA | GCAATACTAT | 60 |
| 25 | CTCCTAAGCC TTTCATTGGC ATTG | | | 84 |
| | (2) INFORMATION FOR SEQ ID NO: 1715: | | • | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | |
| | | • | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: | 1715: | | |
| • | GTTTGAATTG ACTGACTTCG TTTTACCGCG TGTTTAATAT | TGTTATACAT | ATAT | 54 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1716: | | | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 77 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · · · · · · · · · · · · · · · · · · · | | |
| | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 | .716: | | |
| 50 | GAAGCCTGTC AGTGGATCAA ATTATTGAAG ATAACTTGGG | TGGCATTTTT | GGAAAGTCCA | 60 |
| | AATGCTGGGA ATGGTCA | | · | 77 |

(i) SEQUENCE CHARACTERISTICS:

| 5 | (A) LENGTH: 154 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1717: | |
| 10 | GGGCCTTTT TTTCCCAAAA AAAAAAACCC CCCCAACCCC AATTTTGGnC CCCCTTCCCC | 60 |
| | TTTAAAAATT TAAAAATTGG GCCAAAAGGC CCCCCAAAA AAAACCCCCA ATTGGAATTG | 120 |
| 15 | GAAAACCATT GGAACCAATT CCATTGAACC AGGA | 154 |
| 4. | (2) INFORMATION FOR SEQ ID NO: 1718: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1718: | |
| | ATTGTCTACA CTGCCACTTT ATTTTCATTA ACCATTTCAC AAATGTGTTC ATCATTCAAC | 60 |
| 30 | ATGAACATCA ATTGTTCAAT TACATCGACA CCTGATGCCT AAnCACGCAC CTTTTGCACA | 120 |
| | (2) INFORMATION FOR SEQ ID NO: 1719: | |
| 35 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 54 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| • | (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1719: | |
| | TTCATTTGTT TGTAAAAGTG GCATTTCTAT GTCTTAAAAG TGACGAAACT TCAC | 54 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1720: | • |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 55 base pairs(B) TYPE: nucleic acid | |
| 50 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (mi) CROVENCE DESCRIPTION, SEO ID NO. 1720. | |
| | | |

| ٠, | (2) INFORMATION FOR SEQ ID NO: 1721: | |
|----|---|-----|
| | (i) SEQUENCE CHARACTERISTICS: | • |
| _ | (A) LENGTH: 71 base pairs | |
| 5 | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | * · · · · · · · · · · · · · · · · · · · | |
| | | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1721: | |
| | | |
| | TTTGGATTAT AAATTGACAT GTAAGTACGA GGCAGCTGTA CCCGATATAT AATTGCTAAG | 60 |
| | | • |
| 15 | AGTTAGGGCT G | 71 |
| | (2) INFORMATION FOR CEO ID NO. 1722. | |
| | (2) INFORMATION FOR SEQ ID NO: 1722: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 325 base pairs | |
| 20 | (B) TYPE: nucleic acid | |
| | (C)-STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | 4 |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEO ID NO: 1722: | |
| | (XI) BEYOBNED DESCRIPTION: BEY ID NO: 1722: | |
| | TTTTATCTTT ATTACTAAAA CCAACTGCAC CAAAGTTTGC AGTCATTACC ACACGTTTAA | 60 |
| | | |
| 30 | CACCCGCATG TTCTGCAGCT CTTAAAATAC GTTGTATACC TTCAATTGCA GGCTTCGCCA | 120 |
| | | |
| | TCACTTCTGC ATCGTCTGTT TTACCGAAAA ACACCGGAGA TGCTACACTC AAGACATACT | 180 |
| | TGCAATCTTT CATTGCTTCA TCCCAATGTn CATCTTGTGA TAAATCCGCT TCGACAAACA | 240 |
| | | |
| 35 | TTAAATCGCT CTGTGGAAAT GCCCATGTCT TGCATTGTTT nAATTACTTT ATCAGCTTTA | 300 |
| | | |
| | CTTAAATCAA GNATCGTCGT TTGTA | 325 |
| | (2) | |
| | (2) INFORMATION FOR SEQ ID NO: 1723: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 71 base pairs | |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 45 | | • |
| | | |
| | () GROUPHOR BROOKING GROUP HOLDER | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1723: | |
| • | CAGTATTGCA GTCACGACAA TGTGATGACT AAATTATCCA AAGTATGAAT TCCATGCGGC | 60 |
| 50 | CHARLES GIGGEORY INTOINION WATTINGCA WARTHINGTH ICCUTOCOCC. | 60 |
| | ATTAATCCTA G | 71 |
| • | | |
| | (2) INFORMATION FOR SEC ID NO. 1724. | |

| 5 | (A) LENGTH: 53 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|----|--|-----|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1724: | |
| 10 | TTGCAACGAT ATTAGGCTAT CTAGTCGGCA TATTTGTAAA ACAAGATCCA ATT | 53 |
| | (2) INFORMATION FOR SEQ ID NO: 1725: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1725: | |
| | ATCTATTCAT CTTCGTACAC GGACAGGAAA TGAGTCCAGT AGATGCACAT TGGGAATTAA | 60 |
| 25 | TCGAAGCTAG C | 71 |
| | (2) INFORMATION FOR SEQ ID NO: 1726: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1726: | |
| | CATCTTGCAG GTCTACATTA TAAAATGTGA AGTTTTCTAC GATAACAATT GGGAAACTCA | 60 |
| 40 | GGGGCATCTC C | 71 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1727: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 235 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1727: | |
| | TTCHTTTTTA AAAATTCCCC ATTCCTTTT AAATTCTTT CCCGCTGGAT TAAATGGATT | 60 |
| | TTAAAAATTC CACCCCAACT TANAATTAAA TGGCTTGTGG AAAATTAACG GGATTGGCAT | 120 |
| | | |

| | TCCAGCTTAA ATGGTTTTTT TGGAGGCTTC CACGTTAAAA ATGGCGGGTG GCTTT | 235 |
|-----|--|-------|
| , | (2) INFORMATION FOR SEQ ID NO: 1728: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 61 base pairs | |
| 10 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | | 4 · 4 |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1728: | |
| 15 | TAGAGTGGCT ATAAAGCTAA GTTCAATTGA CCAATTTACA ACAGGTTATT GAGGACAATA | 60 |
| | A | 61 |
| | (2) INFORMATION FOR SEQ ID NO: 1729: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54-base-pairs | |
| • 0 | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| 25 | (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1729: | |
| 30 | ATCACCAAGA AGTTCTAATG CTTGGTATAA ACGTTGAATA CGACGTTCGG TATT | 54 |
| | (2) INFORMATION FOR SEQ ID NO: 1730: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid | |
| 35 | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| | · | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1730: | |
| | CGTCCCGAAG CGTTGGAGGC GGGAACATCC AGAGTAATTG GCACAGATTA TGACCATAT | 59 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1731: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| 50 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1731: | |
| | (AI) DEGULACE DESCRIPTION. OBY ID NO. 1731: | |
| EE | | |

| | (2) INFORMATION FOR SEQ ID NO: 1732: | |
|------------|---|-----|
| 5 ` | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (2) 19192991 1211002 | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1732: | |
| | TATGTGGTGT TCAATGCAGT GGTCATTATG GTGCATCTTA CCAGATTCGG CATTCTTATT | 60 |
| 15 | ATAACTATAC TTGTAATAAA TGGCGACATG CAGACACGnC AATAC | 105 |
| | (2) INFORMATION FOR SEQ ID NO: 1733: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | • • |
| | (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1733: | |
| | TTTACGTTCC ATAGCAAAGT GATACAAACG TCAGCATCAA TGTAAGGCAT AGATCATAGT | 60 |
| | | |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1734: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid | |
| 35 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | () CDC//DVCD DDCCD//DDCCV CDC TD VC | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1734: | |
| 40 | TTCCATCATA CATTCGCGTT TTACTTTTCT TCTGGTATGA TCAAATATTC ACATAA | 56 |
| | (2) INFORMATION FOR SEQ ID NO: 1735: | |
| | (i) SEQUENCE CHARACTERISTICS: | • |
| 45 | (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (2) 10102001. 111041 | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1735: | |
| | AAATGGGGAT GAAACAGTTA GTGTACAGGT GAAAGCTTAA CAGCAGCTAC AATTGCA | 57 |
| 55 | | |
| - | | |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 61 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|--|------|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1736: | |
| | GATTTGCAAT TAAACTTAAA TGTAATTTTT CGGAATGTGT ATTTGGTTTA CTTAAAGTAA | , 60 |
| | A . | 61 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1737: | . , |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 0 | | |
| | (xi) SEQUENCE DESCRIPTION: SEO ID NO: 1737: | |
| 25 | AAAGAAGCTA AAGAAAAAGT TGATAAAACA GCAAAAGTGA TTATTAGCTA CAGCATT | 57 |
| | (2) INFORMATION FOR SEQ ID NO: 1738: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1738: | |
| | CAATAATATC GCTAAAACCG CCATTTGTAC CAAATGAATT TGATAATGCT GCAG | 54 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1739: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1739: | |
| 50 | TAGAGCCCAA CCGGCAACCC ATCCATGGAA ATTCACCAAA ATAATACATT GACCCCAAG | 59 |
| | (2) INFORMATION FOR SEQ ID NO: 1740: | ננ |
| | | |

| | (A) LENGTH: 136 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 5 | | * | |
|-----|--|-------------|----------|---------------------------------------|-------|
| 5 | | | νT | | |
| | | | | | ÷. |
| | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 174 | 10: | | |
| 10 | CCTTTTTGGn AATTTAAGGG GGTTCCCAAC CA | AATTCCCC CA | AATTTTTT | TGGGTTAAA | A 60 |
| | AAACCCGGCC CAAAAATTTA AGGGAATTTG GA | AAAAGGTT TG | GTTCCCTT | TTTTTCCCA | A 120 |
| | GGCCCAAAAT TTGGAA | | • | . ` | 136 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1741 | | | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid | | * | | * |
| 20 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | • | • |
| | | | ÷ . | ** | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 174 | 1: | | |
| | CATTCAACCA ACGACTGACA ACAGAACATT TAX | AGAGTCTA GG | ACATTGAT | TGA | 53 |
| | (2) INFORMATION FOR SEQ ID NO: 1742 | | | | * |
| 30 | (i) SEQUENCE CHARACTERISTICS: | | * . | | 3 |
| · · | (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | * = | | · · · · · · · · · · · · · · · · · · · | |
| 35 | (D) TOPOLOGY: linear | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 174 | 2: | | |
| 40 | GCTCGTCTGA TTCAGTCACA AAATTGTCTT GTT | TATACTTG TC | ACCTATCA | тс | 52 |
| | (2) INFORMATION FOR SEQ ID NO: 1743: | | | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs | Ŷ | • | * (4) | |
| 45 | (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | | | | 130 |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 174 | 3: | * | |
| | TGTTATTTAA AGAĞGCTCAA GCTTTCATAG AAA | • | GAGAGTGT | CAT | 53 |

| 5 | (A) LENGTH: 94 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|------|--|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1744: | |
| 10 | TCTGAGTTAA AGACGTCTCA CTTAAAGCTT TAGCAATTCC AACAATCAGA TATCTTCACA | 60 |
| 4 9 | CGTGTTATAT GTGTCCATTA ATATATCCTG TGGC | 94 |
| | (2) INFORMATION FOR SEQ ID NO: 1745: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 212 base pairs (B) TYPE: nucleic acid | |
| 20 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1745: | |
| | GGAAAAAAnn TTTTTAAAAA AAGGGAAAAG GGAATTGGGG TTCCCGGCCC CTTTTTAAAG | 60 |
| 25 | CCCCAAATT AAGGAAATTT TAAATTTTGG GGAAGGGGAT TTTCCACCGG TTAATAAACC | |
| | GCCGATTTTG AGGGGGTTGA ATTAATTGGC CCAAATTTAA AAACCTGGAT GCTGGGTCCA | 120 |
| 30 | · | 180 |
| . •• | ATTTTTACC GGGACCAATT GGTCCTGCAT GA | 212 |
| | (2) INFORMATION FOR SEQ ID NO: 1746: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1746: | |
| | TATCTTCCGA TGAAGAACAA GATGCACAAG AAGTACGCCA ATGATTTAAG AAAGTGGT | 58 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1747: | |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 105 base pairs(B) TYPE: nucleic acid | |
| 50 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1747: | |

| | AAAATTAAGn CCTTTTTAA CCTTTCCCTT CCCCAATTGG GGCCT | 105 |
|----|---|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1748: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 52 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 10 | (D) TOPOLOGY: linear | |
| | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1748: | |
| 15 | AGTGCCTATT ACTITGATTG ATGTCCAAGT TTCCTATCAC ACAACTTAAT TT | 52 |
| | (2) INFORMATION FOR SEQ ID NO: 1749: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 20 | (A) LENGTH: 95 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1749: | |
| | | |
| | AAAGCATCAT CCGAACTCCA ATGATTATAC TCCCTAGATA TTATTATGTG ATGCTTTGAG | 60 |
| 30 | CATTAATTAG AGATGGGACG ATTCCATGAA AGATA | 95 |
| | (2) INFORMATION FOR SEQ ID NO: 1750: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 35 | (A) LENGTH: 63 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1750: | |
| | TTGACACATC TACTCACATT AAAAGTAGAT GAAGCGTTGA GATTAACATT TCCACATTTA | 60, |
| 45 | CAA | 63 |
| | (2) INFORMATION FOR SEQ ID NO: 1751: | |
| | | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 50 | (A) LENGTH: 116 base pairs | |
| 50 | | |

| | THE TAX TO COURT AND ACTUAL AND AND ACTUAL A | CAAGATCTAC | | ,60 |
|-----------|--|--------------------|-----|-----|
| - | CAATATAAAC AGCGGCTATA TGATATAAAT GCTCAGACAC ACCCACTGCG | ATCCAT | | 116 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1752: | | | |
| | (i) SEQUENCE CHARACTERISTICS: | | | |
| | (A) LENGTH: 114 base pairs | | | |
| 10 . | (B) TYPE: nucleic acid | | | |
| 10 . | <pre>(C) STRANDEDNESS: double (D) TOPOLOGY: linear</pre> | | | |
| | | * 1 gt | · • | |
| | | | | |
| | (vi) SPOUDNOE DECORATION OF TO THE | | | e |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1752: | *- , | | |
| | TATGATTAAG CTTAGTGCAG ATTTGATTTA TTMAACAACG CTTCACTACA | TTAAAAATAG | | 60 |
| | GGCACTCGCA CATATAGTTG TATCAATAGC CTTTATCAAT TITTTGGGAA | GGTT | | 114 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1753: | | | |
| | (i) SEQUENCE CHARACTERISTICS: | | | |
| | (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid | i i | • | |
| | (C) STRANDEDNESS: double | | | |
| 25 | (D) TOPOLOGY: linear | • | | |
| | | | | |
| | the system of th | 4 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1753: | * | | |
| 30 | | | | |
| • | AACTTCAAAT GTGCCAAGTG TTGAATCACA TCAAAATCAT TTTTATTTAA | CG | | 52 |
| | (2) INFORMATION FOR SEQ ID NO: 1754: | * | ٠ | |
| | (i) SEQUENCE CHARACTERISTICS: | ÷ | | |
| 35 | (A) LENGTH: 75 base pairs | | | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | | |
| | (D) TOPOLOGY: linear | | | |
| | | | • | |
| 40 | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1754: | ÷ · | | |
| | ACTANTCCCT TGCGTGTTTC CAATCAATTG CATTATTAGT GGCCATTTGT | ITGATATAA C | | 60 |
| 45 | TGACAGCTT TAACC | | | 75 |
| | (2) INFORMATION FOR SEQ ID NO: 1755: | | * | |
| | (i) SEQUENCE CHARACTERISTICS: | | | |
| 50 | (A) LENGTH: 53 base pairs | | | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | | |
| | (C) STRANDEDNESS: GOUDIE (D) TOPOLOGY: linear | | | |
| | | ٠ | | |
| | • | | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1755: | |
|----|--|-----|
| | GTGAACAAGG GTAGATGTAA ATAGTTGATG CATGTGTACA CATCATAACA AAA | 53 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1756: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1756: | |
| | TTATTTGGGC AGGCAAATAC CCTTAATATA TTCAAATCAT GTTAATATCA TTGCTATTGC | 60 |
| | TAAACC | 66 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1757: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1757: | |
| | ATTAATCGGA GCACTTGGGT TCGCAATTTA TGCTGAAATG GATCATCTA CATCATC | 57 |
| - | (2) INFORMATION FOR SEQ ID NO: 1758: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1758: | |
| | CGAACAATAA CTCTAAGTAT CCAACAAATG CTGCAAGTGT ACCTACTGTG ATTGATCCAG | 60 |
| 45 | AAATAGCAAG ATATGCACCA ACACCGATGA CAATAATTGG TCCAATATCT GTAACTGTAT | 120 |
| | TAATTGCGGC AAAGGAATAG GCATTCCATC TTGTATGTTT CAACGCACGT GTTAGGAAAT | 180 |
| | TAGTATTCTT TTTATCAAAG TTTTTCGCTT CATTGTCTTC AATCGCAAAA CTTTTAACGA | 240 |
| 50 | CTGAAATACC TTGAACACGT TCATGCAAGA ATCCTTGAAC CTCAGCTAAT GCTTGAGATC | 300 |
| | TITCANGTGT CAATTTTCTT AATCTTCCAA AGAAAACGTA CACCGTTAAA ATGTAAAATG | 360 |

| | (2) Interest for Por SEQ ID NO: 1759: | |
|----|---|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 139 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1759: | |
| • | HATTATGTCA TGCTAGGTCA CTTGCATCAT CCATTTAGTA TAGAAGACGA CAAAATTAAA | 60 |
| 15 | TTATAGTGGG CTCCTTGATT GGCAGTATTC ATTTTCGGGA AGCGGGGTCC AGGCTTAAAG | 120 |
| | GGTATTAGAC GTGGTTACC | 139 |
| | (2) INFORMATION FOR SEQ ID NO: 1760: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: | - |
| | (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 8 |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1760: | |
| | | • • |
| 30 | TCGCCCCTCC AGGCTATTAT TTCATCTATA TCATTGTCAT CAGTTAAATT CAGCCTCGAC | 60 |
| | ATTTCCATTT CAATAGACTG TTCATTCAAT TCTAAGTCAT TATTGTAAGT TTCTAGTTGA | 120 |
| | TTTTCATAAT GATTTAGATT ATTTTGCTCA ATTAACTTTC TTTGAGACAA TTGCATTAAC | 180 |
| 35 | TTATCTTCAA TCTCCTTTGA GAGTTCTTGA TGCTGATTCA CATCTTGAAC ATACTTCTTA | 240 |
| | TAATCCACCT CAAAATTAGT GATATTANTA TATNTCGAGA GTGTTTCAAA TTCAGTGATG | 300 |
| | AGATCTCGAC ATAAT | 315 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1761: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 399 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 15 | (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1761: | |
| | TAAATCCTCG AGATTCTTAA TAGGGTAGAT ATCTAACGTT TTCGCAAAGC TCTTTTTGAT | 60 |
| | TTGTTCTTCT TTTGAATCTC CAATGATCTT ATTATCACCA TCACAAGATG TAACAAAGAT | 120 |

| | CCATCCTCAT CATTCATCAT CTTCATCTAC CTTCGCGGCT GGAAATTCAA aGAATCTATT | 240 |
|-----------|--|------|
| _ | ACTGACAAAT CGCTTTTTCC ACCTTTTGAA AAGTCAATTT CCAACTTTTT ATAACCCACA | 300 |
| <i>5</i> | GAACTTCCTT TCAAATTACC ATCAATATGC ATTTTTAATA CCGGTGCTTT ATCAGTAGGA | 360 |
| | ATATTATAAC GACTTCTTAA TTGCTTAACA TTTTCATCT | 399 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1762: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 224 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1762: | |
| 20 | GTATAGAAGA CGACAAAATT AAATATAGTG GCTCCTTATT GCAGTATTCA TTTTCGGAAG | 60 |
| • | CGGGTCAAGC TAAAGGGTAT AGACGTGTAC AATTAATGAT GGCATTATTA ACGATGTATT | 120 |
| | TATTCCTCTT AAGCCACTTA GACAATTGGn AATTATCTCA GGCGAATATA ATGATGTTAT | 180 |
| 25 | TAATGAAAA GTTCATGTGA AAAATAAAGA TAATTATnTA CATT | 224 |
| | (2) INFORMATION FOR SEQ ID NO: 1763: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| 33 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1763: | |
| | AGCAACCAAC GCCAGATAAA GCAGAAGATA ACGCATTTCC CCCCATCACC ATAT | , 54 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1764: | |
| 45 · | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1764: | |
| 50 | ATTCCCTTAT CGCATTCTGT AAAATGATCT TCATCAGAAA TTGCTTCGAT ACGTTTATG | 59 |
| | (2) INFORMATION FOR SEQ ID NO: 1765: | |
| | | |

| 5 | (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-------------|--|-----|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1765: | |
| 10 | GATTCAATTC ATCTGTATAG ACGATATATC CTGATATGAA TTGGAAATGG AATA | 54 |
| * * + + * * | (2) INFORMATION FOR SEQ ID NO: 1766: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 15 | (A) LENGTH: 85 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1766: | |
| | ATCGCATAGA AGCATTAGAC TCAAACTATT TTCGGTTATG AGAATAACTC TGACATCCAT | 60 |
| 25 | ATGGATACTT AGTTTCCAAG TTAGA | 85 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1767: | • |
| | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs | |
| 30 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (b) Torobod1: Timear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1767: | |
| | CAGTACTGCT GAATGATGCT ATTGATTTTC TCATGAGACA TGGCGATAAC ATCG | 54 |
| | (2) INFORMATION FOR SEQ ID NO: 1768: | |
| 40 | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| 45 | (D) TOPOLOGY: linear | |
| | | |
| ** | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1768: | |
| 50 | GRCACTACTA ATCGTATCAG GATCACTAAT TAAGGCATCC AGCATCAGAT ACGAGCGCAC | 60 |
| | GTCAGACTAA TCTACTGTCA TGATAAAGCA GCTGCTAACC TTGTAAGTTC GTGAAA | 116 |
| | (2) INFORMATION FOR SEQ ID NO: 1769: | |

(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid

| 5 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1769: | |
| | GTTCTATCCA ATATGGAAAT GAGGACATTA TGCGTGAAAG CTATGGACGA TGGACGATGG | 60 |
| 10 | GITCTATCCA ATATGGAAAT GAGGACATTA TGCGTGAAAG CTATGGACGA TGGACGATGG | |
| * | TACACGCATG TTGTGTAAGC AG | 82 |
| | (2) INFORMATION FOR SEQ ID NO: 1770: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 152 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| 20 | | * • |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1770: | |
| 25 | TATCTGTATT GTAGTAATCC GCTTCTCCCA TCTATATAGG GATCTTTCGT AGATATTCAC | 60 |
| | TTTATGCCTA GGATCCAAGA TGTGTAAGCA GCACTTTGCA TTATCTAATG CAAAGGGNAC | 120 |
| | ATGCGGCTGT AAGCCCTGTT CTGATAATCA TA | 152 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1771: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid | |
| 35 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1771: | |
| 40 | TGGAGGCGAA GTAAATGAAA AGTATTACGT TTGAAGAACA TTATGTCATT G | 51 |
| | (2) INFORMATION FOR SEQ ID NO: 1772: | • |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 232 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1772: | |
| | NGAAACAAAT ATCTGATGAG ATATGCAATG ATGACTATAA GTAACATTAA AATGAAGCCC | 60 |
| 55 | | |

| | CGTACACCAA TTATATCTTT GTGGNTGTTA TATTAAATCT ATATTATGTT CATTTAACAG | 180 |
|----|---|------|
| 5 | CATATGTTAA AAATTGACAG TTAACACATG TAGCTATTTG ATGTGAATGT GC | 232 |
| 3 | (2) INFORMATION FOR SEQ ID NO: 1773: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| , | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1773: | |
| | TAATGTCCCC CAGAATGTAG GCAAATGCAG AACCTGGTTT TAGGGTCAAC TGTTTnTTCT | 60 |
| | CCAAGCAGAA ACAAAGTTCT TGTGTCAGTG CACTTTTGGT CCACCATT | 108 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1774: | • |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 111 base pairs (B) TYPE: nucleic acid | |
| 25 | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | 1.1 |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1774: | |
| | CGCAATTGAA GGATACACTA TTTTAAGAGC TGCAAACATG CGGGTGTAAC GTGTGGTATA | 60 |
| | CTGCAACTTT GGTnATTGGT TTAGTATAAG ATAAAATCAT CACAATGAAT C | 111 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1775: | |
| | (i) SEQUENCE CHARACTERISTICS: | . 44 |
| | (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid | |
| 40 | (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1775: | |
| 45 | CAGGTTATCA GCTAATAGAT ATGTTGAAGA GGCAGTTGCA GGCCAAATGA AACTGCAGAT | 60 |
| | GTAGTTCAGT ACC | 73 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1776: | · |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 67 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| | (0) 11,1111111111111111111111111111111111 | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1776: | |
|-----------|---|-----|
| | TAGACACAGT GCAAAATCTG GTACAGCTTA TGGAATTAGA CGGGTAAAGC AAATTACTGA | 60 |
| 5 | GTACCCA | 67 |
| | (2) INFORMATION FOR SEQ ID NO: 1777: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1777: | |
| | GTATGCCAGT GTCATTGCTG AAAACATCAA CCATTCCCTG CACCAAAATT ŢTTTGGTAGA | 60 |
| 20 | GTTTGATGCT GGCCATCCTC CAAGGGACTA AGGGTAATTT TGnTTAAAAA GAGCCAAAGG | 120 |
| | CCCAATG | 127 |
| | (2) INFORMATION FOR SEQ ID NO: 1778: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 236 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| <i>30</i> | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1778: | |
| <i>35</i> | GAACCCAAAA ATTAGCAACA GTGGCTACAA TAGTTGGGCA CTGAAAGCCA GCCAAGTGGG | 60 |
| 55 | ATTTTTAGCC CTTGATTTGA AAGCGGGGTC CCCAGGATTA AAAAATTTAA ATTAGCCTAA | 120 |
| | TAAGCCCAAA ATTCCCATTT GGAAAAGGAA ACCTCCTTAA ATTGGGTTGG AAAAAAGnTT | 180 |
| 40 | AAAAAAAAA AGGCCCAGnC CTTGGAATTT TTTGGAATTG GAAAAAGGAA TTAAAA | 236 |
| | (2) INFORMATION FOR SEQ ID NO: 1779: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1779: | |

| | (2) INFORMATION FOR SEQ ID NO: 1780: | |
|----------|---|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 231 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1780: | |
| | GACGACTCGC TTCTATTTTA AAATCCGGCG TACTTGGTTA TATAAATATC ATAATGGTTA | 6 |
| 15 | AAATTAAAAA GCAATGTCAG TTCACACTAT TACTGACATT CTTTTAGTTA TGTGTATATT | 120 |
| 75 | ATTCATTCAC AAGCTTTTGG TCTATAAATC GAGTGATTTG CTTTGTTTGT ATATAACCAT | 180 |
| | CTGCTACATA TTCATCGTTC ATTGTAATTA ATGGATAAAA TAGTTCATCn n | 23: |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1781: | • |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 209 base pairs (B) TYPE: nucleic acid | · · |
| 25 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1781: | |
| 30 | GTCTCCCTGC CCCACATTTA ACATTGTAAT TTTGTGATGT GAAATTTGTTG GAAACGTTAT | 60 |
| | TAATAATGTC AGAATAATTA TAGTCCAAAA CGTAACCAAT ATATATTTAC GTTTAGCCAA | 120 |
| 35 | TAACCAAAAT ATGTAATAAA CAGAAATTAT AAATACTATA AATATCCAAT CATTAAACTT | 180 |
| 35 | GGGAACAGAA AAATGTGATT GCTTGATTC | 209 |
| | (2) INFORMATION FOR SEQ ID NO: 1782: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1782: | |
| | GTTAAACTTA GTTAGATAAA ATGCAAATCA CATTATTGTA GATAGTCTCT TTTC | 54 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1783: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs | |

(C) STRANDEDNESS: double

| | (b) Topologi: Timear | |
|----|--|------|
| 5 | | |
| _ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1783: | |
| | TCTGGAATGT CTCCTTGTCT CTCTATATAG CTATAGTCCG TCGCAAGCGG ACGTAATGTT | 60 |
| 10 | CATTITCATA ATGATTATAG TATGAAAGCG CITTCITGTA TATGTGACAT GTGCGTGTnG | 120 |
| | (2) INFORMATION FOR SEQ ID NO: 1784: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1784: | |
| | CTACCATTTA CATAAAGACC GTCTAATTCT TCAGTTTCAA TGGCATTTTG GAGCAAT | 57 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1785: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 30 | (D) TOPOLOGY: linear | |
| | • | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1785: | |
| 35 | TCATAACCAT TACCAAGTAT CCAAGCAGCT TTTAAACAAT ATGGCATAAA CATT | . 54 |
| | (2) INFORMATION FOR SEQ ID NO: 1786: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1786: | |
| | GGATGGGTGA TTTTAGCAGG TTTGGCTATG AGTACCGTAT TTGCATTAGG ACCGATTTCA | 60 |
| 50 | TTTAACAAAA TCATAATTTT GGGC | 84 |
| | (2) INFORMATION FOR SEQ ID NO: 1787: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 134 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|--|-----|
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1787: | |
| | CCGGTTTACC CTTAAAATTA TTTTTTGGGG GGTTCCATTA AACCTTCCAA TTCCCAATTA | 60 |
| 10 | ACCCCHACCC CCCTGGGTTT TCCTTAAAAA CCAAAAGGCC CTTTTTTTC CCAACCCAAC | 120 |
| | CTTGGGGGAA TTGG | 134 |
| | (2) INFORMATION FOR SEQ ID NO: 1788: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 70 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1788: | |
| | TATATCAACT AAAAAGCGCA TCTGCAACCG ACGGTTGAAA ATTTGGACAG GAGACAGATA | 60 |
| 25 | ATGTAATATA | 70 |
| | (2) INFORMATION FOR SEQ ID NO: 1789: | - |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1789: | |
| | AATATCCAAT TATACAAGCA GGTATGGCAG GAAGTACGAC ACCGAAATTA | 50 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1790: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 45 | (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1790: | |
| 55 | TGATTTACTA GCTGAATCCG ACATGCTTGA TGATACACTA TGTGAATTCA | 50 |
| | (2) INFORMATION FOR SEQ ID NO: 1791: | |

| 5 | (A) LENGTH: 58 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|----|---|------|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1791: | |
| 10 | CCGGACGCTT TACTTCCAAC TTTAGGTGGT CAACACAGGT TTAAACATGG CGATGTCA | 58 |
| | (2) INFORMATION FOR SEQ ID NO: 1792: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1792: | . 50 |
| | CATCATCCTC TAATTTAGTC CAAACTCCTG GATGATATCC AAATGAAGTT CCAATTGA | 58 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1793: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 62 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1793: | |
| 35 | CACAAGTTTT AGAAGGAAAC CAATAACAAA TGACGAGATT AATTGCCACA AACATTAACG | 60 |
| | AC | 62 |
| | (2) INFORMATION FOR SEQ ID NO: 1794: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 103 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| 45 | (b) Topologi. Timedi | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1794: | |
| | AAGGCCCGGG GGGTTTAAAA AAAAAGGTTT AAAAAAGGTT TTGGCCCTTT AAACCCAAAG | 60 |
| 50 | GGAAATTTTA ACCCCAAAAA AAAAAAACCC CTTTGGGAAA GGG | 103 |
| | (2) INFORMATION FOR SEQ ID NO: 1795: | |
| | | |

| 5 5 | (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|--------------|--|------|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1795: | |
| 10 | TATCGATCGA TCATGTCGAA TCGATCTGTC GATCGATCGT ATCGATCGAA TCGCGTCGAA | 60 |
| an 's elemen | TCGAATHCGT CGAATCGATG CTATCGATCG AATGCTATCT GAGTCGAATC ACGTCGATCT | .120 |
| | G | 121 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1796: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 62 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1796: | |
| | AATTCATGTT AAAATCCTCC TGATATTAGA TGGCCCATTT TTATTTTTTT CGTTTCCATA TA | 62 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1797: (i) SEQUENCE CHARACTERISTICS: | |
| <i>3</i> 5 | (A) LENGTH: 397 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1797: | |
| 40 | CATACTOGAC AATTTAGATG GTGAATACTT ATCATTTAAG TCCTTTGACA CCTCATCTAA | 60 |
| | AATTCTAGGA CTTTTAACAA TTTCTTTATA CGTATTTACA AGTTGAATAT TACTTTGAAC | 120 |
| | CTCTTGCGCC ATAAACTGAG GATTGTCACC CTTAGTTTGA TTCACTAAAA TTTGAGTATT | 180 |
| 45 | AGCTTGATAT TTAGGTGATA AGACGAAAAA TGTAACAATA GCGCTAATAA TTAAAAATAA | 240 |
| | TAGCGGTAAA ATAATTAAAA TCTTCAAGTT TTTTTGTAAT ACTTCTTTAA TTTTTGTTAA | 300 |
| 50 | TTCTAATGTA CTTTCCATTA TTTACCTCCC TTAAAAATTT TCATTAAAAT TGGTATTATA | 360 |
| <i>30</i> | TATATAGTAT TTACATATTA CATATCGTTT AAACAAT | 397 |
| | (a) Typesty Top Ope TD NO. 1700 | |

| 5 | (A) LENGTH: 66 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|---------|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1798: | |
| 10 | CGGGTAACAG CGAATGGTGT GTCACCGTAT ATAACTTTAC TATTTAATAT TTGGCCTGTT | 60 |
| | GCTTTC | 66 |
| | (2) INFORMATION FOR SEQ ID NO: 1799: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 77 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| • | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1799: | |
| 25 | GTTGCTAAGT TTGTATTACA ATTTAAATGA TTTTTAGCTT GAGTAAGTTT ATTTAAAGAT | 60 |
| | GCAGTAATTT CGCTAGG | 77 |
| | (2) INFORMATION FOR SEQ ID NO: 1800: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 172 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (b) Topologi. Timeal | |
| | (| |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1800: | |
| 40 | TAATGCTATT TAATTTTCTA CTTCCTAAGC TTCCACCCAT AACGAGTAAN ACTTTTTTAT | 60 |
| | TITCATTAAA GCCTGTTAAT TGATAACCAT TATGTGCATT ACCATTTITT AAATCTTCTC | 120 |
| | GAATTGTTGC TCCAATAAAA TCAGCTTTCT CTTTAGGTAA GTAGTTTAGC GT | 172 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1801: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 140 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| <i></i> | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1801: | |

| | AGTAAAATTT GTCATCACGA TCAGCAAAAG CTTTTGATTC TGACGTATCT TCCATAAATG | 20 |
|----|---|----|
| 5 | ATCTAAAAAT TGGTAGTTCG | 40 |
| | (2) INFORMATION FOR SEQ ID NO: 1802: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs | |
| 10 | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1802: | |
| | ATCCCCCGTA CAGACTTCAG CTTACGTAAA CATGCTGAAC ACTCTAGTGA AGATTTCAAA | 60 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1803: | |
| | (i)_SEQUENCE_CHARACTERISTICS: | |
| | (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | • |
| 25 | (D) TOBOLOGY, linear | |
| | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1803: | |
| 30 | CAATTTAAAT GCATCTTTCC CATTAATTTC ATTTGTTGTC GCTTTAGCTG TGTTAATTAA | 60 |
| | (2) INFORMATION FOR SEQ ID NO: 1804: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 35 | (A) LENGTH: 50 base pairs | 1 |
| * | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1804: | |
| , | ACTTGATCGA AAAGGTTTCA TACCGGTAAA CGATAAAGTT GAAACAAATG | 50 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1805: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid | |
| 50 | (C) STRANDEDNESS: double | |
| 55 | (D) TOPOLOGY: linear | |
| | | |
| | | |
| 55 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1805: | |
| | | |

| | (2) INFORMATION FOR SEQ ID NO: 1806: | |
|------------|--|---------------------------------------|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 70 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1806: | |
| | AAGAACTGTC TATGAATATT GGATGACGCT TTGATGAGAA CATTAGTAAG CCATTTGTTC | 60. |
| 15 | AAGGAGTACA | 70 |
| | (2) INFORMATION FOR SEQ ID NO: 1807: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 77 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1807: | |
| | TAGCATTTCT AATGGAATCC AATCTTACCG AATGACAATT GGAATATAAC TGGTGATAAT | 60 |
| 30 | GTTGAATGGT CCTGTGA | 77 |
| | (2) INFORMATION FOR SEQ ID NO: 1808: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · · · · · · · · · · · · · · · · · · · |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1808: | |
| | CCCGGCCCAA AACCCCTTTT TTGGGTAAAA AATTTTTTTT AAAAAGGGAA AAATTTCCCC | 60 |
| 4 5 | TTTTTTGGTT CCCAAATTTT AAATTAGAAA GGGCCCCCCC TTCCCCCCCA AATTTTTCCC | 120 |
| | A | 121 |
| | (2) INFORMATION FOR SEQ ID NO: 1809: | |
| 50 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| | (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 1809: | |
|----------|---|------|
| 5 | AAGTTTGGTG AAGGAACCAC GTGCATGATG GTGTTCAAAC AATGCGTTAC GATGTTGACG | 60 |
| • | (2) INFORMATION FOR SEQ ID NO: 1810: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 base pairs | |
| 10 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | * |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1810: | |
| | TGGTTGAGAA AACACAGCGT TAAAGTTGAG GTATTTCAAA AGACAAGTTG GAACATTA | 58 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1811: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| • • | (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid | - |
| 25 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | - 0. |
| 3 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1811: | |
| 30 | CTTAAATAGC AAGTGGTTTT ATAACAACTT TGAGTTATCT CAATATAGTT ATCGC | 55 |
| | (2) INFORMATION FOR SEQ ID NO: 1812: | , |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEO ID NO: 1812: | |
| | (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 1812: | |
| | TAAGTCTTCA ATTTTTCAG TTGATACACC TAAGTGATAC AGCCATTCTT | 50 |
| 45 | | 50 |
| 45 | TAAGTCTTCA ATTTTTTCAG TTGATACACC TAAGTGATAC AGCCATTCTT (2) INFORMATION FOR SEQ ID NO: 1813: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs | 50 |
| 45 50 | TAAGTCTTCA ATTTTTTCAG TTGATACACC TAAGTGATAC AGCCATTCTT (2) INFORMATION FOR SEQ ID NO: 1813: (i) SEQUENCE CHARACTERISTICS: | 50 |
| | TAAGTCTTCA ATTTTTCAG TTGATACACC TAAGTGATAC AGCCATTCTT (2) INFORMATION FOR SEQ ID NO: 1813: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 50 |
| | TAAGTCTTCA ATTTTTCAG TTGATACACC TAAGTGATAC AGCCATTCTT (2) INFORMATION FOR SEQ ID NO: 1813: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 50 |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1002 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1814:

| TGGTCATGCG | GGAAATACTA | GGACATGAAA | ATTATGCTAA | AGGCATCAAA | GTAACTGAAA | 60 |
|------------|------------|------------|------------|------------|------------|------|
| ATAATGGCGT | AGTGGATATA | GATATGTACA | TTATTGTAAG | TTACGGTGTG | AAAATATCTG | 120 |
| AAGTTGCCAA | TAATGTACAA | TCAACAGTGA | AATATACTTT | GGAAAAATCA | CTTAATGTAT | 180 |
| CAGTAAATTC | AATCAATATA | TATGTACAAG | GTGTACGTGT | GAATAATACA | GGCAAGAAAG | 240 |
| CTTAGGAGGA | CAACTTGAAA | TGATTAGCAA | AATTAATGGT | AAATTATTTG | CCGATATGAT | 300 |
| TATACAAGGG | GCACAAAATT | TATCTAACAA | TGCAGATTTG | GTAGATTCTT | TGaATGtGtA | 360 |
| TCCAGTGCCA | GATGGtGATA | CAGGAACAAA | TATGAATCTT | ACTATGACTT | CAGGTCGCGA | 420 |
| AGAAGTAGAG | AATAATTTGT | CGAAAAATAT | CGGCGAATTA | GGTAAAACAT | TCTCGAAAGG | 480 |
| TTTACTAATG | GGTGCAAGAG | GTAACnCTGG | TGTCATCTTG | nCACAATTAT | TCAGAGGATT | 540 |
| TTGTAAAAAT | ATTGAAAGTG | AATCTGAAAT | TAATTCAAAA | TTGTTAGCTG | AAAGTTTnCA | 600 |
| AGCTGGTGTT | GAAACGGCAT | ATAAAGCTGT | TATGAAACCA | GTTGAAGGTA | CAATACTTAC | 660 |
| AGTTGCAAAA | GATGCTGCGC | AAGCTGCAAT | AGAAAAAGCA | AATAATACTG | AAGATTGTAT | 720 |
| AGAATTAATG | GAGTACATTA | TTGTAAAAGC | CAATGAATCA | CTTGAAAACA | CACCAAACTT | 780 |
| ATTAGCTGTA | CTTAAAGAAG | TTGGTGTTGT | TGATAGTGGC | GGTAAAGGTT | TGTTATGCGT | 840 |
| TTACGAAGGA | TTCTTAnAAG | CGCTTAAAGG | TGANAAAGTT | GAAGCCAAAG | TTGCAAAGAT | 900 |
| agataaagat | GAATTTGTAC | ATGATGAACA | TGATTTCCAT | GGTGTAATTA | ATACTGAAGA | 960 |
| TATTAATTTA | TGGCTATnGT | ACTGAGATGA | TGGTTCGTTT | TG | · | 1002 |

(2) INFORMATION FOR SEQ ID NO: 1815:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1815:

| | CHAITATH CHAITATHE ATAATATH CACTCAAAAA | 120 |
|----|--|-------------|
| 5 | CTGTTTTCCA ACATTGATTT ATTGTTGGAA AATCTCGAAA ATCTAGTCTA TTTCTCCAAC | 180 |
| | AATCGAAGA: TTATGCCCTT TTTTCTCCCT TTAAATAAGT CATAATACGA GGCATACATG | 240 |
| | CAACATTTAC AATAAAATAT GTTCCTACAT CGTATTATAC GAATGCTCAC ACTTATAGTT | 300 |
| 10 | GTTTAGTAAA CCCAGATGTA TTGCTAACAT ACCCATNANC NCTATATAGT T | . 351 |
| 1. | (2) INFORMATION FOR SEQ ID NO: 1816: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 62 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (b) Topologi: Tillear | •: |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1816: | 2 |
| | ATATCGTATC CCATGCGGGA AGGGCTTTAT TTATACTGTG CACGATGAAT GCGCACAACG | 60 |
| 25 | GG | 62 |
| | (2) INFORMATION FOR SEQ ID NO: 1817: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 70 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | : |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1817: | |
| | AAAGGGGGA AATTTTTTT TTTTGGGTTT GGGGGGAAAA TTTTTTTT | 60 |
| 40 | TTTAAATTAA | 70 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1818: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1818: | |
| | CAAGTTCGGA ATGCGAACGC GTCTTAATCT ATATACAAGT GATGCACTCC A | 51 . |
| 55 | (2) INFORMATION FOR SEQ ID NO: 1819: | |

| 5 | (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|------------|--|-----|
| - | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1819: | |
| 10 | TCGCCATACT ATCGACAGCT GCTAAAATTG CGCTCTTCTT GTGTCGCAAT CG | 52 |
| | (2) INFORMATION FOR SEQ ID NO: 1820: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1820: | |
| | CAAATTGGGG AAATTACTAG AAATGAAGAT ATTTATAAAG ATGACTGGAC GTCAACTT | 58 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1821: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 58 base pairs (B) TYPE: nucleic acid | |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1821: | |
| | ACTGCTTCAG CACCTGTATT CATTGGGGAA AGCTTTATCG TTGACCGGCC AGTTTACA | 58 |
| : . | (2) INFORMATION FOR SEQ ID NO: 1822: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 190 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1822: | |
| | ACCTGTTGCT CGTGTCATAA ATAGGTGACT ATAAATCTCT GTTCAATATA CTTTTCGTTT | 60 |
| 50 | TTCCAATCTT AAAGGTCGAT GTTCGTGAGT AATCTTATCT CTGGnCCAAT TTTAATGTCA | 120 |
| | TGATATGTTC ATAGTATCAC CCCTTTGTTG TGTAATAATA ATCAGGTGGG TGGTTAGAAC | 180 |
| 55 | GGTGTGAATA | 190 |

| <i>5</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|--|-----------|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1823: | ٠. |
| | AGCnTTAGCn TATGGTTTAG ACACAACTGn TAAAGATGCn AAGTTCTTGT | -50 |
| | (2) INFORMATION FOR SEQ ID NO: 1824: | |
| 15 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1824: AAAAATTGGA AAAAAGGGGC CCAAAGGTTA ACCCAAATTG GAAAAAAACC CAAATTTTTT GGAAATTAAC CCAAAAATTG GCCCCCAATT GGAACCCAAA AT | 60 102 |
| | (2) INFORMATION FOR SEQ ID NO: 1825: | 102 |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1825: | |
| 40 | ACGTACCAAT GTCATAATCA GTCATTTTAC CACTCTTAAT AATCTGCTTC CGGGCAA | 57 |
| | (2) INFORMATION FOR SEQ ID NO: 1826: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 61 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ÷ . |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1826: | |
| | ACCATCTTGT ACAAAGTGGA TGTCATATGC ACCATCTTGT GTTTTGAGCT GCATTTAATT | . 60 |
| <i>55</i> | G · | 61 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|--|----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1827: | |
| | ACCOTTTCGC CAAGCCGACC TAATTTCTCA GCAATATTTC TTTCTACGCC ACCAAT | 56 |
| | (2) INFORMATION FOR SEQ ID NO: 1828: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 62 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 20 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1828: | |
| 25 | ACTTATAGGG CGCACTTATT TTTCGCTTCC ATAGCGAAAC TAGTGTCACT TATACGTATG | 60 |
| | TG | 62 |
| | (2) INFORMATION FOR SEQ ID NO: 1829: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (b) Toronosi. Timear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1829: | |
| 40 | GCTACACACG ATTTACCTTT CTTGTCACGT TTTGCGACCA TCATTGTGAT GATA | 54 |
| | (2) INFORMATION FOR SEQ ID NO: 1830: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 67 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1830: | |
| | GTAATGACCA TCGCTGATTT ATGACATTGT TAGATCTCAT GTGCCATTTA GTCTGCTGAA | 60 |
| 55 | TCTTGGG | 67 |

| 5 | (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear |
|----|--|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1831: |
| | ATAACTCTTC GnCAAACTCC TCAACAAACT TCTTGTGTTC CATCTTCTGG |
| | (2) INFORMATION FOR SEQ ID NO: 1832: |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 base pairs |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear |
| 20 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1832: AAACGTMAGA ATATTTAATG GAGCCAAGAA TGGTTTACAG ACGGAGAAAT GGGATATGTT 60 |
| 25 | GAAGCGAGGC GTACGCGGAA AGCGTACTAG GCTAGAACAC T 101 |
| | (2) INFORMATION FOR SEQ ID NO: 1833: |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear |
| 35 | (2) 10102001 111041 |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1833: |
| 40 | TCGTCATCAT GTCTGTGTTA CCAACGTTTG ACGATTTANT TCATGCNGAA 50 |
| , | (2) INFORMATION FOR SEQ ID NO: 1834: |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1834: |
| | ATAAGTTAAT TGATTTATTG ATAAAGAGAA GCCAGATTTA AATATTATTA AACGT 55 |
| 55 | (2) INFORMATION FOR SEQ ID NO: 1835: |

| 5 | (A) LENGTH: 58 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|----|--|-----|
| 5 | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1835: | |
| 10 | AAACAAGAAC CCCCATATGG TTAAGCTGCG CGTTTCAACA TACGGGGGGT TTTCATAT | 58 |
| | (2) INFORMATION FOR SEQ ID NO: 1836: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1836: | |
| | TACGTTTTAT AAAAACAAGA ACTAAAGTAT GCAGTGTGAA TTGTTCACTT TChTGGCGTT | 60 |
| 25 | GGAATTGATT AAAACGAGAT ATGGTGTTGT GGAAGTTGTT TGTGTTTGCA TATTTTAAAC | 120 |
| | CGATT | 125 |
| | (2) INFORMATION FOR SEQ ID NO: 1837: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1837: | |
| 40 | AATCTACAAT CCTGAATCAC TCGTTAAGAT TAAAAGTATC GACAATGAGT ATCTGAACAT | 60 |
| | GAGCTCATCT GCCGTTTTTA ATGCNAAAAA CCGGCGGCGG GATATTTTTG ACCACGGC | 118 |
| | (2) INFORMATION FOR SEQ ID NO: 1838: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 50 | (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1838: | |
| | AUTOROGO DE DESCRIPTO DE CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA DE LA CONTRA DEL CONTRA DEL CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DEL CONTR | 60 |

| • . | GTCCCAGTIT TTGGGATTGC C | 141 |
|-----------|--|---------------------------------------|
| | (2) INFORMATION FOR SEQ ID NO: 1839: | * * * |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 10 | | * * * |
| i-a. | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1839: | |
| 15 | TCTGGGGACT AAGTATGTCT CAGGCTTTAT GCTGTTATGT TTGAAAATGA AAGG | 54 |
| , | (2) INFORMATION FOR SEQ ID NO: 1840: | • |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 20 | (A) LENGTH: 133 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | · · · · · · · · · · · · · · · · · · · |
| | (D) TOPOLOGY: linear | |
| | | * * |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1840: | |
| | ATTAAAAAAC CTTTTTAAAC CGGGAACCCA AGGAAAAATT CCGGGTTTTA ATTAAAACCT | 60 |
| 30 | TTTGTTAATT GGTTCCAAAC CAACCTTTTG GGTTAATTTT AACCAGGAAT TTTGGAAAAC | 120 |
| | ngttttattt gga | 133 |
| | (2) INFORMATION FOR SEQ ID NO: 1841: | • |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | , |
| • | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1841: | e . |
| | AAAGTATGGA TTGATCGTGG AGAAGTTCTT CCTACTAAGA ACACTAGTCG | 50 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1842: | 131 |
| • | () CHOWNESS OF THE PLANTAGE | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid | |

| 5 | (2) INFORMATION FOR SEQ ID NO: 1843: | |
|----|---|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs | |
| 10 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1843: | |
| 15 | CTGAGATGAA TATTGTGTTT CGCCATACAT ACTGGGTAAT ATCCCAACCA TTGCTGTAAA | 60 |
| | (2) INFORMATION FOR SEQ ID NO: 1844: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1844: | |
| | CATTACCTGT AAAAGGAAGC TAAAGACGAT GAGTATTTAT AGAAACCAAT TGCCGACCAT | 60 |
| 30 | TTGCAGCCAT TAGGAGGGTA GGAGGGCAAT CGCGnCCAAA GGTTATTAAC CGTCAATTAC | 120 |
| | CTTGA | 125 |
| | (2) INFORMATION FOR SEQ ID NO: 1845: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 126 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 40 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1845: | |
| 45 | ATCCACCTGG GTTTGTTCTT AATTTAACCT GNTAATTAAT TGGGTTGGGT CCGGCAAAAG | 60 |
| | TCCGGACCTG CAAATCGGAT TTTATCGTTA AATCTTGAAT TCTATTGCCC ATATTAAATC | 120 |
| | GCAAAT | 126 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1846: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1846: | |
|----|--|-----|
| 5 | TTTTGGGAAT AAACCAATTA ATCATGGGCA AAAAATAAGC AATCCAAGTA CTTACTA | 57 |
| | (2) INFORMATION FOR SEQ ID NO: 1847: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1847: | ÷. |
| | TGATAAATAT TTCATCTAAA GAGAGGGAGT CATTATGACA CTACTTACTG | 50 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1848: | |
| 25 | (i)-SEQUENCE-CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | - , |
| , | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1848: | • |
| 30 | ATCTAGGCAA TGAATGGACG GACTTAATAT TGATGTGCAA CAAGAAGAGG AGAAGCGAAT | 60 |
| | CAATA | 65 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1849: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 244 base pairs (B) TYPE: nucleic acid | |
| 40 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1849: | |
| 45 | CGTGTGAAGT CATTACTTTT AATCCCATGA TGATGGTGAT GGATGAGACG ATATCTCTCT | 60 |
| | GTCTTTAACA GTTAAGTCCA ATTCTTCCAA CGAAACTTTT CCATAGGTTG TTTTATAAGT | 120 |
| | TGGAATACTT GCACAAATCA TACCTAATTG CTTATCAATT TTCTCAAGAC TGTCATCAGT | 180 |
| 50 | TATAAGATCA ATTITATTAA TAATAATCAT GTCACTTAGT TTCAACTGAT CTTCCATCAG | 240 |
| | GCGA | 244 |

(i) SEQUENCE CHARACTERISTICS:

| 5 | (A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|--|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1850: TTTAAAGGTT CCCGGAAAGG TTTGAAACCA AACCTTTGCC CCGGCCCCCC GGGAAAAAAA | 6(|
| | AAAnttegtt taacccccgg ggggggggc ccttaaaaaa acccaa | 106 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1851: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1851: | |
| 25 | TTTTTTAAGG CCCTTGGGGG GCCAATTTC CCCCCCCC AACCTTCCAA AGGTTGGGGG | 60 |
| | GCCTTTTTT TTAAATTGGG GGGA | 84 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1852: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1852: | |
| 40 | TCATGATTAA AATTCAACAA TTACAACATC ACTTTGGATC ACATAAGAGT AA | 52 |
| | (2) INFORMATION FOR SEQ ID NO: 1853: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1853: | |
| | ATAAAACATT TCAAGATGCG CTTGTAATTG TATGTGATAC TGCCAATGCT CCACGA | 56 |
| | | 20 |

| _ =- | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid | | | = |
|----------|--|-------------------|--|------------------|
| <i>5</i> | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | |
| | (0, 00000000000000000000000000000000000 | • | | |
| | | | • | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ I | D NO: 1854: | | ř |
| | AAAAGATCAT GCGCATAATG ACATGGTGAT GATA | TGAGTA TGATGGTGGG | TACA | 54 |
| | (2) INFORMATION FOR SEQ ID NO: 1855: | | | |
| 15 | (i) SEQUENCE CHARACTERISTICS: | () | | |
| | (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid | | | |
| | (C) STRANDEDNESS: double | | | |
| : | (D) TOPOLOGY: linear | | | |
| 20 | | | • • • | |
| | · | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ I | D NO: 1855: | | |
| 25 | ACAACAAATG GTAATGCATA AACATACAGC CAAT | AGCTAC AATTGCACGA | CG | 52 |
| 23 | (2) INFORMATION FOR SEQ ID NO: 1856: | | | - |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | • • |
| | | g | | 4 |
| | | * | • | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ I | D NO: 1856: | w | |
| • | ACGGCTGCAC TCATCATGGT CTGTGGCGTG ATTG | TTAATG TTTTAGTTGC | CCGCTTC | 57 |
| | (2) INFORMATION FOR SEQ ID NO: 1857: | | | |
| 40 | (i) SEQUENCE CHARACTERISTICS: | | • | |
| | (A) LENGTH: 192 base pairs (B) TYPE: nucleic acid | | ************************************** | |
| | (C) STRANDEDNESS: double | | | |
| | (D) TOPOLOGY: linear | | 3 | |
| 45 | | | | |
| | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ I | D NO: 1857: | | - |
| 50 | GCAGATAACT TCCTTGATCC TAACAAAGCA AGTT | CTCTAT TATCTTCAGG | GTTTTCACCA | 60 |
| | GACTTCGCTA CAGTTATTAC TATGGATAGA AAAG | CATCCA AACAACAAAC | AAATATAGAT | 120 |
| | GTAATANACG AACGAGTTCG TGATGACTAC CAAT | TGCACT GGACTTCAAC | AAATTGGAAA | 180 |
| 55 | | | | |

| | (2) INFORMATION FOR SEQ ID NO: 1858: | |
|----|--|----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 77 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1858: | |
| | CGCTGCACTT CCTGAACGCA GTGAGACCAG AACGTGGTGT CACTTTCGGT CTATTCCGGT | 60 |
| 45 | TAAGTGTTGG TCTCGGA | 77 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1859: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1859: | |
| | TTTGGCGTTC GTGATTTTCT CTAGACGTAG TAACTTTCCC ACTCTTTGCG TCC | 53 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1860: - (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | THE | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1860: | |
| 40 | TTTCTCACTC GCGCATTTCA GTTTGTTTTG ATTTACCCGT CTCTTCTATT TGTCTTAAT | 59 |
| | (2) INFORMATION FOR SEQ ID NO: 1861: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1861: | |
| | AATGAATGTA TGCACATTAA CATCATCAAT TAATCCTTTT AATAAATTGA GTTGTAATTT | 60 |

| | (2) INFORMATION FOR SEQ ID NO: 1862: | |
|-----|--|------|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| . * | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1862: | |
| | ATTAATACTG AGCAAATGTG CATAAGACAT CATGAATTAG CACCAATTTA CAGG | . 54 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1863: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 89 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| - | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1863: | |
| | TTTAACCATC ATTCTATGTC AAAGTTTTGA AATGATGGTT ATTTTTATT GCTTAAATTT | 60 |
| | ATTATTGCTA CTACTATACC AATGAAAGT | 89 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1864: | |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 400 base pairs(B) TYPE: nucleic acid | |
| 35 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1864: | |
| 40 | AAAGCTGGTA CGCCTGCAGG TACCGGLCCG GAATTCCCGG GTCGACCCAC GCGTCCGGAA | 60 |
| | CCAAAATTGC ATCTGATGGT CTCAAGGGTC GTGTGTTTGA AGTGAGTCTT GCTGATTTGC | 120 |
| | AGAATGATGA AGTTGCATTT AGAAAATTCA AGCTGATTAC TGAAGATGTT CAGGGTAAAA | 180 |
| 45 | ACTGCCTGTA CTAACTTCCA TGGCATGGAT CTTACCCGTG ACAAAATGTG TTCCATGGTC | 240 |
| | AAAAAATGGC AGACAATGAT TGAAGCTCAC GTTGATGTCA AGACTACCGA TGGTTACTTG | 300 |
| 50 | CTTCGTCTGT TCTGTGTTGG TTTTACTGAA AAAACGGCAA CAATCCAGAT ACGGGANGAC | 360 |
| ou | CTCTTnTGCT GCAGCACCAA CAGGTnCCGC CAAATCCGGA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1865: | |

| 5 | (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|--|------|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1865: | |
| 10 | AAATGGCGTA TCTTTATGTA TCAACTAAGT AATCACCAAT TTCTTTCGGA T | 51 |
| | (2) INFORMATION FOR SEQ ID NO: 1866: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1866: | |
| | GTGTTGCGGA TAATCCGTCG ACATTAGCGT CTGAAGGTAT CATGAGGCAA CTGCGCAA | 58 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1867: | y. 4 |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid | |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1867: | |
| 35 | ACAGCAACTG ACCCAGTTTA CTACCGTCAC TCAAATCACA CAGGTGGTAT CAAATCAATC | 60 |
| | (2) INFORMATION FOR SEQ ID NO: 1868: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs | |
| 40 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | i. |
| • | (3) 10102001 22.002 | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1868: | |
| | CAATCTCTTA CCATTTATCT CAGCTGGTGA AAACGGTCCA TTACACTTAG AATAAA | 56 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1869: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

- 55

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1869: | * |
|-----------|---|-----|
| 5 | GCTATAGACT AGAGGTACAG CAAATTCATG TGTACAGTGA TTAGAAGGCG ATGAGCAAAA | 60 |
| | GTAAT | 65 |
| | (2) INFORMATION FOR SEQ ID NO: 1870: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 173 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 0 |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1870: | |
| 20 | GCTACTGGCG GGGGATAGTA ACACCCAATG TTACACGTAT ATACGTACGG CTTCTTGATA | 60 |
| | AAAAGATGAA GCCnTTACAA GTAGAGAGCG TAAGAACGTG ATCATCTAAA TGGTAAGGGT | 120 |
| | AGACTATCCC ATGCCATTGT GGGCGGTTGC ATAGGTACCA CGGCACATAG CGG | 173 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1871: | (4) |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 2 8 |
| • | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1871: | |
| 35 | GCTGTGGGAT TGTCCTTTGG CATGGGGTTA GGGAGAGCGT TTCTAAGGGG CGTTTGAAAG | 60 |
| | CCATTGATCC GTAAAAGGAC CATTGTTGGA AGCNGCCTTA AGAA | 104 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1872: | · |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 64 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | · |
| 45 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1872: | |
| 50 | CCATTATCTC AAGAGGTTCT AGTAAGGGGA TGGCATTTGC TTCTTATGAA TTTGACCAGA | 60 |
| | ATAA | 64 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 377 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|---------|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1873: | |
| 10 | GACAACCTAT TGTTTCCCTA CCATACTGTT GTCCGGTTTG ACAAAACGGC GTTCCACAAT | 60 |
| | CCATACATCG TGCACCTTGG ATAGAGGCAT CTTCTTTAGT AAATCGTTGT TGATATGCTT | 120 |
| 15 | TATGATGCTT CAAACGGTCT ACCAGTGATA ATTCACCTAA GTACTGTTTG TCATACTTCA | 180 |
| | TARATCCTTT ARATTCACCC ATCGTATCTC CCCCTTTCCT TARTACACAA CGGCTGGTTT | 240 |
| | ATGTTTAGCA TCGATTGTTT TGACTGTmCA TCGTAAAATG CAGCTAACAT CGCTTCATCT | 300 |
| 20 | TCCATTGTCA TGTGAAGATT TTGTGGCAAA nGGAATTTTT TGCATCAATG AATnGGTGAA | 360 |
| | CCTTTGGGGG TGACCTT | 377 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1874: | |
| ġo | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 78 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1874: | |
| | ATTATCTGAA TACGCAGCAG TTGCAGCACT TGATGGATCA GCAGTATTTA AAAGAGGTTA | 60 |
| | ACACATTACC CAATAGTG | 78 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1875: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1875: | |
| 50 | CTAAAAGAAG TTAAAGAGTG TGATGGTAGA ATTATATTAT TTATTGATGA AATGCCATAT | 60 |
| | GCTTGTAGGT GSTGGTAAAA CAGATGGTGC CATGGATGCA GGCAACATGC TAAAACCAAT | 120 |
| <i></i> | GTTAGCACGA GGAGAGTTAC ATTGTATTGG TGCAACAACT TTAAATGAAT ATCGAGAATA | 180 |

| | TGTTGAAGAT ACAATT | 256 |
|------------|--|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1876: | • |
| . 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 286 base pairs | |
| 10 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1876: | |
| 15 | AGCGCGAAAT TGAGCAAGCG GAACATGCGA CTGATGAAGA AAAACAAGTT GCTTTAAATC | 60 |
| | AATTAGCGAA TAATGAAAAA CGTGCATTAC AAAACATCGA TCAAGCAATA GCANATAATG | 120 |
| | ATGTHAACGT GTTGAAACAA ATGGCATTGC TACACTAAAA GGTGTACAAC CTCATATTGT | 180 |
| 20 | AATTAAGCCT GAAGCACAAC AAGCAATAAA AGCAAGTGCA GAAAATCAAG TAGAATCAAT | 240 |
| | AAAAGATACA CCACATGCAA CAGTTGATGA ATTAGATGAA GCGAAT | 286 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1877: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 74 base pairs (B) TYPE: nucleic acid | |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1877: | |
| 35 | ACTTCCAAAC ATGATAAAGA CAGACTACTT CACAGGTTTA AGGGAAGCAA CCACATTAGC | 60 |
| | GGGATTCACC CTAT | 74 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1878: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid | |
| 45 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1878: | |
| 30 | TTTCATTAAG TTCAAAAAAT CTCAATAACT TTAAGGATTG GTCCGCATAT TA | 52 |
| | (2) INFORMATION FOR SEQ ID NO: 1879: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|------|---|-----|
| | | |
| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1879: | |
| | ATACCCCTGA GATTAATTAC TTGTCCTTTT TTTAGAACAA CATCTCCTGG CTTTGTTTCG | 60 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1880: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1880: | |
| . ' | AATATCATTA ATAATATCAT TGATGCAAGT CCTATTGTGC ACAACTGGGG TGATTGCCTT | 60 |
| | (2) INFORMATION FOR SEQ ID NO: 1881: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | t |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1881: | |
| 7' . | ACAATGGCAC ATGGACTTAT GCCTGGGGTG TCCTGTTCGT CGCAGCATCA AAATGA | 56 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1882: | î |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| Θ., | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1882: | ~ |
| | TGCAAAGCAT TGGCACATGG CCAGTCAGTT TTACAACGTC GTGACTGGGA AAACCCGAGA | 60 |
| | ngcgacgttg taaaacgacg gccagtgcca agcttgcatg cctgcagtcg actctagagg | 120 |
| 50 | A | 121 |
| | (2) INFORMATION FOR SEQ ID NO: 1883: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | *, | | |
|-----------|--|---------------|---------------------------------------|---|
| 5 | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 1883: | | |
| | ACATTTAATG TATAACCAGT TTCAACATTG CCG | ATTTAGT GGCAG | CAGTT GCAGGA | 56 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1884: | 4 | | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | |
| | | * | 4 | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 1884: | • | |
| | TGCATCCATT_TGATTGAATT_TTATGTTTTG_ACC | AAAGCCG_GTTGC | AATGT_AC | 52 |
| | (2) INFORMATION FOR SEQ ID NO: 1885: | | | * |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | |
| 30 | | • • | · · | |
| | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 1885: | · · · · · · · · · · · · · · · · · · · | |
| | TGAAAAGTGG TGGAATGGTG TTAAAAGTTG GTG | GGTAATT TTAGA | GAAGA G | 51 |
| <i>35</i> | (2) INFORMATION FOR SEQ ID NO: 1886: | | · · · | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 95 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | |
| | | | * | • * * * * * * * * * * * * * * * * * * * |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 1886: | *. * | (*). |
| | TACACGAACC ATACTCACCA GGTTTTCGTG TCA | TGAGGCG ATATT | TTTTG TCATTTT | ATA 60 |
| ٠ | TACATTTATC CAAATTCATC TTTTAAATGT TGA | GT | | <u>,</u> 95 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1887: | | | |
| <i>55</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid | | | 1 |
| | (C) STRANDEDNESS: double | | | |

| | (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 1007: | |
|-----|--|----|
| | GCTACCAAAG GCGTTTTACC TATTGCTAGT CACTGCAAGT GGCTTAGCTA TGCAGATCAA | 60 |
| 5 | CTGGT | 65 |
| • | (2) INFORMATION FOR SEQ ID NO: 1888: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| ,,, | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1888: | |
| - | GTGGGACCAA CTGGCCGGTG ACGGTGGTAA AGGTGCTTCA GTCGTATTGA AGTGGGATGA | 60 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1889: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1889: | |
| | TGTTGGAGAA ACAGTTAACG AGGTTTAATG TTAAAAAAGC AACGTATCAT GGGTATA | 57 |
| | (2) INFORMATION FOR SEQ ID NO: 1890: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 64 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1890: | |
| · | TGGGATCTGC TTGCAAATAC ACAAAACTTT CTGGATTTTA TTACAATTGC AATATAATCA | 60 |
| 45 | AACA | 64 |
| | (2) INFORMATION FOR SEQ ID NO: 1891: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | * |

| | (XI) DEGOENCE DESCRIPTION. DEG | 10 10. 1031. | |
|---|--|--------------------|--|
| | GGCATCCACT CAGATAAAAT AAAGATGTCA AAAA | AGGCAAA GATGGTGCTA | AAAAAACAA 59 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 1892: | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs | * | |
| 10 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| · . · · · · · · · · · · · · · · · · · · | | | The second secon |
| | | | |
| ٠. | | | • |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ 1 | ID NO: 1892: | |
| • | GGTATCTCAA CGATCCTTTA GGTTAATTCG GAAA | ATTTCTA CACGTGAGTT | AGCA 54 |
| | (2) INFORMATION FOR SEQ ID NO: 1893: | | • |
| 20 | (i) SEQUENCE CHARACTERISTICS: | H | |
| | (A) LENGTH: 52 base pairs | *** | 10 |
| | (B) TYPE: nucleic acid | | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | 1 | |
| 25 | (D) TOPOLOGI: Tinear | • | |
| | | | \mathbf{r} |
| • | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ 1 | ID NO: 1893: | (F) |
| 30 | TTGTCTTGGC AATGGCAGAG CAACAGAAGT TTAA | AGTGCT TGCTGATCAT | AT 52 |
| | (2) INFORMATION FOR SEQ ID NO: 1894: | * | |
| | (i) SEQUENCE CHARACTERISTICS: | | |
| 1. | (A) LENGTH: 79 base pairs | · * | |
| 35 | (B) TYPE: nucleic acid | | |
| 3. | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | | | |
| | | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ 1 | ID NO: 1894: | |
| | TAAACCTATA CCCTGTAAAA AGAAAAATCG TGGA | ATCGAAA GAACATGTAT | GTGGCATTTA 60 |
| 45 | TGATTGATGC TCAAGCAGA | | 79 |
| | (2) INFORMATION FOR SEQ ID NO: 1895: | | |
| | (i) SEQUENCE CHARACTERISTICS: | | · |
| | (A) LENGTH: 377 base pairs | | |
| 50 | (B) TYPE: nucleic acid | \ | |
| | (C) STRANDEDNESS: double | • | |
| | (D) TOPOLOGY: linear | | |
| | | | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1895: | |
|---|---|-----|
| | TTATAAAGGA GAGAAATCCT TAATTATGAA TAAAGCATCA TTTGATAAAA AAGTTAAAAA | 6 |
| 5 | GCAATTATGG TTTTTGAACA AGAAGGAGAA ACAAGCATTA GATCAACGAT TGTCTTCTAT | 120 |
| | ATCTGATGAT GACAGCGTTA ACTTAAATAA GCCTGTTACC TTTGCTAATG CTTACTTAAG | 180 |
| | ACAAAATGTA TTTCGAAATA AAGAAACAAA AAGTTATAGT ATGTTTGTTA CATTAGTAGT | 24 |
| 0 | GATGATGTTT GCTTATGTTG CTTTATTAGG TTTGTnTTTA TTTGGGCTAA TTACAAGTCT | 300 |
| | ATCTGGCGTA CAATTTTCG TTAGTCCTAA GGTAGATTTA TCTACAACTG TTGTTATTTT | 360 |
| 5 | AACAATHATT GGAGCGA | 377 |
| , | (2) INFORMATION FOR SEQ ID NO: 1896: | |
| 0 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1896: | |
| | TTAGGATCCG TCTTTGCCGC AGCGTGGGTG TTCCGCGAGC GCTTCTTAGA GGTTTTGC | 58 |
| o | (2) INFORMATION FOR SEQ ID NO: 1897: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 445 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * . |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1897: | 4. |
| 0 | ATCGCTCAAA CCGAAATTGA AAATGCATCT ATTACTTCAT TAAGCCGTTT ACCAGACGTT | 60 |
| | ATATTAGCAT TGAAAAGTGG AAAGGTTGAA GGTGCTGTAG TTGAAAAACC TGTAGCAGAA | 120 |
| | GCATATTTAA AACAAAATCC TAAATTAGGA ATTTCCAATG TGAAATTTAA TGAAGAAGAA | 180 |
| 5 | AAAGATACAG TGATAGCAGT GCCAAAAGAT TCACCAAAAT TATTGTCACA AATTAATAAA | 240 |
| | ACGATTAAGG AGGTTAAAGA TAAAGGATTA ATCGATAAAT ATATGACTAA TGCTGCAAAT | 300 |
| | GCGATGAATG ATGACAGTGG TTTTATTTCT AAGTATGGTA GTTTTTTCTT GAAAGGAATT | 360 |
| 0 | AAGATTACAA TATTAATTTC ACTTATCGGT GTTGCATTAG GTTCTATTTT AGGTGCATTC | 420 |
| | GTTGCGTTAA TGAAATTAAG TAAAA | 445 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ÷ |
|-----------|---|-----|
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1898: | |
| | ACCTTTCAA TGTTGCTTTG ATATAAATTC ACAAAGTTGA CTTTTTAATT CTTCAATAGA | 60 |
| | TTCTCTACTG CGATAGCTGA ATTGCCATCT TTTCTACTAC T | 101 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1899: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | - |
| | | -) |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1899: TGCCCTGGAT GCCTTTAACT TGATTCATGA CCTGTGGTTT TATTTCAATT TAGATGAGCT | 60 |
| | ACCTTCAAGA CCTTC | 75 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1900: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1900: | |
| 40 | AGCAATACGG AACTGATGAA CGGAATTGTA ATACGAGAAT ATGAAGCATC AACG | 54 |
| | (2) INFORMATION FOR SEQ ID NO: 1901: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1901: | |
| | AGTACCTGAG TATCGCAGAC CGGCTTCAGG TCGTAGAATT TCTATACGTG GAGCTAGAAG | -60 |
| 55 | | |

| 5 | (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|--|----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1902: | |
| ,, | GTCTAACTAC AGCATGCCGG CTTATTGTTG CACTTTCTCA ATATTTCCAT A | 51 |
| | (2) INFORMATION FOR SEQ ID NO: 1903: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1903: | |
| | GGATTNAAAC GTGCATTAAC GCGTGTNTTA AATAGTTATG GTTTAAGTAG | 50 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1904: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid | |
| 30 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1904: | • |
| | ATCGTATTTA TTTCAGCGAG TAGCGGTAGC CTTCAATACA CAAAGATTTT ACC | 53 |
| | (2) INFORMATION FOR SEQ ID NO: 1905: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1905: | |
| 50 | ATAAGACGCT AGATCTGGTC AATTTATTTC CGATTTTTTC AACACTATTC | 50 |
| | (2) INFORMATION FOR SEQ ID NO: 1906: | |
| 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs | |

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

| | 5 | | |
|---|-----------|--|-----|
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1906: | |
| | | TTCATCTGAA TCGTCGGCTT TCGCGATTAC TTCTTCGTCA GGGTTGCTAT C | ,51 |
| 1 | 10 | (2) INFORMATION FOR SEQ ID NO: 1907: | |
| 1 | 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | (b) Torobosi. Timedi | |
| | | | |
| 2 | 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1907: | |
| | | CAATTGCTAA TAATCCTTTT AAGTCATTAA TGATTTGATC TTCCGTAATG TTGAA | 55 |
| | | (2) INFORMATION FOR SEQ ID NO: 1908: | |
| 2 | ?5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 3 | 30 | | • |
| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1908: | |
| | 35 | TTGCCAAACA GACATGACTT AAATTTCAAT ATCTTCTTTG ACTGCATCGA TAT (2) INFORMATION FOR SEQ ID NO: 1909: | 53 |
| 4 | 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 94 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1909: | |
| | | TGAATTICTA TACAATTATG GGGAAGGGTA TTGGTGAATT GGAATGGGCT CCTAAGTTTA | 60 |
| | | CAAGCCCCCA TTCGATGGCC GTTAAAGTTT TTAA | 94 |
| ŧ | 50 | (2) INFORMATION FOR SEQ ID NO: 1910: | |
| į | 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (XI) SEGUENCE DESCRIPTION: SEG ID NO: 1910: | |
|----|--|---------------------------------------|
| 5 | AACATGATCG TGGGGGGATG TTATGTTTGT TCATATATTT AGGAAGTCGT TTGTAGTTAT | . 60 |
| | TGTTTG | 66 |
| | (2) INFORMATION FOR SEQ ID NO: 1911: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . • |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1911: | • |
| 20 | ATCTTCGCTC CACTTACTGC AATAAGGATT TGCGGCAATC CTAAACCGTT TTTCA | 55 |
| | (2) INFORMATION FOR SEQ ID NO: 1912: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912: | • |
| | AACAATCGTA ACGATACAAC GCAATCTTCG AAAAATAATG CAAGTGCAGA TTTCCGAAA | 59 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1913: (i) SEQUENCE CHARACTERISTICS: | |
| , | (A) LENGTH: 51 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
| 40 | (b) Topollog1. III.eur | |
| * | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913: | • |
| 45 | ACACCACACA CACACACACA ACACCCCACA CAACACACAC AAACACACAA A | 51 |
| | (2) INFORMATION FOR SEQ ID NO: 1914: | · |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · · · · · · · · · · · · · · · · · · · |

| | (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1914: | |
|-----|---|----------|
| _ | TGTTACGACT TGGTCGACCT GGCAAGCGCT TCGCGCACGT TCTGCAGCnT CTCACTTATT | 60 |
| . 5 | GGTATCGCGA TGCGACGTTA AGAAATTTCG GAGTTCTGGT CACCTTATGT T | 111 |
| | (2) INFORMATION FOR SEQ ID NO: 1915: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915: | |
| | TGGTCCGCTC TCAATCGCAT CTTCAGGTTT TACTTGGCAA AAGAGCGCGG TGCTCA | 56 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1916: | v |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 62 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | Ry visit |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916: GCCGACAGTA AAATAAAGGT ACTTGATATA ACATATAACG GAAAGCAACA GTTACTGTCA | 60 |
| | CA | 62 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1917: | 62 |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 103 base pairs (B) TYPE: nucleic acid (C) STRANDENESS: double | : |
| | (D) TOPOLOGY: linear | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917: | |
| | ATGATATTTA TTTGATTGAA GAGATGTTGC TTAAACAAGA AGACGTACAA TTGATANAAC | 60 |
| | GTAAAGATTA TATTCAGCAC CCTAAAGAAA ATGGTTACCG CAG | 103 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1918: | |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 60 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |

| | (XI) SEQUENCE DESCRIPTION. SEQ ID NO. 1910. | |
|-----------|---|-----|
| 5 | CAGTGTAGCG TGTGTCATGC CGTTTTACCA CAATTGAAGA CTGAGCTCTA TCCCTGTGCC | 60 |
| | (2) INFORMATION FOR SEQ ID NO: 1919: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919: | |
| | TCAAATTAAC TTCCAACAAA AACAAATGCA AGGTGAAGAA ATTGCTGAAG AAGATTTACA | 60 |
| | AAAAGCGCAA GAACAAGCGC AAGCAATTGA AAAAGATGAA AACATCTCTn CATTAAT | 117 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1920: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920: | |
| | TGCCTAATGA AACATTTAAA AATATTTTTA AATATATCTA TCAACACATC GTTCTATTAA | 60 |
| | TTGGGATTGT TAGTTTTCTC AAAGGATTTT TAGGATTTTT CATGGAAAAA AATGGAAGTA | 120 |
| 35 | ATTTATATTT TGTTTCATTC CCGTTTTCAG TAGTCGTTGG ATTCTTTATT GTCTTTTAT | 180 |
| | TTATATGGTT TAGTTTTAAA ACAATACAAC TGCAGTGTTT TAACAATTCA AATTGGATAT | 240 |
| | GGATATTCAC CTATTTAGCA ATCATTCTAC TAATTGTAGG ATTTTTCTAT GTATTCTTTA | 300 |
| 40 | TTCCACAATC ATTACTTGCC TTTGGACCAT ATATTCAGGT AAGCAATTGG GTATTTATTA | 360 |
| | TATTTTCATT TATAGTTATG CCTATNGGAT TACGCATTGA | 400 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1921: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 122 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (D) 10200001. 22:000 | |

| | TORONOCCI CATTINATI TOCATITOR ATTENTIONS | • |
|---------|---|-----|
| | CATTAAGATT TATACAAGCT ATCTTTAACA TTGCCTTATC TTTGATATAT TTCTTGCATT | 120 |
| 5 | CG | 122 |
| | (2) INFORMATION FOR SEQ ID NO: 1922: | |
| 10 , | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 410 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | , |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922: | |
| | AGAAGATACC ATACACATTT BATTAGTTAC AGCATAAATC AATTTATACC CTTAATTATT | 60 |
| 20 | ACATTGTTTA TATTTTAAAT TCGGGGGAGT AATTTTAAGT AATATCTTGT TGCTGCTAAT | 120 |
| | TCTATTGTTA ATAAATTGAT ATTAGATGTA GAAATTGAGT GTGAAAGTTA ATAATAGATG | 180 |
| | ATTTAGCTAG TAACATAATT AATTCATATA TAGTCAAAAA GTTCTGTTAG ATACTGTTCT | 240 |
| 25 | TGATGAATAT TCTTTGATGT TAGGTGTTAG CTATTCTAGA TGAGTTTCTT AGATGTGGAT | 300 |
| • | GCCTGTCTTG ATGAAGTTAT CTATGATGTT AATATAATAC TTGATGTTGA TTCTTAGATG | 360 |
| | TTAGTGCGAT TTCAAGATGC TGATTCTTTG TTGTTGCACT ATCTTGGTGA | 410 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1923: | • |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 348 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ٠. |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923: | |
| 40 | TTTCTATGGT TTATCAGGTG ATTTTACGGA AAACAGTGAA GATTATGGCG TATACCGCTT | 60 |
| | TAAACGTGGA TTTAATGTAC AAATCGAAGA ATTAATAGGG GATTTCTATA AACCAATTCA | 120 |
| 45 | TAAAGTGAAA TATTGGTTGT TCACAACATT GGATAAATTA CGTAAAAAAT TAAAGAAATA | 180 |
| | GATGTAAATG ATGTTAGGGC TTATAGTNAT TGATACTATA GGCTCTTTTT TATATGTTTT | 240 |
| | TTAATAAAGC CTCGAATAAT GATATATTAA ATGACAAGTT TAACAAGTGA TTGCAATAAA | 300 |
| 50 | TATAAATnTG AATTGCACAA CCGATTTGNA AATGATTGAG TTGAGGAA | 348 |
| | (2) INFORMATION FOR SEQ ID NO: 1924: | |
| | 14, 61, 61, 61, 61, 61, 61, 61, 61, 61, 61 | |

| 5 | (A) LENGTH: 253 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|--|-----|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924: | |
| 10 | AGGGCAGATT TAAGCTAACT TGGAATGTTT TCGAGTTTTT GAGTTAGTTC TCTATCCATT | 60 |
| | TTTTCAGTTA CATGAGTATA TATGCGAATG GTTGnTTGTT CATCTACATG TCCTACCCTT | 120 |
| | TTCATAATTG CTTTTAAAGA AACATTCATT TCTACTAATA AAGTTATGTG TGTATGTCTA | 180 |
| 15 | AATGTGTGCG TGGTAACTTT CTTATTCATA TTTAAAGCTT TTGTACGTTT TCTTAACGCA | 240 |
| | CACCGGCCAT TTC | 253 |
| • | (2) INFORMATION FOR SEQ ID NO: 1925: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · · |
| 25 | (D) TOPOLOGI: Timear | , |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925: | |
| | GGTATAGGTG CAAGTCCTAT CTTCCGCTCC ATGGTTTAAT GATAATGCGG GA | 52 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1926: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926: | |
| , | TGGTCACTGT TCCTGATGCT TACGTTAGAA TGTAAGATTC CCGATTTATC AGTTATATAC | 60 |
| _ | TGTTTGCTTC ACTTTGGAGA TCTG | 84 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1927: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |

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| | CTTTCTAAAT AATTCTAGTA TAGTTTTTAT TCAAATACGC TAGGCTCAGA GCTATT | 0 |
|----|--|-----|
| | (2) INFORMATION FOR SEQ ID NO: 1928: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 138 base pairs (B) TYPE: nucleic acid (C) STRANDEDNES: double | |
| 10 | (D) TOPOLOGY: linear | |
| | | |
| | and the second of the second o | 1 |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928: | |
| 15 | GCAAATTGTC ATTAGACGGA GTATTATTTA GAATTTTCGG TGATATCCAC CGGCACAAGA 6 | |
| | TCGATGTTGG ACAATATCTA ATATACTGAT ACGCATTTAA ATAGAAGAAG GGAATTAGAG 12 | 0 |
| : | TTTGGTTnTG AATGCAAA | 8 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 1929: | |
| | (i) SEQUENCE CHARACTERISTICS: | . , |
| | (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid | |
| 6, | (C) STRANDEDNESS: double | |
| 25 | (D) TOPOLOGY: linear | |
| | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929: | |
| 30 | ACATCTTTAT ATGCTTCAAC ATCAAATACA CCACATATTG GTAAACAACA AA | 2 |
| | | ~ |
| | (2) INFORMATION FOR SEQ ID NO: 1930: | |
| , | (i) SEQUENCE CHARACTERISTICS: | |
| 35 | (A) LENGTH: 51 base pairs | |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| • | (D) TOPOLOGY: linear | |
| | | |
| 40 | | |
| - | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930: | • |
| | TITAATGTTC ACAACACCGG AATAATAATA ACTAAAGCGC CGCTAATAAA T | 51 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1931: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 400 base pairs | |
| | (B) TYPE: nucleic acid | |
| 50 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (D) LOCOBOOL. Linear | |
| | | |
| | | |

| | ACGAMAATA AATAATCATT TCACCTTTAT AGCCAGTATT TTTAATTAAT ATATTTTCAT | 60 |
|-----------|--|-----|
| | CTATTAGCGC TTCTAAAAAT CTATTTGACT TTTGAACATA CTCTTTAGCT ATATTATTAA | 120 |
| 5 | CAACAGTATA GGATTCCTCA TAATTTAGTT GATTAAATTC TGAGTCGTTC ATTAATTCAA | 180 |
| | CTAATCCTTT TATTACTTTT TGTACAACAT TAATATTTTT ATCAAAATCA AATTTATCTT | 240 |
| | CCTTAGATAA ATTAATAnnn AAAGTCTTAA GAACATTTGT AAATAGCTCT GCAACACTTA | 300 |
| 10 | TAGTTTGGnC AAATTCCTTA AATTTATTTA CACAGTACTC ACACATTAGT TTTAAAAATA | 360 |
| | ATGGATTGTT GAATTCTGGA TTTAATATAG GTAACTTAGG | 400 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1932: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1932: | |
| 25 | ACTTGCGGAA nGACGCAACG TTTATGTACG TTGGAAGAAA AATTCAGGAC TTACGTTCAA | 60 |
| | AACTACCATA GCAATATGCA TTGAAAGATG ACAGTATGCG | 100 |
| <i>30</i> | (2) INFORMATION FOR SEQ ID NO: 1933: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 61 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (b) Torozogi. Timedi | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1933: | |
| 40 | CGCTCTGCTT TAAGCGTTGG GACTTTGTCA ACGGTAGTGG ATGGGAAGTG GTTCTGCTTT | 6Ó |
| | G . | 61 |
| | (2) INFORMATION FOR SEQ ID NO: 1934: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934: | • |

| | (2) INFORMATION FOR SEQ 1D NO: 1935: | | |
|------|--|-------------------------------|----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | | • | |
| 10 | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 1935: | |
| · - | ATGTATTACG GTTTAATTAA GCCACATACC AAC | AAGATTG CATTTATGGT ATCTCA | 56 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1936: | | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 61 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | | | |
| | | | |
| - 25 | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 1936: | |
| | TCGCACCAGA AACAAGGGAT TGTTAAAATT GCG | TAAATCC TTAAATTTAT TTGTAAATAT | 60 |
| | A | | 61 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1937: | | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | • | | |
| | | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 1937: | |
| . ,, | ATGAATAATC ATATTTCTAA TCAAAGTAAT AGC | ATTTATA TTGTGTTTAA A | 51 |
| | (2) INFORMATION FOR SEQ ID NO: 1938: | | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| 50 | | • | |
| | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 1938: | |
| 55 | TTGCTGAAGA TAGAGGCTTC ATGAAGGTGG AGA | AGTTAGC TGATTTCTGG AACAGG | 56 |

(i) SEQUENCE CHARACTERISTICS:

55 .

| 5 | (A) LENGTH: 51 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|----|---|-----|
| | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939: | • |
| | ATCTCAATGT ATTCCTCTAG TGTAAGTTCT TCATAAATAA CCGGTGATTC C | .51 |
| | (2) INFORMATION FOR SEQ ID NO: 1940: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940: | • |
| | CTCAGGTCGA CTCTAGAGGA TCCCCTGTTA AATAAAACTT CTTAAGCACA TACTTATTTC | 60 |
| 25 | ACTATGCCTT TTACGTTCCC CTTATACTTT TCTCACATCT TTCTCTTAGA CTACTCCCTT | 120 |
| | ATACGCCCCG CTCAATATCT TTAATCATTT CATCTACAGT TATTTTCGCA CTCGTTAAGA | 180 |
| 30 | CAATAGGAAC GCCTGGCACC TGGATGCGTA CTTGCACCTG CAAAATATAW ATCTTTATAA | 240 |
| | TCTCGCGATA CATTYTGTGG ACGATAATAA TTACTTTGCG CTAAAGTTGG GCATTAAACC | 300 |
| | GAATGCCGAA CCAAATTC | 318 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1941: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid | |
| 40 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| ٠ | | |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941: | |
| | CCGGGAAAAT TTTTGGAATT AAGTGGAAAA AAAATCCCCT TAAAATTCCC CTGGCCA | 57 |
| | (2) INFORMATION FOR SEQ ID NO: 1942: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 378 base pairs (B) TYPE: nucleic acid (C) STRANGEDNESS: double | |
| | (D) TOPOLOGY: linear | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942: | |
|----|---|-------|
| _ | TGTTCTTCTT TTGAATCTGT TTTATTCGTT TGTTCCTCTT TTTTCTGTTC ATCTTTCATA | 60 |
| 5 | TTTCCACATC CCCCAATAAA AATGATTAAA AGTAATACAC TCATGTACAA AGCAATTTTT | 120 |
| | TTTATATACT CCATCATTTC ACATCTCTCT GTTTTAATTT TATAAACATT TGAATATTTC | 180 |
| 10 | ATACAACTTA TTAAAATAGT GATTATTCAA CTTTTATGTT ATCAAACAAA ACTAACTTAT | 240 |
| | TCAATTTAAT ACATGTAATT CATTTTAACT TTATTATTAA ATGTTCTAAC GTNATTTTTT | 300 |
| | ATATTAGTAA TTATATTTAT TTATCCTCGC TTGGATTAAA GTAGATACTA TCTGTGAAGT | 360 |
| 15 | Anatattttc tgccttgn | 378 |
| | (2) INFORMATION FOR SEQ ID NO: 1943: | |
| | | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 394 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 25 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943: | • |
| | AAGAAGAAGT CAAAATTCAG CTAAGTAAAA GCTCGAGTTA TAAAAAAGTC TAAATTGATT | 60 |
| 30 | CAACAGGAGT AGAAAAGGAA ATTAGTCTTG CATATTTTAG AAAATGAATA AAAACAGTTA | 120 |
| | CTATATGCAA CTCAAGAATT AAATATTATT TAAGCCACAT ACCTATTAGA GTACAAAATA | 180 |
| | TACAAGTTGT ACTTATATCT AGGTATGTGA CTTTTGATTT TAAGCGTAAA GTAAAAGTTT | 240 |
| 35 | TTATGTTTGT ATTAGTTCTA AATTATTTTG CACTTGGATG ACACGTATTT TTGAGTTTAA | 300 |
| | GTGGTGACTC AAGTTCAATA AAATAAATAT CAGATAGGAT AATTTGANAA TNATATGAAA | . 360 |
| 40 | GGGTTATCTC CAAAATnATC TCCATATTAT AAGG | 394 |
| | (2) INFORMATION FOR SEQ ID NO: 1944: | |
| • | (i) SEQUENCE CHARACTERISTICS: | • * |
| | (A) LENGTH: 52 base pairs | |
| 45 | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (D) TOPOLOGI: Timear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944: | |
| | TATTCGTGAT GACGATTGTC GGTGACATGA AGTTCTATTT GCTGGCACTG AT | 52 |

(2) INFORMATION FOR SEQ ID NO: 1945:

| 5 | (A) LENGTH: 82 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|--|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945: | |
| 10 | CGTTTAAAAA ATGATATCAA TCTTTATTGT GGATTGCAAC ATCCGTGTGC TCCATAAAAC | 60 |
| | GTGTGGCGAG ACTTGGGAAA GG | 82 |
| | (2) INFORMATION FOR SEQ ID NO: 1946: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 70 base pairs (B) TYPE: nucleic acid | |
| 20 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946: | |
| 25 | GTATTATTGA TGAAGAAACA GCTCTCCAGT TGTAGATGCA TGCTACGTTC ACGTTACCAC | 60 |
| | TGTATCAATT | 70 |
| | (2) INFORMATION FOR SEQ ID NO: 1947: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | æ. |
| 35 | (D) TOPOLOGY: linear | |
| 33 | e Transition of the Control of the C | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947: | 盖·6 |
| 40 | TATCACCAGC ACCAAGGNTA ATGACATGCT GATCTTTTGC AGTTATGGTN | 50 |
| | (2) INFORMATION FOR SEQ ID NO: 1948: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948: | |
| | ATTGTATGAA TCTTTGGGGA ATGAACTTTM AACGAACGGA CATCTTGCAA TGACGCATCA | 60 |
| 55 | ABATGGTTTT ABCACATGTA ATCGGCTCTC GGTACTATTC GTGTGATGTA CACATGG | 117 |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 64 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----|--|----------|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949: | |
| ,,, | TTTGATGATT TCGGGATGGA TTGGTATTGT GGTGAATGAA TTTTTTAGCT CATCATCAAA | 60 |
| | TTAG | 64 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1950: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950: CTCTAGTGGC CATTCATATT TGTCGCTGAA TGATGTTGGT ACATCCATTG CTGCTGT | 57 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1951: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 68 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | | |
| • | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951: | |
| 40 | CTGTCCTTCT GAAACTTGGG TATTTAATTA GGAATAGTTA AAAAAATCAT TCACAGAAAC | 60 68 |
| | (2) INFORMATION FOR SEQ ID NO: 1952: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952: | |
| | TTAAATTAAC CTTAAGGTTG GNATTTTTAA CCCCCAAATT TTTGGGGTGG TTAAAATTCC | 60 |
| 55 | | |

| | (2) INFORMATION FOR SEQ ID NO: 1953: | |
|----|--|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953: | |
| ~ | GACATTTACA CCTGCTTCAA TCTGGTCCAG TGCAGCATCT AATTCTTCGA | 50 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1954: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954: | |
| 23 | ATTTGGCCAA CTGTTCAGCA CGGTATTGGT TCAATGCAAC ACTTTATCAT TGCTTCAGGG | 60 |
| | CTATATCGGT GGTATGGGnT GTATCACTTC TTAGAACGTG GTATTAA | 107 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1955: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1955: | |
| 40 | GAAGTGAATA TGAAGCTGCT AAAGACTCCG GAATGCTACC TCAGACAACT GATG | 54 |
| | (2) INFORMATION FOR SEQ ID NO: 1956: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 365 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1956: | |
| | ATGATTATTT TAGTTCCATT TGTTGAGTCG ACTGCTAAAG TTCCATTTAA ATGTTGTACA | 60 |
| 55 | | |

| | ATAAGCAGTA ATTTATGATT GTTTACAGTT TTTAATTTAC CATGAACTTT TGAAGCATTT | 180 |
|------|---|-----|
| | GCATGTTTAA TAACATTATT TATCGCTTCA CGCGTAATCA TAACTAACAT AGATTGTTTA | 240 |
| 5 | GTAGGACTTA ATACTTGCGC TAATTCTTTA TTTTCAAATG TAAAATCAAT ATCAGCATCN | 300 |
| | NTHAAAACTT TACGTATACT ATCAATCTCT TCAATAAATG ATGGTAATTT TACATCATCA | 360 |
| | ATAAT | 365 |
| 10 | (2) INFORMATION FOR SEQ ID NO: 1957: | |
| . 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 346 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 111 |
| | (D) TOPOLOGY: linear | |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957: | |
| | AAATAATGTC ACAAAAGTTA AAGATACTAA TATTTTTCCA TATACTGGTG TAGTTGCTTT | 60 |
| | TAAAAGTGCA ACTGGATTTG TAGTTGGAAA GAATACTATT TTAACAAATA AACATGTGTC | 120 |
| 25 | GAAAAATTAC AAAGTGGGCG ATCGTATTAC TGCACATCCA AATAGTGATA AAGGTAATGG | 180 |
| | TGGTATTTAT TCGATTAAAA AGATTATTAA TTATCCAGGT AAAGAAGATG TATCAGTCAT | 240 |
| 30 | TCAAGTTGAA GAGCGTGCAA TAGAACGTGG ACCAAAAGGC TTTAATTTTA ATGATAATGT | 300 |
| • | AACGCCATTC AAATATGCGG CAGGGGCTAA AGCTGGTGAG CGAATT | 346 |
| | (2) INFORMATION FOR SEQ ID NO: 1958: | . * |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 390 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| . 40 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958: | |
| | TTTTCCAGTT AATTTTTCCA GTTCACTAAA TACTTTATTG ACTGTACCAG ACCCAATAAT | 60 |
| 45 | AATTTGGTAT TGTCCCCCAG TAGAAAACGT CCCTTTAACT ACATCCATAT TGTTTAGCGC | 120 |
| | CTCTTCATTT ACTAAACTTT CATCATTTAA AACTAATCGT AGTCTCGTTG CACAATGCGC | 180 |
| 50 | CATTGCATCT AAATTCTCTT CTCCGCCTAT CGCGTTCAAA ATTTCTTCTG CGGATTGCTT | 240 |
| 50 | ATAATTCATA TATTTAGCCT CCTAATTAGA ACCGGTTCCA TTTATTCCAC TTTATTGTAA | 300 |
| | CCGGTTCCAA AAATATTTGC AACACTCTAT TATCATTTTA TATAAACACC TACACCATTT | 360 |
| 55 | COGITCON ANIATITO ACCIONI INCIDITI INICIDIA | |

| | (2) INFORMATION FOR SEQ ID NO: 1959: | |
|----|---|----|
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 50 base pairs | |
| 5 | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | (2) 101020011 22::002 | |
| | | |
| 10 | / 1) | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959: | |
| | GATTGCATAT AATAGTAAAA ACATTACATC TTGAACAGTA CTCGTTTTGT | 50 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1960: | |
| | (i) SEQUENCE CHARACTERÍSTICS: | |
| | (A) LENGTH: 57 base pairs | |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| 20 | (D) TOPOLOGY: linear | |
| | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960: | |
| 25 | (na) ongomica poortial troit ong to the | |
| 25 | AATITGAACC AGACACTGAT ACAAGTCACA CCCAGAAACT TTTAAGGACG TAAATGT | 57 |
| | | |
| | (2) INFORMATION FOR SEQ ID NO: 1961: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 30 | (A) LENGTH: 50 base pairs | |
| | (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | (b) Totaled1: 12med1 | |
| 35 | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961: | |
| | AACGCTATAT TAGCGATATA CAATGATGCC ATTATCAATA nTACAnCTGn | 50 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1962: | |
| | (5) THEOMESTION FOR DDA ID NO. TSAS: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 60 base pairs | |
| | (B) TYPE: nucleic acid | |
| 45 | (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962: | |
| 50 | TACAACGTCA GTTGGCAGAC ACCAGAAGAA GGATTCATAA GTATATTCAG GAACTTGTTA | 60 |
| | | • |
| | (2) INFORMATION FOR SEQ ID NO: 1963: | |

| 5 | (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | - |
|------------|--|-----|
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963: | |
| 10 | AATTTTTCCC CCTTTTTAAA TTTCCCAAAA AAAAnCCCCC AAnAAAAAAA | 50 |
| | (2) INFORMATION FOR SEQ ID NO: 1964: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964: | |
| | CAACAAGTAG ATGCATCAGA GAGTAGTGTT CAAACGTTAA TAGATGTGGC ATG | 53 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1965: | |
| 30 · | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965: | |
| 35 | AGCAAAGGCA TAACTGCTAA TGACCATGTA AATGAGACGA GTCGATCGTG GCCA | 54 |
| | (2) INFORMATION FOR SEQ ID NO: 1966: | |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 252 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 45 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966: | |
| | CTCAAATAAC TGGCTCAACT CAACCGGTCT ATAACACCAT AACACCGCAT GCCACTCTAG | 60 |
| 50 | CATACTCAAT CGCTCTGGTA CCAGCCCTCA AATAACTGGC TCACGCCAAC TGTCTATAAC | 120 |
| | ACTAACACGC ATGCACTCTA GCCTACTCAG AGCTCTGGTA CAGCACTCAA TAGCTGACTG | 180 |
| <i>5</i> 5 | TCACAGTCCA CACACACTCA ATACTGGCTG ACACAGTTCA CACACAGCTT ACTCGCTCTC | 240 |

| | (2) INFORMATION FOR BEQ ID NO: 1907. | • | | * . | | | |
|------------|--|----------|---------------|---------|----------|-----|----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | in the second | 3 = | | | |
| | (D) TOPOLOGY: linear | | . 1 | | | | , |
| | | | * | | | | |
| 10 | | | | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ | TD NO- | 1967: | | | | |
| | (XI) DEGODAGE PROCESTITION. DEG. | 10 1.0. | | | • | * . | |
| | CAGTITAAAC TOGATGTTGT GTACTACTGT GCC | AGCTGGA | ATGTT | A ATATT | TGGTGATG | | 59 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1968: | | Lu , | | | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | * * | | | | | |
| 20 | (D) TOPOLOGY: linear | | | | | | |
| | | 100 Sec. | | | | | , |
| | | | | , | . * | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: | 1968: | | | | |
| | GTTACATGGC ATCACGCCAA ACCTGTCTAT AAC | ACCATAA | CACGG | CATTG C | c . | | 52 |
| | (2) INFORMATION FOR SEQ ID NO: 1969: | • | · | | | | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | * | * 6 | | 7. |
| | (b) lorobogi. limear | | | ÷ ' | • * | | |
| 35 | * | - | | | | | |
| , | Same Control of the C | | | | | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: | 1969: | | | | • |
| | ACAATTITAA TTATATAACT CCAGGGGCTA CAG | TAATACG | ATTTC | CCAG A | CTCCAAA | * | 58 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1970: | | | | | 1. | |
| | (i) SEQUENCE CHARACTERISTICS: | | | | - 3 | | |
| | (A) LENGTH: 59 base pairs | 1 | | 0 1 | | | |
| | (B) TYPE: nucleic acid | | 1. | | | | |
| 45 | (C) STRANDEDNESS: double | | | | | | |
| | (D) TOPOLOGY: linear | | | | | | • |
| | (*, *********************************** | | | * * | * . | 1. | |
| | | | | | | | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: | 1970: | | 200 | | |
| | | | | | | | |
| +7 | TGACGTATAA TGGATGAAAG TCTATTAAGT TTA | | AATAC | rgtga a | ATCTTTCT | | 59 |
| | (2) INFORMATION FOR SEQ ID NO: 1971: | *. | , - • | | | | |
| 5 5 | * | | | | | | |

| 5 | (A) LENGTH: 52 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|-----|--|-----|
| | | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971: | |
| 10 | TATCATGTTA TCTTCAATCG TTCACCAACA GTCATTTGCT GCATCAGTAA CG | 52 |
| | (2) INFORMATION FOR SEQ ID NO: 1972: | · · |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • |
| | | |
| 20 | | |
| | (xi-)-SEQUENCE-DESCRIPTION:-SEQ-ID-NO:-1972: | |
| : . | TTGCTGGTGC CATAGACTAC ACTTGTTTGA TATCAGAAAT GGGATCTGTT CCATTACC | 58 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 1973: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 209 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | ٠. |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973: | |
| | AGTTAAACCG AGTCCAACCC AAACCTCCAA TCCACCTAAT GGTTAAAATT CCAAACCATT | 60 |
| | ACCAGGAGG GACCAAAAAA CGGAATGGGG CCTATTGGTA GGGTACCTAT CCCATTTAAA | 120 |
| 40 | AATCCATCCA AAAGCCCAna TTATCGGACC ATTTTCGCCA AAAATAATTT AAGCGGAAAT | 180 |
| | TGAATACCTT AAAATTCTCn GGGCCCACT | 209 |
| | (2) INFORMATION FOR SEQ ID NO: 1974: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974: | |
| 55 | ATCTGAGTAT TTATAACATA AATCACTAAT ATCGTTATTA CATAGGGATA GGGTAAAAGT | 60 |

| | (2) INFORMATION FOR SEQ ID NO: 1975: | |
|-----------|---|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975: | |
| | TTCCTGCATC CGAGTCTGAA TCGCTGTCGA ATCACGTCGA GTCGATCGCT ATCAGGTCGA | 60 |
| 15 | GTCGCGTCGA ATCGnTCGCT ATCGAGTCGA TCGCGTCGAA TCGAATCACG TCGAGTCG | 118 |
| | (2) INFORMATION FOR SEQ ID NO: 1976: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976: | |
| | TTGCAACNTT TGATCTAGAT ACTACCTTAG TTGGATTGTA CTACTTGATT CTACTTCACC | 60 |
| 30 | TTTAGTTGGT TTTGTAGCAG GCGTTTTGTC TTTACCTGAC TCACTAGATG CGTCATTTTC | 120 |
| | TTTTTCAACA CTTGGTAATT GTTTATTGTC ATCTTTTTGG CTGTCTTGTT TTTGTGATTC | 180 |
| | TTTTTCAACA GGTGATGGTG TTGGTTTGCT AGGCGTACTG GAGTAGCTTC CTTCTTAGCT | 240 |
| <i>35</i> | GAGTTATCTT GTTGTTCTTT TTTGTTAGAT TTATCGGTAT TGGCTTTTGT AAATGCTTCT | 300 |
| | NTATCAACGA TTCTGACATG GTATTGTCCA TCATAATCAA TCGTTTTTAC GTGAACTTTA | 360 |
| | ACGATAGCAT CATATAGAGT TTACCTTCAA CATATGGGAA | 400 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 1977: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 74 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977: | |
| 50 | TAGACAAAGA CAGTAACAGT AAAGTACGCT TCAGAACTGA TGGCTCACTG CGAGTATAAA | 60 |
| | | 74 |
| 55 | AACTTGTAGT GTCC | 7-1 |
| 55 | | |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 72 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
|-------------|--|-----------------------------|----------|
| | | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID | NO: 1978: | |
| ,, <u>.</u> | ACTCAAAAAC TCGGAAAACA TTCCAATTTA GCTTA | AATCT GACCCTTTTT TTGACCCTTA | 60 |
| • | TATTTTTAC AA | | 72 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1979: | | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | · · · · · · · · · · · · · · · · · · · | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ II | | 60 69 |
| | GCACCATAA | | 69 |
| 30 35 | (2) INFORMATION FOR SEQ ID NO: 1980: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ II CAGAGAGTTG TCGCTCATTA AACGCCACnT GATGA | | 60 |
| | GTATGGATAA TTTTCACCTG TTGCTGAGTC TTTG | ATAAGC CTCGACTGT | 109 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1981: (i) SEQUENCE CHARACTERISTICS: | | |
| 50 | (A) LENGTH: 55 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | | |
| | | | ٠., |
| | (xi) SEQUENCE DESCRIPTION: SEQ I | O NO: 1981: | |

(2) INFORMATION FOR SEQ ID NO: 1982:

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----|---|-----|
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982: | |
| | GAATCTGTTC AAGTTAGAAT TATCCCGGCA TAATGATAAA GGCGAGTAAA TGG | 53 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1983: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 252 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983: | |
| 25 | GnCTTTTGAA TAAAGAAAAA TTCATCAATA GAAAAACCGT CTTTATCGTC TATTTTTTTA | 60 |
| | ACTAGTAAGT TCGGCGTTCT TAGAGACTCA AATATTGATT TTACGTTTTT CTTTGTTACA | 120 |
| | CCACTAACAC TAAATATTCT TCCATCTAAA TCTACTAATT CTGGTACCGC AAAGACATCT | 180 |
| 30 | AAACCATGTG TTTTTCTTT GTATTTATTT TCATCTTTTC CCAATAAAAA CACTTGGAAC | 240 |
| | TTTTGATTTn GT | 252 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 1984: | • |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | • |
| 40 | (D) TOPOLOGY: linear | |
| | | ٠ |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984: | |
| | CGTGTTAATC AACTAATTCT TAGTTTTAAC TGTCGTAATA ATCAACTGAA CACTTTCAAT | 60 |
| | CTA | 63 |
| 50 | (2) INFORMATION FOR SEQ ID NO: 1985: | |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 63 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985: | |
|------|---|---|
| | TCCTAAAATG ACCGCTAATG CCTATGGATT GTTATCACCG ACCGCAGGGA CAGCACGACC | 60 |
| 5 | TAC | 63 |
| | (2) INFORMATION FOR SEQ ID NO: 1986: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | • - |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986: | |
| | GGCATATAAA AATTAGAGAA ATTATTTCAA ATGAACAGAT AGAGGCACAA GATGAATTAG | 60 |
| 20 | TTAAACGATT AAACGATTAT GNTTTAAATG TCACTCAAGC AACTGTTTCT CG | 112 |
| | (2) INFORMATION FOR SEQ ID NO: 1987: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 base pairs | 8 |
| , | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 30 | | * |
| 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987: | * |
| | TTTATCAATT TGTAACGAAC ATGAATTACA TGTTTCAGGA AAATATATTT CATCCCATTT | 60 |
| 35 | TTAAAAAGTA TAAGATTTTA TGAAAAATTA AACCAATTNA GTATAA | 106 |
| | (2) INFORMATION FOR SEQ ID NO: 1988: | |
| 40 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | |
| . 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988: | |
| | AATGGCGTAG TTACAGCATT TATGATTGTG TTAATCTTTT CTTCTGATAA ACATAATCTG | 60 |
| 50 | TTTGACCAAA AGTATTTAAG TGTTCAATTA ATTAGTTTTA TTATTTACGT CGTATGGCAA | 120 |
| | GTTTTATTGA TAATGTTTTA TTATCATTCA AAACCAAAAA ATAATTCATT TTCAAAATTT | 180 |

| | TGGTTAGGTG GACATCAGAT TCACTTCCAT GAAAGTAAAT TAATTGAATT TGTTGGTTTC | 300 |
|----|---|-----|
| | TTAGGAATTT CTTATGTTAC ATTCAAAAGT GTGCAGTTAA TTATGGAAAT TCGTGATGGT | 360 |
| 5 | TCTATCAAAG AAATTAAAGT ATGGAAATTA ATTCAATTTA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 1989: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989: | |
| | TTCAGCTTAC AATAATGAGC AGGTTGGGGT GGGCTCCAAC GCAGAGAATT TCGATAAGAA | 60 |
| 20 | ATTCCACAAA TAATACAAGT TGGCCCACTC CCATTCTGTA ATAAATATAG GAGGTCATTG | 120 |
| | TTATGCAAAT AGAACTTACT GATGCAGCAG TAACTTGGTT TAAAAATGAA CTTGAGTTGC | 180 |
| | CTGAAAATAA TAAAGTGCTC GTGTTTTTTG TAAGATATGG TGGCGAATTC CAACTCAAGC | 240 |
| 25 | AAGGATTTAG TCCTGCTTTT ACAGTTGAAC CAAAGGAAGA TGTTGATATT GGCTATGAAC | 300 |
| | AACAATATGA CGATTTAAAT GTTGTCGTAG CGGAAAAAGA TTTGTGGTAC TTTGAAGATG | 360 |
| | ACCACATTAT TGTAAATGTA GTTGTCACGA AGATGAATTT | 400 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1990: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990: | |
| | CAATTTATTA TGTAACTAAT TATAGCATTG ATGAACAAGG CGCTCAACGT AATANTACAA | 60 |
| | TTAATGGATT GTTTCACAAG ATGGTAAAGC TAGGATGTCT TTTTATTAAG A | 111 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 1991: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 50 | (D) TOPOLOGY: linear | |

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| | TARACARATT CATCARTTGT TAGTGGCATA TCCTARTGTA ATTAGAGAGG AGTT | 34 |
|------|--|--------|
| | (2) INFORMATION FOR SEQ ID NO: 1992: | |
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 10 | (D) TOPOLOGY: linear | |
| - 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992: | |
| 15 | GAACGATAGA TTGATGAAAA GTTTAAAAAA GTACGTATAT GTTTATTAAG TTTGAGTTT | 59 |
| | (2) INFORMATION FOR SEQ ID NO: 1993: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs | |
| 20 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | (D) TOPOLOGY: linear | - ' |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993: | |
| | CGAGACCAAA ATATTCGAAC GAATAATTTC AGTGTTTTGC TCCTTTATTA TAGATTCAAG | 60 |
| 20 | CTATGGATAA TAG | · . 73 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1994: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994: | |
| | ATCCATACAA ATGTAACAAG CACAATTGCn GCCATACTTn GCATGACAGT | 50 |
| | (2) INFORMATION FOR SEQ ID NO: 1995: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (b) 1010000 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995: | |

| | (2) INFORMATION FOR SEQ ID NO: 1996: | |
|----|--|----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996: | |
| | TCANTTAANA TTAATGTNCG TTGGGGCTCT AATAAAATTT GTTTACAACG | 50 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 1997: | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 61 base pairs (B) TYPE: nucleic acid | |
| 20 | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | , |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997: | |
| 25 | TCATGATTTG AAATGACTTT CAATGACTTG GGTGGGACAC TTGTTGCACA GCTGGATGTG | 60 |
| | c | 61 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 1998: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs | |
| 35 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998: | |
| 40 | CATGCATTGA TGnTCTCAAA GAACATGATG AAACAGGTCA nCACATGNCA | 50 |
| | (2) INFORMATION FOR SEQ ID NO: 1999: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999: | |
| | GGTTCGCTAC TGATTGGGTA TACATCTGAT TTAGCAATCT TGCGCACTTG TT | 52 |
| | | |

| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | | |
|----|--|--------------------|------------|-----|
| | | | | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 2000: | | (· |
| .0 | ATGTGGTTAG ATATCTGCAC ACTTGAACGT TAT | TGTGGGA TATACTTGGC | CAT | 53 |
| | (2) INFORMATION FOR SBQ ID NO: 2001: | | a sale | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | * | |
| 20 | | | | |
| | | ID-NO:-2001: | | |
| | ATCTCAGTAA GGGTAAGCGT CAAAGTCTGC ACG | GATGCTA ATGTTTACCA | GGTT | 54 |
| 25 | (2) INFORMATION FOR SEQ ID NO: 2002: | • | | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | * | · . | , |
| | | | . * | |
| | (xi) SEQUENCE DESCRIPTION: SEQ | ID NO: 2002: | | |
| 35 | CTAAAGATTG TAATGCTTGA ACAATTGGTT CAG | TGAATTT TTGGAAATTG | TGGAAACTGT | 60 |
| | TACCATCATC ATCTGTTATA AAACTAAAGT TTA | AATTGCC AGTATCATGA | TAAACAGCGC | 120 |
| 40 | CACCACCAGA AATTCTTCTT ACTACATCGA TGT | TGTGAGC ATCGATATAT | GTCTGATTTA | 180 |
| , | CTTCCTCTAT CGTATTTTGA TTCTTTCCAA CAA | TGATAGA TGGTCTATTT | ATGTAAAATA | 240 |
| | AAAAGTAACT TTCTTCTGCT GGTAAATTTT TTA | AAACATA TTCTTCCATT | GCTAAGTTTA | 300 |
| 45 | AAGTTGGATC TGTAATATTA TTATTACTAA TGA | ATTTCAT TACAATCTCT | CCCTTATATC | 360 |
| • | TATATATATn CTCTACTTAT TTATGCCTTA ACT | TTGCTCA | | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 2003: | | | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | | · 2 |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003: | |
|----|---|-----|
| | CCGAAATAGG ACGGGCAGTT GGATTTATTC GAAATGGGTG GCGTTAATAT ATACAGT | 57 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 2004: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004: | |
| 13 | NAGTAGTTGA AGGCGACCGC GGTCCACAAG CTGCAAACGT TGTTAAACTA TAATTCTTAG | 60 |
| | ATTTGAATCA TTGATTTTAA CTAACACCTT ACCAAGAAGT AAGGTGTTTT TA | 112 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 2005: | |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005: | |
| 30 | AAATCTTGAC ATAGGCACAG GAATGTATAT TGATCTCGAT CACTTAAGTC | 50 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 2006: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | (with appropriate programmer, SEO ID NO. 2006. | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006: AAGGTGGGTT TAAATTTCCC AAAAAAAAAA GCCTTTTAAC CTTTTGGGGG GTCCCCTTTC | 60 |
| | CTTGGAATTG GAAAGGGGCC AAAATTGGAA TAAGGGGTTT GGAAAAACCC AAGCC | 115 |
| 45 | (2) INFORMATION FOR SEQ ID NO: 2007: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007: | |
|-----|-----|--|-----|
| ٠. | | TGAAGAAATA GCAAATGAAC TCAATATTTC TATTGAACGT CAATATTTCA ACCAATTATA | 60 |
| | 5 | TCGCTTCAAT AATCAAGATT TAAAGCATCT TGAACAAGAN TTTGA | 105 |
| | | (2) INFORMATION FOR SEQ ID NO: 2008: | |
| | 10. | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 67 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | · . |
| | | \(\frac{1}{2}\) | |
| . : | 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008: | |
| | | ATTGGCTACT AAAGTTAAGG ACATGATGGA TTGGATTAGT GGTATGCGCT TTGAAAAGAT | 60 |
| | 20 | CAATTAT | 67 |
| | | (2) INFORMATION FOR SEQ ID NO: 2009: | |
| | - | (i) SEQUENCE CHARACTERISTICS: | |
| | 25 | (A) LENGTH: 73 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
| | | | |
| | 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009: | |
| | | TATAAATTAG CGTCCTTCAT ATCACAACGA TGATGCTCTG TGCGAAGATC TGATTTATTT | 60 |
| | | CAATGTGCGC ACG | 73 |
| | 35 | (2) INFORMATION FOR SEQ ID NO: 2010: | |
| | 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| | | (D) TOPOLOGY: linear | |
| | 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010: | |
| | | CTTTGTTTAT GTTTCGTTTA ATTTGTAACC CTCTCTTTGG ATACCGAGGT T | 51 |
| | | (2) INFORMATION FOR SEQ ID NO: 2011: | |
| | 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 88 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|----------|--|----------|
| 5 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011: | |
| | TAACGACCAA GCTTAAAGAG ATACGCTCTT ATGCGATTGG ATAGGTCGTT AAAGTTAACT | 60 |
| 10 | ACAATACCTC ATAAGTAGAT TTAGAATC | 88 |
| | (2) INFORMATION FOR SEQ ID NO: 2012: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | . • |
| | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012: | |
| | GTCAACCCTT GCCAAGCTTA TATCACGATA CTGGGATGTG ACTTCCGGTG AATTAC | 56 |
| | (2) INFORMATION FOR SEQ ID NO: 2013: | <i>;</i> |
| 25 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013: | v. |
| 35 | AGCTTATAGT ACTTGTGACT TCATAATGGA TGAAGTTGAA GTACCAAAAG AATTAACACA | 60 |
| | ATTACACGAA TAATTTAAAT AGAGAGTGTG ATAGTAGGTG GAATTATTAA ATAGTTATAA | 120 |
| | TTTTGTTTTA TTCGTATTAA CTCAAATGAT ATTAATGTTT ACAATACCAG CTATAATTAG | 180 |
| 40 | TGGTATTAAG TACAGTAAAC TTGATTATTT TTTCATCATA GTAATTTCGA CATTATCGTT | 240 |
| | ATTTCTATTT AAAATGTTTG ATAGCGCGTC CTTAATCATA TTAACTTCAT TTATTATTAT | 300 |
| | AATGNATTTT GTCAAAATCA AATGGNATTC NATTTTGTTG ATTATGGCTT CGCAGATTAT | 360 |
| 45 | CCATACTGGT GCCAACTACA TGGATATAGT TATATATGCA | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 2014: | |
| 50 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | <i>:</i> |

| | (XI) SEQUENCE DESCRIPTION: SEQ ID NO. 2014: | | |
|-----------|---|---------------------------------------|------|
| 5 | TCTTTCGAGG ACAGTAGAGG GTCCACCCTA TTGGACGTGG TACTGTACTA C | TTTTAAA | 58 |
| | (2) INFORMATION FOR SEQ ID NO: 2015: | - | *. |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | |
| | | | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015: | | |
| • | TCTACCTGCA GGCATTCAAG CTTGGCACTT GCCGTCTTTT TACAACGTCG T | GACT | 55 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 2016: | | |
| | (i) SEQUENCE CHARACTERISTICS: | | |
| | (A) LENGTH: 66 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | • | |
| 25 | (b) Topologi: Timear | | |
| | | | • |
| - | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016: | ē | |
| 30 | TACTCTTAAG CTAACAACGG CGGTTATGAG TCCTTTGACA AGGTATCGGA G | GAAAGACCG | . 60 |
| | | | |
| | TAAAGC | · · · · · · · · · · · · · · · · · · · | 66 |
| • | TAAAGC (2) INFORMATION FOR SEQ ID NO: 2017: | Q. | 66 |
| 35 | (2) INFORMATION FOR SEQ ID NO: 2017: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | 66 |
| <i>35</i> | (2) INFORMATION FOR SEQ ID NO: 2017: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid | | 66 |
| | (2) INFORMATION FOR SEQ ID NO: 2017: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | 66 |
| | (2) INFORMATION FOR SEQ ID NO: 2017: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | 66 |
| | (2) INFORMATION FOR SEQ ID NO: 2017: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | ATTGTTCAT | 66 |
| | (2) INFORMATION FOR SEQ ID NO: 2017: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017: | ATTGTTCAT | |
| | (2) INFORMATION FOR SEQ ID NO: 2017: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017: CCAATAAGCA CACTGCCATT ATTGAGGACG GTACATNTAC GGTTAGACCC AND | ATTGTTCAT | 60 |
| | (2) INFORMATION FOR SEQ ID NO: 2017: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017: CCAATAAGCA CACTGCCATT ATTGAGGACG GTACATNTAC GGTTAGACCC ACGCGGTGGGC ACATAGTGTT TGGCTTTGAG GAGGTTACCA TTGCC | ATTGTTCAT | 60 |
| 40 45 | (2) INFORMATION FOR SEQ ID NO: 2017: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017: CCAATAAGCA CACTGCCATT ATTGAGGACG GTACATNTAC GGTTAGACCC ACGGCGTGGGC ACATAGTGTT TGGCTTTGAG GAGGTTACCA TTGCC (2) INFORMATION FOR SEQ ID NO: 2018: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 58 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | ATTGTTCAT | 60 |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018: | |
|-----------|---|-----|
| | CCTTCCAATA GTAATTGATT GATGTATGAG TATATTAGGT GTGAAATCAA GAGGATTC | 58 |
| 5 | (2) INFORMATION FOR SEQ ID NO: 2019: | |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019: | |
| | TITCCTCGTA GGTGGTTCTT CTTCATCTTC GTTGTTTTGT CCGAAGTTTG GA | 52 |
| | (2) INFORMATION FOR SEQ ID NO: 2020: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs | |
| 25 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020: | |
| 30 | ATAGTTTAGG TGAGGATGTT GRGGTACGAC AGGAAGAAGA ACGGCAAACA | 50 |
| | (2) INFORMATION FOR SEQ ID NO: 2021: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 300 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 40 | | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021: | |
| | TIGICACAAI AATIICIICA GGATCATAGG AAAAATGATA ACGATTIITG AAGTATIGAC | 60 |
| 45 | TAATTGCTTC GCGAGTTTCT AATAACCCTT TATTGTGAGA GTATGATGTC TTGTCATTGT | 120 |
| | TAATAGCATC AATATATGCC TTTTTCACAA CATCAGGCAT CGGGAAGTCT GGTTGGCCAA | 180 |
| | TAGTTAAATT AACACAATCA TCCAAATTAT TCATACGATT TGAAAATTGG CGATACTTGG | 240 |
| 50 | GTGGCTCCTA AAATAATTAG GAAATGAGGA NTTNAAGGAA GGTTTCCATT TNGTGGACAC | 300 |
| | (2) INFORMATION FOR SEQ ID NO: 2022: | |
| <i>55</i> | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs | |

| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
|-----------|--|------|
| 5 | | - |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022: | , . |
| | TCATCCAAAT TATTCATACG ATTTGAAAAT TGGCGAATAC TTGGTGCTCT TAAATATTTA | 60 |
| 10 - | GAATTAGAAT TTAAAGAAAG TTTCATTTGT GACACCTCAA ATATAAATCA AATATTGTCT | 120 |
| | AAAAATTTAG AAATTAATAA TATCATAACA TACTTTTAAA GCAAAAAAGG GTAAATTACT | 180 |
| | TAAGCTTTAT TTGAAAAACG AAAAATGTCT AAATACACTG TAGTAACTAC TTTTCAAAAT | 240 |
| 15 | GAATAAAGTG GTTACAGTTA ATGTACTTAG ACAGTATAAA ATTATGAATC TTTAAACTGT | 300 |
| | GATGGTCTTT GTAAATTAAT TATTGGATTT GTCCATTTAC AAACAAGGTT TGTAGATAAT | 360 |
| | ACATATACGA TGATTACAGA TATACTTATT AAATAAAGAT | 400 |
| 20 | (2) INFORMATION FOR SEQ ID NO: 2023: | 400 |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs | |
| 25 | (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| ٠. | | |
| .` 30 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023: | |
| | TTHAAATATA CCAATCACGT TCATCCACAG TGATCCTAGA CCAATCCAGA | 50 |
| | (2) INFORMATION FOR SEQ ID NO: 2024: | : |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | . • |
| 40 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024: | |
| 45 | TTTTTAATGG TTTAAAAATT CCCTAATAAA ATTTTGGAAA ACCTAAATTC CAAGGGGTTA | 60 |
| | AATTCC | . 66 |
| | (2) INFORMATION FOR SEQ ID NO: 2025: | |
| 50 55 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 64 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |

| GTAAGAGCAA TGCCGCAAAA TGCCTGTAAT GATATTGTGA ACGTAATTGA ATCAGTAGAG GACC (2) INFORMATION FOR SEQ ID NO: 2026: (i) SEQUENCE CHARACTERISTICS: | | (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 2025: | |
|---|----|--|----|
| (2) INFORMATION FOR SEQ ID NO: 2026: (3) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026: CTGTCGCTGC GTGACTTAAT TCTTTTGCCC CGTTGGCATA TGAGGAAATG TCA 20 (2) INFORMATION FOR SEQ ID NO: 2027: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027: CATTTCACTA TTATTGGTTT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA (2) INFORMATION FOR SEQ ID NO: 2028: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | | GTAAGAGCAA TGGCGCAAAA TGCCTGTAAT GATATTGTGA ACGTAATTGA ATCAGTAGAG | 60 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026: CTGTCGCTGC GTGACTTAAT TCTTTTGCCC CGTTGGCATA TGAGGAAATG TCA 20 (2) INFORMATION FOR SEQ ID NO: 2027: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027: CATTTCACTA TTATTGGTTT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA (2) INFORMATION FOR SEQ ID NO: 2028: (3) (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (2) INFORMATION FOR SEQ ID NO: 2029: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 5 | GACC | 64 |
| (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026: CTGTCGCTGC GTGACTTAAT TCTTTTGCCC CGTTGGCATA TGAGGAAATG TCA 53 20 (2) INFORMATION FOR SEQ ID NO: 2027: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027: CATTTCACTA TTATTGGTTT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA (2) INFORMATION FOR SEQ ID NO: 2028: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028: CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA 46 AACGGAATCG TCA (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | (2) INFORMATION FOR SEQ ID NO: 2026: | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026: CTGTCGCTGC GTGACTTAAT TCTTTTGCCC CGTTGGCATA TGAGGAAATG TCA 20 (2) INFORMATION FOR SEQ ID NO: 2027: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027: CATTTCACTA TTATTGGTTT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA (2) INFORMATION FOR SEQ ID NO: 2028: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028: CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 10 | (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| CTGTCGCTGC GTGACTTAAT TCTTTTGCCC CGTTGGCATA TGAGGAAATG TCA 20 (2) INFORMATION FOR SEQ ID NO: 2027: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027: CATTTCACTA TTATTGGTTT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA (2) INFORMATION FOR SEQ ID NO: 2028: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028: CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 15 | | |
| (2) INFORMATION FOR SEQ ID NO: 2027: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027: CATTICACTA TTATTGGTTT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA 53 (2) INFORMATION FOR SEQ ID NO: 2028: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028: CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA 60 AACGGAATCG TCA 73 (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026: | * |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acidd (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027: CATTTCACTA TTATTGGTTT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA 53 (2) INFORMATION FOR SEQ ID NO: 2028: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acidd (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028: CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA 60 AACGGAATCG TCA 73 (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acidd (C) STRANDEDNESS: double | | CTGTCGCTGC GTGACTTAAT TCTTTTGCCC CGTTGGCATA TGAGGAAATG TCA | 53 |
| (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027: CATTICACTA TTATIGGITT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA 53 (2) INFORMATION FOR SEQ ID NO: 2028: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028: CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA 60 AACGGAATCG TCA 73 (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 20 | (2) INFORMATION FOR SEQ ID NO: 2027: | |
| CATTTCACTA TTATTGGTTT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA (2) INFORMATION FOR SEQ ID NO: 2028: (3) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028: CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA (A) ACGGAATCG TCA (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 25 | (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | * |
| CATTTCACTA TTATTGGTTT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA (2) INFORMATION FOR SEQ ID NO: 2028: (3) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028: CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA (A) ACGGAATCG TCA (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | | |
| (2) INFORMATION FOR SEQ ID NO: 2028: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028: CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA AACGGAATCG TCA (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 30 | | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028: CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA AACGGAATCG TCA (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028: CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA AACGGAATCG TCA (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 73 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA 45 AACGGAATCG TCA (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 40 | | |
| CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA 45 AACGGAATCG TCA (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028: | |
| AACGGAATCG TCA (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | | 60 |
| (2) INFORMATION FOR SEQ ID NO: 2029: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | 45 | | |
| (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | | | |
| | 50 | (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029: |
|-----------|---|
| | AATAATAATT CTGGAATAGT GTTTAATACT TATTnTCCGT TTAAGATTTC AACTTAATAT 60 |
| 5 | GGTTTACAGC GCGTAGCTCG TCTAATTCAT CATCACGTGT AGAGTGCTCT GCCTTATCAG 120 |
| | ATCAGTT 127 |
| | (2) INFORMATION FOR SEQ ID NO: 2030: |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 61 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double |
| 15 | (D) TOPOLOGY: linear |
| | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030: |
| 20 | GCAAGTGAAT TGAAGTGACA TGTGGCTGGT GCTTCATGGT AATGATAAAC CAACACCATG 60 |
| | 61 |
| | (2) INFORMATION FOR SEQ ID NO: 2031: |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 78 base pairs (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear |
| 30 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031: |
| 35 | ATAAATATCT ATTTAGATAT AAGTATTGAT AAGTTGCTTG AATTTATAAA GTGAAGGAGT 60 |
| | AGGTGTCATT AGTATAGT 78 |
| | (2) INFORMATION FOR SEQ ID NO: 2032: |
| 40 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 229 base pairs(B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear |
| 45 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032: |
| 50 | GAATAGTGTT TATAAAATGT TGACACTGTA GTGGCATATT GTAAATTAAA TATTATTATG 60 |
| ອບ | TGATCATTTT GTTTAAATAT TAGTTATAAG AAGTGAAATA nTCATTTTAA AAGGAGACTT 120 |
| | AAAACTTGAA ACGATCAACG AATCAAGAAA AATTTCTTGA TACACTAATT AGACTTAATA 180 |

| | (2) Infoldigation for SEQ ID No. 2003: | |
|----|--|------|
| 6 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033: | ē . |
| | TTTTGTCATC TGTATAGGTA TGCGCGCCGG TGTCTTTATT CACTTTGAAC TGTGCGT | 57 |
| 15 | (2) INFORMATION FOR SEQ ID NO: 2034: | |
| 20 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 62 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | - ST |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034: AAGGCATTGG ATATAAGACT TGATGTTGCA TGGCAATCAC ACTGCCTAAT CCTTGCATAT | 60 |
| | AA . | 62 |
| 30 | (2) INFORMATION FOR SEQ ID NO: 2035: | |
| 35 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| - | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035: | |
| 40 | ATGGCAAATA CTATACATCG TCCAATTGAT TGAAAAATAT GGTTATTAAA GA | 52 |
| | (2) INFORMATION FOR SEQ ID NO: 2036: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 86 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036: | |
| | AAGGTGTTTT TATATGCTTA TTACAAATAC TTAACGCGAT GAGTTTCTCA ACCAAATTGA | 60 |

| | (2) INFORMATION FOR SEQ ID NO: 2037: | |
|--------------|--|-----|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| 10 | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037: | |
| | TACCCACCC CAAACCCAAG GTTTTAAAAA ACCCCTTCCA AAAGCCCGGA AAAACCAAAA | 60 |
| | | |
| 15 | GGAATTATTT T | 71 |
| | (2) INFORMATION FOR SEQ ID NO: 2038: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| 20 | (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid | |
| | (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (2) 10102001 111001 | |
| | | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038: | |
| • | CARROCCOCA ACERACA ACERT COERCOCA CARRA ECCERA CECCARETTA C | 50 |
| | GAATCCCGGA AGTACAATTT GGTACGTGAA GAAAATGGTA GTGGAATTAC | 50 |
| | (2) INFORMATION FOR SEQ ID NO: 2039: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: | ٠, |
| | (A) LENGTH: 400 base pairs | |
| | (B) TYPE: nucleic acid (C) STRANDEDNESS: double | |
| 35 | (D) TOPOLOGY: linear | |
| 33 | | |
| | | |
| ٠ | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039: | |
| 40 | CAGTATCTCT TGGTATTTTA ATTGGTGCTT TATTAAACGT AATTTTACCT TTATATATCG | 60 |
| | ATGGAGCGAA GAGTATTTTC GTATACGTTT ATAGTGCGTC TATTTTACCA GGTATGATTC | 120 |
| | CTTGGTTTAT GATTTTATTC AGTCATTTAC GTTTTAGAAA ATTACACCCT GAAGAATTGG | 180 |
| 45 | AAGGTCACCC ATTCAAAATG CCTGGTGGCG CAGTAACTAA CTATTTAACA ATCTTATTCT | 240 |
| | TAATATTAGT ATTGGTTGGT ATGGTATITA ATGTTGAAAC TAGAATATCA GTGCTTATTG | 300 |
| <i>50</i> . | GTGTCATCTT CTTAACGATT GTAACGATTT ATTATTTTAT TAGATATAAT AAAAnTAATG | 360 |
| - - . | TAAAGCANAA TAGTATGTTA TAANGAGCGN TACTTATGAC | 400 |
| | (2) INFORMATION FOR SEQ ID NO: 2040: | |

| 5 | (A) LENGTH: 79 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear | |
|----|---|-----|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040: | |
| 10 | AAGCTGATTT TTCTAAATGT TGAAAATCAT AAACTGCTTA ATAATAAATA ACGAGATCTA | 60 |
| | AGTAATAGTG CTCCATTAA | 79 |
| | (2) INFORMATION FOR SEQ ID NO: 2041: | |
| 15 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 54 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double | |
| 20 | (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041: | |
| 25 | AATTGAACGG ATCGTTCCCA ACCGTTATCA ACCCAGACCG GTGTTTGAAC CCAA | 54 |
| | (2) INFORMATION FOR SEQ ID NO: 2042: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042: | |
| | AATGGGATTG GTTCAAACTG AAATGGGCTG TTAGTCCCTG TAAAACCAAG | 50 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 2043: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs | • |
| 45 | (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043: | |
| 50 | ATTGGNATAA TCAAAGCATT GAATCATACA TAGTCACATT GATTGTTTCC TCAGAGTTTC | 60 |
| | AACACTCTAT AACTCATTTT AGTAATTTGC TGATTGCGCA CTTCATGTG | 109 |
| 55 | (2) INFORMATION FOR SEQ ID NO: 2044: | |
| 55 | | |

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|----|---|-----|
| 5 | (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044: | |
| 10 | TTTTATGGAG GTGATGAAGT GGGTGAAGCT GAAAGGAAGC AAAAGCTTGG | 5 |
| | (2) INFORMATION FOR SEQ ID NO: 2045: | |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 20 | | |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045: | |
| | TTGGCCCCCT TCCAACCCTT GGAAATTTTA AAAGGCCAnT TTTGGGGTAA AACCCTTGGT | 60 |
| 25 | TCCAAGGACC CCCAAAAGTT TTTTAACCTT CCAATTATTA T | 101 |
| | (2) INFORMATION FOR SEQ ID NO: 2046: | |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2046: | |
| | ACCCTTTCCA AAAAGCCCAT TTTGAATTCC CCAAAGGGAG CCAAATTTAA GATGGCCGCn | 60 |
| | AAAAAGGACC GGGGGTCCA TGTTTTAATT TAAGCCGGAC | 100 |
| 40 | (2) INFORMATION FOR SEQ ID NO: 2047: | |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear | |
| 50 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047: | |
| | GTTAGTTATG AGCAACGTAT TAATGAAATT ATTGAGCAGT AATTNACCAG | 50 |
| | (2) INFORMATION FOR SEQ ID NO: 2048: | |